2013

HIGH THROUGHPUT DATA FRAMEWORK BASED CHARACTERIZATION AND EVALUATIONS OF THERMOBIFIDA FUSCA FOR INDUSTRIAL APPLICATIONS

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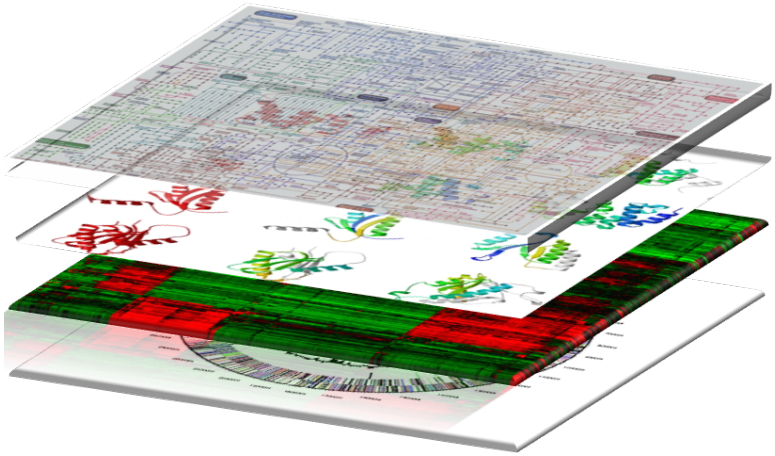

A DISSERTATION SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE DOCTOR OF PHILOSOPHY AT VIRGINIA COMMONWEALTH UNIVERSITY

BY

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DECEMBER 2013

DEDICATED TO MY PARENTS

Dr. Sanjeev Kumar & Dr. Manorama

ACKNOWLEDGEMENTS

This dissertation marks a major milestone in my career. I feel very fortunate to have the supervision, mentorship and support of a few very special people around me. I am grateful to them for their guidance and words of encouragement when I needed it the most.

The first and foremost pillar of my success is my advisor Dr. Stephen S. Fong. I express my regards and gratitude to him for being an ideal mentor for me. He recognized my capabilities and stirred my thoughts in the direction to which I could excel and perform the best. I admire his patience in listening to all my random views and stringing them together to make it sound a cohesive thought. I can't thank him enough for providing a platform and laboratory surrounding that works the best for students like me to achieve our goals.

I would like to extend a note of thanks Dr. James Paul Brooks (Virginia Commonwealth University), Dr. Bruce Cooper (Purdue University), Dr. Oleg Krochin (University of Manitoba) and Dr. Sheryl Baldwin (Virginia Commonwealth University) for giving their invaluable suggestions and time to train me in the different facet of my work with their expertise. Not only that but they were always available as and when I needed their help in understanding and overcoming the hurdles that I came across during various sections of my work.

In 2007 when I was starting to find my direction to my research, three people introduced me and initiated the seed of research in Systems Biology in my mind. I could not have reached to where I am today without meeting them. This trio includes Dr. Gregory Buck, Dr. Stephen Fong and Dr. Seth B. Roberts. I am indebt to them for all the time and attention they gave me to train my mind and plan my future goal.

I would like to express my gratitude toward my dissertation committee Dr. Danial Bonchev, Dr. James P. Brooks, Dr. Sheryl Baldwin and Dr. Gregory A. Buck for supporting my

work and valuable insight for improvement. I really appreciate their time for reading my thesis and hearing me during my proposal and final defense.

My laboratory culture played an important role in making my experience at work the best. I would regard my colleagues and administrative incharges for making this story a success. This team includes: Christopher Gowen, Yu Deng, George McArthur, Adam Fisher, Allison Yaguchi, Cythina Lovelace and Jack Schreiber. I wish to thank them all for sharing my sorrow of failures, multiplying the joy of success though out the span of 4.5 years at SBEL.

I extend my gratefulness to VCU Life Sciences and Department of Integrative Life Sciences for providing me an opportunity to purse my degree and financial support for three years.

I would like to thank my friend Preetpal Sidhu for his timely critical analysis, feedback and invaluable hours to review my write-ups and provide comments. His constant word of encouragement and intellectual discussions played a vital role in thinking through some of the rationales of my project.

I was among a very few people who were fortunate to have my first best friend for life my sister, Shubhra, with me while I was going through the though phases of my life. She was here to sing and dance along for the good and bad patches of time by non-stop talking, feeding good food and scolding me when I am slacking. Her words of encouragement that goes like *"You are a genius that's why mom dad name your Gennie"* is something that always rings in my ear and give me smile and energy to move on.

In the course of my study I feel fortunate to have met the special person in my life whose confidence on me fired my desire to perform the best. My husband, Dr. Pramod Mishra, whom I can't thank enough for taking all the toll of my stress, unavailability and yet keeping extremely

calm and patient. Being from the same background, he was always aware of my progress and knew the best way to walk me through the phases of graduate school life and talk me out of the terrifying tough times. I feel blessed to have such an understanding companion who stands by be and inspires me to perform the best in life.

Finally, I want to thank my family for emotional and intellectual support and foundation without which nothing could have been possible. My parents had always trusted me for all my plans and encouraged me to achieve my goals. I feel proud not only for achieving this success in my education but more proud of rising up to the expectation my family. I don't think I have enough words to thank my parents for all their life long love, care and support in all the good and bad swings of my life. I hope I can be as good as you all are in the course of time when required.

TABLE OF CONTENT

LIST OF TABLE

LIST OF FIGURES

LISTS OF ABBREVIATIONS

CBP – Consolidated bioprocessing

CoA – Coenzyme A

COG – Cluster of Orthologous Proteins

DNA – Deoxyribonucleic acid

EC – Enzyme Commission

FBA – Flux Balance analysis

HOV – Higher Order Variables

IMG – Integrated Microbial Genomics

KEGG – Kyoto Encyclopedia of Genes and Genomes

MILP – Mixed-integer linear programming

mmol / g-DW / hr – millimoles per gram of dry cell weight per hour

MOMA – Minimization of metabolic adjustment

NCBI – National Center for Biotechnology Information

RNA – Ribonucleic acid

TBB – Terpenoids Backbone Biosynthesis

TFU – *Thermobifida fusca*

ABSTRACT

HIGH THROUGHPUT DATA FRAMEWORK BASED CHARACTERIZATION AND EVALUATIONS OF *THERMOBIFIDA FUSCA* FOR INDUSTRIAL APPLICATIONS

By Niti Vanee

A dissertation submitted in partial fulfillment of the requirements for the degree doctor of philosophy at Virginia Commonwealth University.

Virginia Commonwealth University, 2013.

Major Director: Stephen S. Fong, Associate Professor, Chemical & Life Sciences Engineering

Cellulolytic organisms are being heavily studied for the production of biofuels, given that lignocellulosic biomass would be a cheap, abundant, and renewable starting material for chemical production. A challenge with cellulolytic microorganisms is that they are typically poorly characterized and often difficult to genetically manipulate. Our group focuses characterization and engineering of a thermophilic aerobic, cellulolytic actinobacterium, *Thermobifida fusca*. The wider range of optimal temperature and pH for the growth condition, besides the secretion of several group of cellulases, have made this microbe a potentially efficient host system for industrially application. After the development of first ever successful genetic manipulation protocol by for *T. fusca* in 2011 in our group the quest continues to better understand and further explore this microbe with such remarkable capabilities.

Available genome annotation of the bacteria gives a preliminary clue towards the exploration of its biological system. Genome-scale metabolic reconstruction provides one such framework to populate all the available piece of information to mimic the biological systems to the closest functional state. Further, this skeletal base network can be made

more realistic by applying the constraint that controls the flux through various reactions in the pathway network thereby providing the optimal solution space for operation. For the purpose of curation of this *in silico* model, we aim to integrate the experimental datasets (proteomic and metabolomics) and optimize the agreement between the *in silico* and *in vivo* conditions at a steady state condition. Once the model considerably imitates the original biological network, it will be used for the fundamental understanding of the microbial system for the application towards production biofuel and high yields of compound of pharmaceutical interest.

The ultimate objective of this project is to design the candidate strain for the cellulolytic production of Natural products. Natural products play an important role in manufacturing of several active pharmaceutical ingredients (APIs). APIs or precursors of APIs can be produced in living organisms with the major challenge of designing and optimizing metabolic pathways to obtain the compounds of interest. In this capacity, living organisms can act as renewable catalysts with high product specificity to produce APIs with potential cost savings over purely synthetic chemistry synthesis routes. This is an effort to understand and design industrially usable microorganism *T. fusca* to act as a host system for the purpose of production of these compounds. The present project focuses on, *in silico* characterization and experimental validation of *T. fusca,* with particular focus on the terpenoids backbone biosynthesis (TBB) pathways using a genome-scale metabolic model, transcriptomics, proteomics and metabolite analysis. The DXP pathway leads to the production of terpenoids precursors that have applications in nutraceutics and pharmaceutics.

This study generates the metabolic model, *i*TFU975 for *T. fusca* based on the proteomics dataset as the starting point. Further the model and the experimental dataset together helps to characterize the secondary metabolites pathways and compounds in the network associated with the production of terpenoids.

In conclusion, this is an effort to characterize the natural products biosynthesis in *T. fusca* by establishing a bridge between the analytical methodologies and computational efficiencies on "-omics" knowledge to prove the diverse applicability of Systems Biology.

CHAPTER 1: INTRODUCTION

1.1. BACKGROUND

Lignocellulosic material from Plant biomass is the most abundant and inexpensive raw material that can be used in the fermentation industry for the production of biofuels, pharmaceutical ingredients and other biotech products. However, this potential carbon source experiences a hurdle of pretreatment (milling and enzymatic degradation). The plant biomass contains strongest biopolymers that need to be converted to the fermentable sugars before they can be used in bioreactors for the purpose of production of known extensive range of compounds. This process is known as saccharification and is carried out by a class of enzyme called cellulases. Cellulases are readily produced and secreted by a class of bacteria, actinomycetes, known for its high cellulolytic activity. (Lamot,E. and Voets,J.P. 1976)

Actinomycetes are widely studied for their highly expressed cellulolytic system that can degrade plant biomass and convert it to fermentable sugars. This pretreated plant biomass is further fed to the fermentation processes using the industrially applicable microbes for the production of biofuel, pharmaceutical ingredients, renewable materials and other biotech products. It will be of great importance to biotech and other industries to consolidate this multistage bioprocess into single step using a platform organism having the capabilities of both the lignocellulose degradation and fermentation processes. The combined process, also defines as a consolidated bioprocess (CBP), is illustrated in Figure 1. (Carere,C.R.,

Sparling,R., et al. 2008, Carroll,A. and Somerville,C. 2009, Demain,A.L., Newcomb,M., et al. 2005, Lynd,L.R., Weimer,P.J., et al. 2002, Lynd,L.R., van Zyl,W.H., et al. 2005)

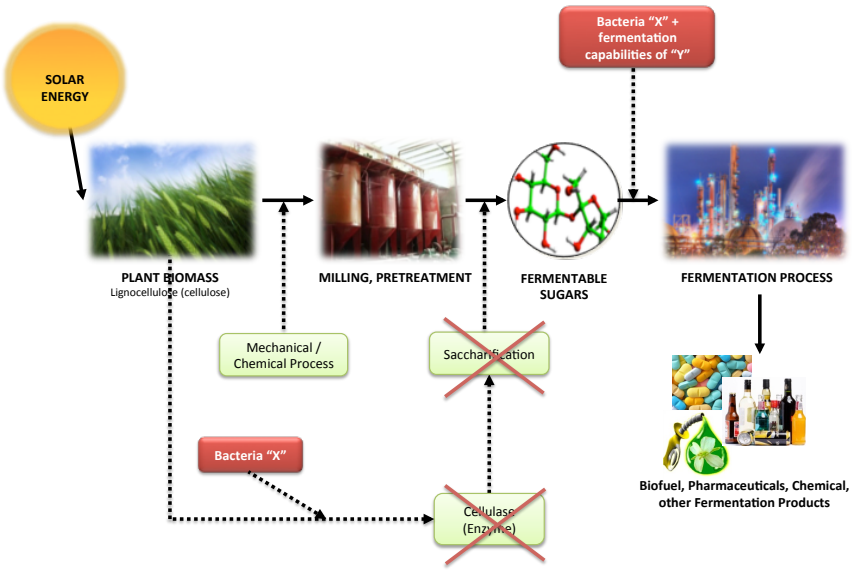


Figure 1: *The prospective use of cellulolytic microbes such as T. fusca may help in reducing the multiple steps towards the fermentation bioprocess there by reducing the need of pretreatment of plant biomass to feed into an industrial process as a source of carbon. Bacteria-X denotes the cellulolytic capabilities of microbes such as T. fusca and Bacteria-Y denotes the fermentations potentials of industrial microbes*

The consolidation of the cellulolytic capabilities of actinomycetes and the long cited history in production of medically relevant molecules such as antibiotics (roughly two-thirds of clinically used antibiotics are produced by the actinomycete, *Streptomyces*), they prove to be a great platform microorganism to be studied. This is supported by the fact that approximately 45 percent of all bioactive compounds obtained from microorganisms come from actinomycetes family.(Mahajan,G.B. and Balachandran,L. 2012)

1.2. *Thermobifida fusca*

In the actinomycetes classification, *Thermobifida fusca*, aerobic thermophilic gram-positive filamentous bacteria (shown in Figure 2), is known for its high temperature and pH stability as well as highly expressed cellulolytic system. The cellulolytic system comprises of three endocellulases (Cel9B, Cel6A and Cel5A), two exocellulases (Cel6B and Cel48A) and a processive cellulase (Cel9A) (Wilson,D.B. 2004, Wilson,D.B. and Kostylev,M. 2012). Numerous studies in past have reported the lingo-carbohydrates degradation ability, the enzymatic system and the cellulases expression of *T. fusca*. Efforts have been made to clone several individual cellulase genes into *Streptomyces lividians, Streptomyces albus, Bacillus subtilis* (Ghangas,G.S. and Wilson,D.B. 1988) and *Escherichia coli* (Irwin,D.C., Zhang,S., et al. 2000, Spiridonov,N.A. and Wilson,D.B. 1998). The cloned enzymes were isolated in good concentration but failed to show a comparable level of cellulolytic activity to that of *T. fusca*. This may be due to the complex cellulose degradation system. It is not defined by a few genes but is an intertwined network of various enzymes (Kukolya,J., Nagy,I., et al. 2002, Wilson,D.B. 2004). Hence, it is a recommended solution to utilize the innate capacity of *T. fusca* by optimizing the production capability of industrially applicable compounds. Since actinomycetes are important player in the production of compounds such as siderophores (Lee,J., Postmaster,A., et al. 2012), polyketides (Niraula,N.P., Kim,S.H., et al. 2010, Takahashi,S., Toyoda,A., et al. 2011) and terpenes (Cane,D.E. and Ikeda,H.

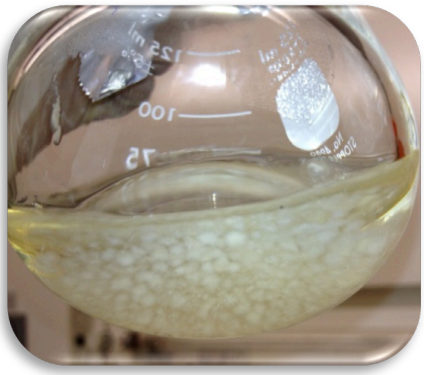


Figure 2: *Cell growth for T. fusca in Cellobiose at 55°C*

2012, Citron,C.A., Gleitzmann,J., et al. 2012), it suggests the naturally suitability of *T. fusca* for production of medically-relevant compounds such as antifungals, antibiotics (antibacterials) and chemotherapeutics. The successful characterization and targeted analysis may lead to an alternative route through consolidation of bioprocesses (Figure 1) i.e. to exploit the natural capabilities of *T. fusca* and to obtain/optimize the secondary metabolites of interest.

The prospective competence of producing a chemicals of industrial importance using the inexpensive lignocellulosic biomass has brought this microbe in focus. The sequencing of its genome by Department of Energy (DOE) in 2005 sets up a milestone towards understanding this industrially applicable microbe (Lykidis,A., Mavromatis,K., et al. 2007). Besides proving an excellent host microbe for biofuel production (Deng,Y. and Fong,S.S. 2011b), it also showed success towards utilization of untreated (without any preprocessing) lignocellulose source. This has shown a ray of hope toward making use of the cellulolytic capabilities of this microbe to reduce the complex multi-step bioprocess to a CBP (Carere,C.R., Sparling,R., et al. 2008, Carroll,A. and Somerville,C. 2009). The potential approach is illustrated in Figure 2.

Prospects of CBP has encouraged further utilization of the microbial subsystem by cloning genes of interest into the standard cellular systems such as *E. coli* and *S. cerevisiae* (Wilson,D.B. 2004). The cloning certainly showed some promising results but direct use *T. fusca* for the industrial purpose motivated our research group in past. In 2011, Deng & Fong established the first ever genetic modification protocol

for production and optimization of the propanol in *T. fusca* (Deng,Y. and Fong,S.S. 2011b). The initial developments in the characterization of *T. fusca* are listed in Table 1. Following along the same lines, we continue to further understand the other capabilities of robust cellulolytic system of actinomycete for use in manufacturing industries. Thus, our group aims to present a systems level understanding of the metabolic network of *T. fusca*.

Table 1: *Significant milestones for T. fusca research and characterization*

YEAR	DEVELOPMENT	GROUP	CITATION
1998	Genus Constructed	Zhang et al.	Int. J Syst Bact. 1998 Apr
2002	Physical Characterization	Kukolya et al.	Int. J Sys Evol Micr, 2002 Jul
2005	Genome Sequenced	DOE	JGI Finished Genome, 2005
2004-2006	Plant biomass degradation study and analysis of enzymatic system	Wilson et al.	Chem Rec. 2004 Biochem. 2006 Nov
2007	Sequence Annotation	Lykidis et al.	J. Bacteriol. 2007 Mar
2010	First Genetic Modification	Deng & Fong	Appl. Environ. Microbiol 2010 Apr
2011	Producing biofuel from untreated biomass	Deng & Fong	Metab Eng. 2011 Sept

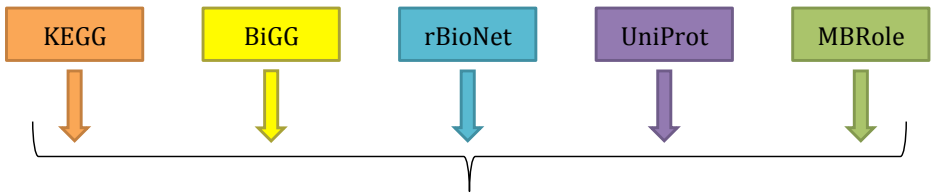
1.3. Metabolic Models and Rational Strain Design

Traditionally, engineering of microbes often involved a long iterative trial-and-error process. Advancement in high-throughput technologies has enabled us to better understand microbial systems as a whole and to filter specific targets in an expedited fashion. With the availability of genomic sequence of the organism, it has become possible to use the annotation information to build the draft metabolic network (Edwards,J.S., Covert,M., et al. 2002). These models can be used for simulating the living state of bacteria, if operated under the defined constraints and boundary conditions. There are various algorithms such as FBA - flux balance

analysis (Orth,J.D., Thiele,I., et al. 2010, Varma,A. and Palsson,B.O. 1994), MOMA - minimization of metabolic adjustments(Segre,D., Vitkup,D., et al. 2002), ROOM - regulatory on-off minimization (Shlomi,T., Berkman,O., et al. 2005) and MCA - metabolic control analysis currently used for the purpose of simulation of these models (Rapoport,T.A., Heinrich,R., et al. 1974, Kacser,H. and Burns,J.A. 1973). In the current study, we will be using FBA, which is based on linear programming algorithm, to simulate and optimize *T. fusca* model for biomass production.

1.3.1 *T. fusca* Model and FBA

Whole genome sequence and annotation of *T. fusca* was used for genome-scale metabolic reconstruction to understand the underlying metabolic pathways (Deng,Y. and Fong,S.S. 2010a, Deng,Y. and Fong,S.S. 2011b, Durot,M., Bourguignon,P., et al. 2009, Lykidis,A., Mavromatis,K., et al. 2007). The reaction database used for drafting the model includes but is not limited to KEGG(Kanehisa,M. and Goto,S. 2000, Kanehisa,M., Goto,S., et al. 2006), BiGG(Palsson's Models Compilation), rBioNet, UniProt (UniProt Consortium. 2013) and MBRole(Chagoyen,M. and Pazos,F. 2011) which will be described later in the chapters. The in-house MetModel reaction database illustration is shown in Figure 3.



Abbreviation	Description	Reversible	Pathway	EcNumber	Formula
R_13BGH	Endo-1,3-beta-glucanglucohydrase	FALSE	Starch and Sucrose Metabolism	3.2.1.58	[c] : 13bdglcn + h2o --> glc-D
R_13BGHe	Exo-1,3-beta-glucanglucohydrase	FALSE	Starch and Sucrose Metabolism	3.2.1.58	[e] : 13bdglcn + h2o --> glc-D
R_13DAMPPOX	1,3-Diaminopropane:oxygenoxido reductase(deaminating)	FALSE	beta-Alanine Metabolism	1.4.3.6	[c] : 13dampp + h2o + o2 --> bamppald + h2o2 + nh4
R_13GS	1,3-beta-glucansynthase	FALSE	Alternate Carbon Metabolism	2.4.1.34	[c] : udpg --> 13bdglcn + h + udp
R_2DGLCNRy	2-dehydro-D-gluconatereductase(NADPH)	FALSE	Alternate Carbon Metabolism	1.1.1.215	[c] : 2dhglcn + h + nadph --> glcn + nadp
R_2DR1PP	2-deoxy-D-ribose1-phosphatephosphorylase	FALSE	Pyrimidine Catabolism	3.1.3.10	[c] : 2dr1p + h2o --> drib + pi
R_2HBO	2-Hydroxybutyrate:NAD+oxidoreductase	TRUE	Propanoate Metabolism	1.1.1.27	[c] : 2hb + nad <==> 2obut + h + nadh

Figure 3: *Illustration of available database used for compiling the MetModel reaction database*

Further, this draft model will be accessed for any missing links or gaps (in a given metabolic network). This process is called gap filling. This model when patched up with the suitable missing reactions this model can be operated under constraints such as substrate uptake rate or production optimization rate. Once the model provides a framework to understand the cellular process, it can be used for finding target for focused metabolic engineering to yield products of biotechnological value (Joyce,A.R. and Palsson,B.Ø. 2007). Most widely used algorithms for design and simulation of genome scale constraint based metabolic models are based on flux distribution and flow through chemically balanced reactions. Flux balance analysis (FBA) uses Linear programming to optimize the objective functions as follows:

$$\text{Maximize: } Z$$
$$\text{Subject to: } S \bullet v = 0,$$
$$a_i \leq v_i \leq b_i \text{ for all reactions } i,$$

where, Z is the flux through objective function (biomass production and product optimization), S: stoichiometry of the reactions represented as matrix form shown

in Figure 4, v is reaction flux vector, a_i and b_i are the constraints placed on the flux v_i of the reaction i. (Palsson,B.Ø. 2007)

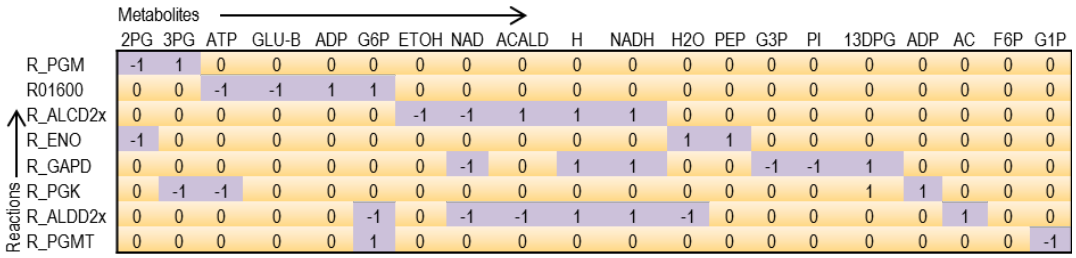


Figure 4: *The chemical reactions converted to the matrix format, confined through mass balance and flux constraints to solve using linear programming*

Although a reconstructed network has been synthesized using various databases and biochemical information for literature, it is most likely never a complete. The network model provides formalism for integrating other high-throughput data and put "content in context" (Palsson,B.Ø. 2007). This validation can be done using multi-scale high throughput experimental data such as transcriptomics, proteomics and metabolomics. This step reconciles *in silico* predictions with experimental results and thereby helps enhancing the characterization of the cellular activity. As a result, of this more closely mimicked model would support the optimal strain design and efficient implementation of experimental manipulations.

1.4. High-throughput Experimental Data

Advancements in the analytical techniques to aids the characterization and quantification of biological molecules that play role in structural, functional and dynamic traits of organism. This involves processing the cells, running them

through the respective instrument and analysis of this high throughout data to interpret the biological inference. These techniques can be broadly classified into sequencing, microarray and spectrophotometric methodology. The four basic levels of these datasets are genomics, transcriptomics, proteomics and metabolomics defining the information for the DNA, RNA, proteins and other macromolecules respectively.

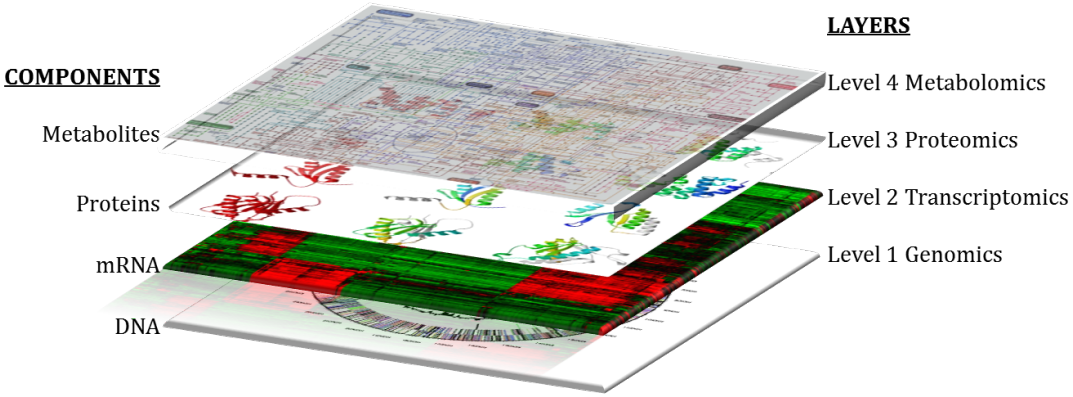


Figure 5: *Omics layers of high-throughput data starting from genome annotation to metabolites characterization*

With the availability of genomics information for *T. fusca* YX strain from Lydiski et al(Lykidis,A., Mavromatis,K., et al. 2007), the next aim was to use the spectrophotometric methodologies to characterize the macromolecules of the strains viz the proteomics and metabolomics or the small molecules when grown on two different media formulations – Cellobiose and Avicel.

1.4.1. Proteomics Dataset

The whole genome sequence information provides a unique signature to classify various strains; proteins are the key players that support functional machinery i.e. biological, cellular and molecular processes. Thus, detailed analysis of

proteins is warranted in order to utilize the functionality for different applications of a microbial strain. As shown in Figure 5, proteins are at the 3rd level in the-omics hierarchy succeeded by genomics and transcriptomics and preceded by metabolomics. Well-established technologies like High Performance Liquid Chromatography (HPLC) combined with Mass spectroscopy and Tandem Mass Spectroscopy has enabled the proteome level characterization of organisms feasible. List of proteins expressed in a strain indicates possible existing functional capacities of the cell. When proteomic data is combined with genome scale models, it further provides insight into the catalytic components of the metabolic pathways.

In the past, several attempts have been made to characterize secretome (Adav,S.S., Cheow,E.S., et al. 2012, Chen,S. and Wilson,D.B. 2007, Irwin,D.C., Zhang,S., et al. 2000)and cytosolic proteins (Adav,S.S., Ng,C.S., et al. 2010, Adav,S.S., Ng,C.S., et al. 2011, Adav,S.S., Cheow,E.S., et al. 2012) of *T. fusca* with the focus on studying the cellulosome and extracellular proteins. The proteomic dataset generated in the current study proves the most exhaustive coverage of experimental evidence. This will be integrated with the metabolic model to validate its outcome and find the agreements between the *in silico* and analytical chemistry results.

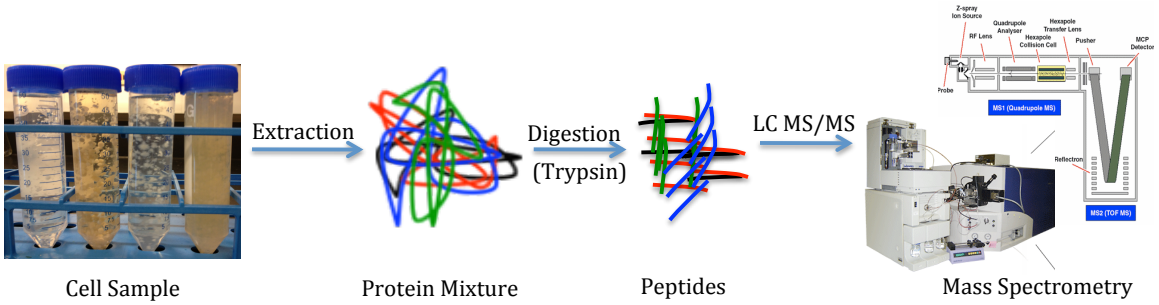


Figure 6: *Flow of process for protein purification, digestion and analysis using spectrophotometry*

1.4.2. Metabolomics Dataset

The concept of systems biology came into existence due to development of omics technologies such as genomics, transcriptomics, proteomics and metabolomics. Quantitative/semi-quantitative data is being derived from different levels of hierarchy from sequence to functional capacities down to substrate and products. All of the levels in the hierarchy are important in completing the entire puzzle unveiling the complete picture however; the best strategy is to measure the outcome of the systems (metabolites) rather than predicting the potential outcome by studying the machinery. This would offer a more practical approach toward the measurement of the global system activity via accessing the metabolite profiles resulting from the combination of factors - genetics and environmental conditions of the microorganism.

If a well-structured study can be performed to attain an exhaustive metabolite profile of the microbe, it is possible to perform a top-down approach to forward engineer of a synthetic microbe with *de novo* synthesized genetic information to reach designed targeted production. This may be developed as the designing principle for new synthetic microbes with most efficient manufacturing genetic and proteomic system.

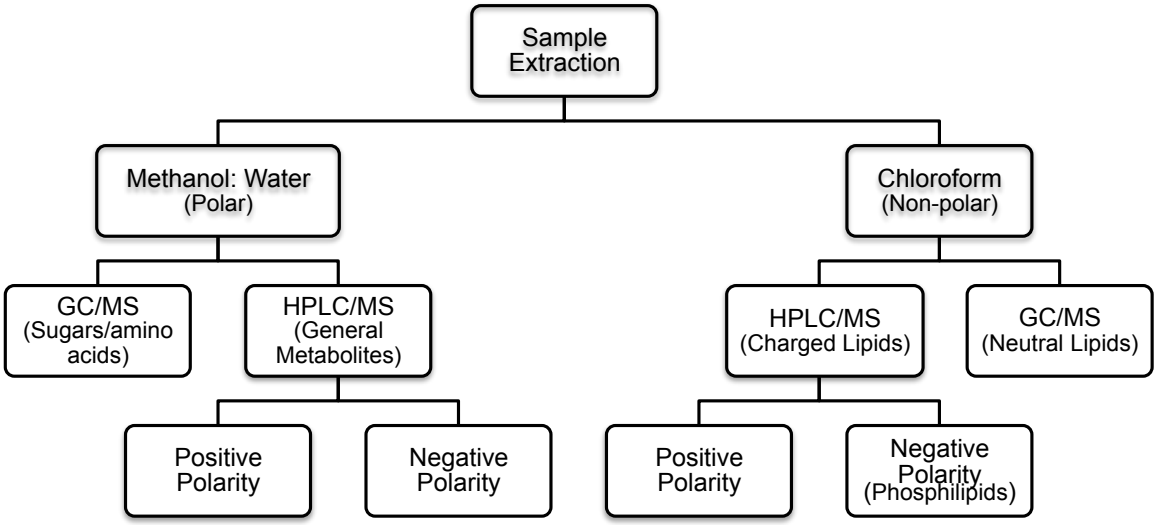


Figure 7*: Combination of metabolite profiling techniques used to exhaustively identify the maximum metabolites present in the cell at a given time. For both polar and non-polar metabolites, positive polarity mode is known to cover more exhaustive range of compounds than negative polarity and hence preferred for first set of compound analysis*(Wang,Y. and Griffiths,W.J. 2008)

Isolation of metabolites is a long process, which involves multiple combinations of techniques to cover the exhaustive range of metabolites present in any cellular system (Wang,Y. and Griffiths,W.J. 2008). Figure 7 shows the compound and technique classification that may be used for targeted or untargeted metabolite profiling. In the current scope, only untargeted metabolite profiling using HPLC/MS TOF in positive polarity will be conducted.

1.5. Natural Product an Application towards Pharmaceutical Industry

Rational strain deigns and developments are proving to be of great advantage in pharmaceutical manufacturing (Citron,C.A., Gleitzmann,J., et al. 2012, Ferrer-Miralles,N., Domingo-Espin,J., et al. 2009, Klein-Marcuschamer,D., Yadav,V.G., et al. 2010). Out of the newly introduced 877 small molecule new chemical entities (NCEs) between 1981 and 2002, approximately 49% were comprised of natural

products or their derivatives (Koehn,F.E. and Carter,G.T. 2005). Structural complexity of these compounds makes direct chemical synthesis or modification of natural products (NP) less feasible.

A conventional route to obtain NPs is extraction from native natural resources but associated with drawbacks such as low-yield, inefficient extraction and significant commercial and environmental expenditure. For example, Taxol (paclitaxel) is one of the well known pharmaceutically NP that is used as cancer treatment drug. To extract the amount that is sufficient to treat one cancer patient, about six 100-year old Pacific yew trees are needed (Horwitz,S.B. 1994). An alternative approach for obtaining natural products is biosynthesis through recombinant microbial engineering and development of fermentation protocols to obtain the desired product at scaled up level. This method of biosynthetic production has proved useful in NP production (Chang,M.C. and Keasling,J.D. 2006, Keasling,J.D. 2010, Menzella,H.G., Reid,R., et al. 2005, Peralta-Yahya,P.P., Zhang,F., et al. 2012, Pfeifer,B.A., Admiraal,S.J., et al. 2001). The class of natural products discussed here are terpenoids that are produced through the Mevalonate pathway shown in Figure 6 (left side pathway). Another known pathway to produce terpenoids is the DXP pathway or the non-mevalonate pathway, shown in Figure 6 (right side pathway). The DXP pathway has the capability to produce higher yields as compared to mevalonate pathway (Martin,V.J., Pitera,D.J., et al. 2003). Therefore, this project focuses on characterizing the DXP pathway in the cellulolytic microbe *T. fusca*. Ultimately, we strive to achieve high process and product optimization, as this actinomycete is known to use unprocessed cheap carbon source and the DXP

pathway to produce high yields of terpenoids precursor compounds (Farmer,W.R. and Liao,J.C. 2001, Kajiwara,S., Fraser,P.D., et al. 1997, Kim,S.W. and Keasling,J.D. 2001).

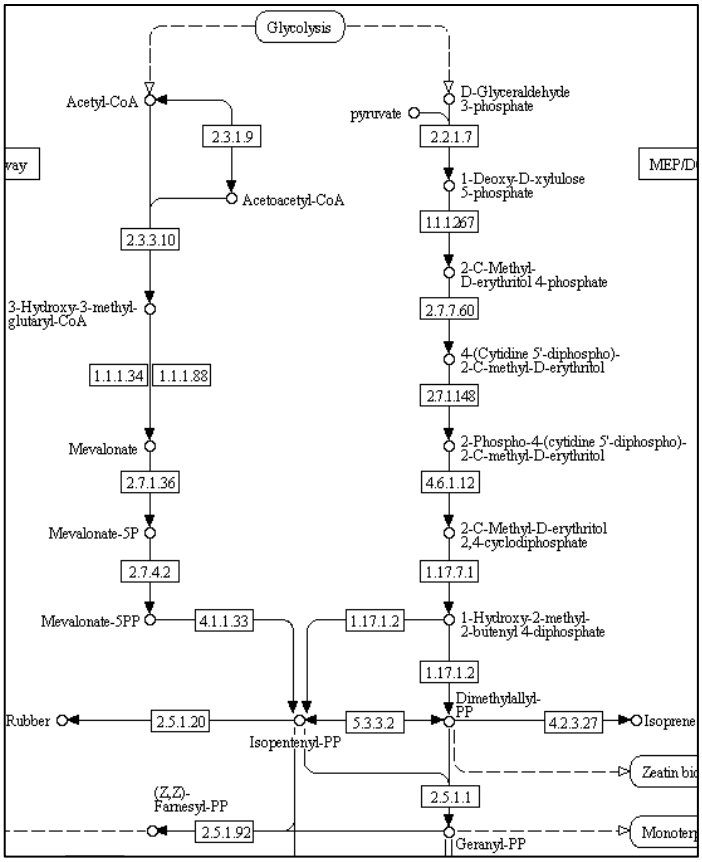


Figure 8: *Pathways for terpenoids backbones synthesis: mevalonate and non-mevalonate or DXP Pathway*

1.6. Dissertation Plan

1.6.1. Develop a Computational Toolbox for *in silico* Design and Analysis of *T. fusca*

This section provides a genome scale metabolic model with *in silico* optimization for biomass production simulated with the experimental substrate uptake rate for Cellobiose at 0.25mmoles/gDW/hr. The three different starting points were used to

draft the *T. fusca* model. A comparative analysis of feasibility and applicability was done using in house python scripts that implements linear programming algorithm. The steps involved in this were: design the model, gap fill and simulate for the defined boundary conditions. This defines the efficient entry point of the experimental dataset for a more accurate model.

1.6.2. Characterize Transit/Ultimate Entities of Cytosolic Components *in vivo* using Metabolite Profiling of *T. fusca*

The general metabolites detection experiment was conducted for T fusca YX strain to enlist polar and non-polar metabolites. This strain was grown on two different media formulations - Cellobiose and Avicel to characterize the cytosolic metabolic entities. The LC/MS Time of Flight analytical methodology was used for mass detection and Omics Discovery Pipeline was used for data handling and preprocessing. In conclusion, this section presents the detected compounds summary along with the current limitations of metabolomics dataset towards a systems level analysis.

1.6.3. Characterize Functional Machinery *in vivo* using Proteomic Analysis of *T. fusca*

In this section, we generated the most exhaustive proteome map of *T. fusca* using LC-MS/MS Quad TOF-based proteomics profiling. This provided approximately 70% coverage (compared to the *T. fusca* annotation) when studied with 2-Dimensional separation and detection for growth on Cellobiose media. This extensive

experimentally verified data was directly implemented for drafting the metabolic model as a starting point. It also accounts for experimental evidences to 355 proteins that were marked as "unreviewed" for *T. fusca* in the protein database - Uniprot unique proteins in this study. These finds were cross examined with the past proteomics map of *T. fusca* published in 2011 by Adav et al. (Adav,S.S., Ng,C.S., et al. 2011). Further, we assessed and characterized the stable cellular network that is resistant to the environmental variation by characterizing the proteins expressed in two different media conditions viz. Avicel and Cellobiose.

1.6.4. *T. fusca* as Industrial Microbe – *Case Study on Secondary Metabolites*

This section brings together the techniques and implementations by defining the applicability of *T. fusca* in the industrially significant compounds. The target family of compounds in this context was secondary metabolites. Actinomycetes are known possess capabilities to produce this class of compounds. We hereby characterize the nodes to which these pathways are complete. These finding were used as the basis for suggesting the strain design for an efficient reverse engineering. The focused backbone pathways were the mevalonate and non-mevalonate pathway for the production of terpenoids precursors.

As an implication, we aim to suggest a novel industrial microbe that is advantageous due to its economical and efficient cellulolytic properties. The computational and experimental evidences presented will substantiate this finding

thereby validating a multi-layered analysis and validation of metabolic models through integration of experimental datasets.

CHAPTER 2 – METABOLIC MODELING OF *T. FUSCA*

2.1. INTRODUCTION

Cellulolytic organisms are a focus of study in the production of biofuels, as lignocellulosic biomass provides a cheap, abundant, and renewable starting material for chemical production. However, cellulolytic microorganisms are poorly characterized and often difficult to genetically manipulate. Here we propose the approach for characterization framework using systems biology approach. This framework will establish a metabolic network scaffold to which the experimental data will be superimposed. Subsequent analysis will be used to propose strain designs for industrial application in the production of biofuels.

Genome-scale metabolic models have been created for many prokaryotic microbes and a variety of applications (Palsson's Model Compilation). Several of these models have been able to incorporate experimental data matching cellular processes. Once the model closely resembles the biological systems, it will be optimized for defined objective function. This objective function may range from production of biomass to chemical target. Following the *in silico* optimization of yields may eventually be replicated for applications in industry, therapeutics or health-related predictions.

In the scope of current study, the three different approaches for the model drafting were used and analyzed for their capability to mimic the cellular process of substrate uptake rate. The three versions will be designed as follows:

1. Autobuild from Model SEED (Overbeek,R., Begley,T., et al. 2005) named as **Tfu_v1**,

2. In-house autobuild based on organism specific annotation named **Tfu_v2** and reaction information from KEGG (obtained in 2008) (Kanehisa,M. and Goto,S. 2000, Kanehisa,M., Goto,S., et al. 2006),
3. Experimental data from 2D proteomic experiment of *T. fusca* grown in Cellobiose media named **Tfu_v3**

This will describe the multiple approaches for the network reconstructions. Tfu_v3 will then be used for detailed study and analysis of the metabolic reactions. To characterize the cellular network the major focus will be on studying the central metabolism mainly carbohydrates and amino acids metabolism pathways. The overall goal of developing genome scale metabolic model for the actinomycete *T. fusca* will be to gain a systems level understanding of the cellular network with the experimentally defined constraints of the substrate uptake rate.

2.2. MATERIALS AND METHODS

2.2.1. Metabolic Network Reconstruction

Tfu_v1: SEED. The autobuild draft model was made in Model SEED (Henry,C.S., DeJongh,M., et al. 2010, Overbeek,R., Begley,T., et al. 2005) and used as the draft network. The *.xml file downloaded was converted into in-house MetModel format to run the FBA using python script created and maintained on Brooks' server.

Tfu_v2: yaml. The *.yaml autobuild drafts were created by our group in 2008 using the then available organism specific annotations and reaction database from KEGG (Gowen,C.M. and Fong,S.S. 2010, Roberts,S.B., Robichaux,J.L., et al. 2009, Roberts,S.B., Gowen,C.M., et al. 2010, Vanee,N., Roberts,S.B., et al. 2010).

Tfu_v3: Proteomics. The draft model was constructed using the 2-dimensional proteomic experimental dataset generated at the Proteomics Core Laboratory facility at University of Manitoba, Canada. A 2D-HPLC-MS/MS analysis was performed on the Cellobiose grown sample across 13 concatenated fractions in the first dimension, each run over a 1-hour HPLC-MS/MS session. This collection of runs yielded 276,129 MS/MS spectra; when searched using the Global Proteome Machine (GPM) these yielded 126,471 peptides (16598 non-redundant) spanning 2101 proteins (of 3097 total, ~ 68% proteomic coverage). Protein expectation values were computed using a Bayes theorem application of its member peptide expectation values following the design by Beavis and Fenyo (Beavis,R. and Fenyo,D. 2004) on X!tandem (Craig,R. and Beavis,R.C. 2004); over 1700 proteins have expectation values of log(e)<-100 (a one in ten-to-one hundred probability of random miss-assignment). The Total Intensity Count (TIC) values for the 1881 proteins identified by at least two peptides span from 11.8 to 28.2 in log2 scale, with a mean of 19.9 and a standard deviation of 2.87. The method was designed and developed by Dwivedi et al in 2008 (Dwivedi,R.C., Spicer,V., et al. 2008).

Open source *T. fusca* (Taxon identifier: 269800) database KEGG (Kanehisa,M. and Goto,S. 2000, Kanehisa,M., Goto,S., et al. 2006), IMG (Markowitz,V.M., Chen,I.M.,

et al. 2012)and Uniprot (Gattiker,A., Michoud,K., et al. 2003) was used to map the gene identifiers to the EC numbers which was then looked up as the search identifier in the reaction database compiled in-house. Further, manual curation was done using the published biochemical literature specifically for Cellobiose utilization as explained in Figure 9.

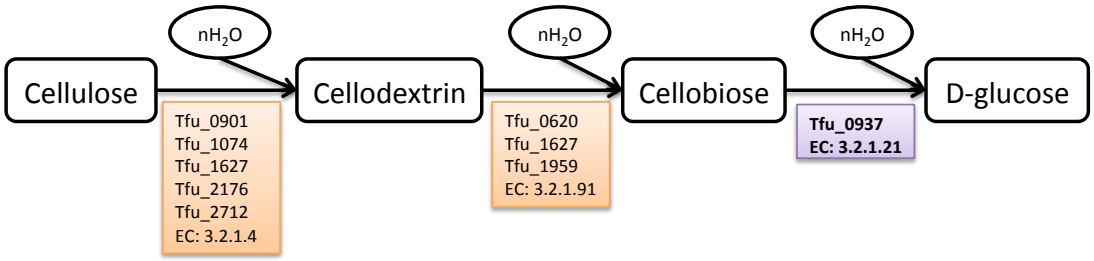


Figure 9: *Cellulose degradation reaction in presence of water: The reaction to convert the Cellobiose As per the experimental dataset Tfu_0937, EC 3.2.1.21 was expressed and thus the associated reaction was added to the model* (Karp,P.D., Riley,M., et al. 2000).

2.2.2. Linear Programming for Flux Balance Analysis

In-house python scripts were used to run the FBA simulations using the linear programming algorithm as follows:

$$\text{Maximize: } Z$$
$$\text{Subject to: } S \bullet v = 0,$$
$$a_i \leq v_i \leq b_i \text{ for all reactions } i,$$

where, Z is the flux through objective function (biomass production/product optimization), S: stoichiometry of the reactions represented as matrix form shown

in Figure 10, v is reaction flux vector, a_i and b_i are the constraints placed on the flux v_i of the reaction *i(Edwards,J.S., Covert,M., et al. 2002, Palsson,B.Ø. 2007).*

Metabolites →

Reactions ↑	2PG	3PG	ATP	GLU-B	ADP	G6P	ETOH	NAD	ACALD	H	NADH	H2O	PEP	G3P	PI	13DPG	ADP	AC	F6P	G1P
R_PGM	-1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
R01600	0	0	-1	-1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
R_ALCD2x	0	0	0	0	0	0	-1	-1	1	1	1	0	0	0	0	0	0	0	0	0
R_ENO	-1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
R_GAPD	0	0	0	0	0	0	0	-1	0	1	1	0	0	-1	-1	1	0	0	0	0
R_PGK	0	-1	-1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
R_ALDD2x	0	0	0	0	0	-1	0	-1	-1	1	1	-1	0	0	0	0	0	1	0	0
R_PGMT	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	-1

Figure 10: *Chemical reactions converted to the matrix format to solve using linear programming*

2.2.3. Objective Function: Biomass Equation

This draft model aims at growth optimization. The best estimates used in various metabolic modeling scenarios in related species provides guidance for this "biomass equation", which was then designed by slightly manipulating the biomass equations from these closely related species and from other available published information about *T. fusca* growth conditions (Feist,A.M., Herrgard,M.J., et al. Feb 2009). The box below shows the biomass equation used for the simulation of all the version of the model.

BIOMASS EQUATION

```
34.7964805 C00001 + 40.1701382 C00002 + 0.00780937 C00003 +
0.00780937 C00006 + 0.00780937 C00010 + 0.00780937 C00016 +
0.00780937 C00018 + 0.00780937 C00019 + 0.25601316 C00025 +
0.00780937 C00034 + 0.59580299 C00037 + 0.00780937 C00038 +
0.50005823 C00041 + 0.20910125 C00044 + 0.33354560 C00047 +
0.23467873 C00049 + 0.00780931 C00059 + 0.28827498 C00062 +
0.12987656 C00063 + 0.25601316 C00064 + 0.20970184 C00716 +
0.00780937 C00070 + 0.14934101 C00073 + 0.14026667 C00075 +
0.00780937 C00076 + 0.05515731 C00078 + 0.18056213 C00079 +
0.13425080 C00082 + 0.08898018 C00097 + 0.00780937 C00698 +
0.43865670 C00123 + 0.01174687 C00131 + 0.09262265 C00135 +
0.21542571 C00148 + 0.23467873 C00152 + 0.00780937 C00175 +
0.41159840 C00183 + 0.24664683 C00188 + 0.00780937 C00238 +
0.00780937 C00255 + 0.01174687 C00286 + 0.00780937 C00305 +
0.28255111 C00407 + 0.01174687 C00458 + 0.01174687 C00459 +
0.09247649 C04574 + 0.00780937 C14818 + 0.00780937 C14819 +
0.00780937 C00229  -->
40.0000000 C00008 + 39.9921906 C00009 + 0.60239528 C00013 +
```

```
40.0000000 C00080 + 0.00780937 C03688
```

2.2.4. Gap Analysis and Model Comparison

The draft model consists of the list of reactions however there are patches in the network that obstruct continuous flow of flux through the pathway. These links are filled in by using the reaction databank and suggesting the list of reactions required to complete the network. This process of suggesting the connection nodes/reactions is called Gap analysis (Brooks,J.P., Burns, W.P., et al. 2012). It is done using in-house python scripts maintained on Brooks' server. The use and application of these scripts have been described in past by Roberts et al.(Roberts,S.B., Robichaux,J.L., et al. 2009, Roberts,S.B., Gowen,C.M., et al. 2010), Gowen et al. (Gowen,C.M. and Fong,S.S. 2010) and Vanee et al. (Vanee,N., Roberts,S.B., et al. 2010). All further comparisons, analysis and summary were performed using R and excel.

2.2.5. Data Integrations and Model Validation for Tfu_v2

The mixed integer linear programming algorithm (MILP) published in 2008 by Shlomi et al. (Shlomi,T., Cabili,M.N., et al. 2008) was used for integration of proteomics data to the Tfu_v2 version of model. This algorithm was re-written in python by Gowen et al. (Gowen,C.M. and Fong,S.S. 2010) to include in our MetModel package.

2.3. RESULTS AND DISCUSSION

T. fusca is known to use cellulosic biomass and hence as a substrate due to its well studied cellulolytic system (Wilson,D.B. 2004, Wilson,D.B. and Kostylev,M. 2012). Figure 9 shows the theoretical steps for cellulose degradation in the presence of water. In the laboratory conditions *T. fusca* is grown on Cellobiose. To implement this biological growth condition, the Cellobiose degradation reactions were added to the draft model based upon the annotation and experimental evidence (EC 3.2.1.21, Tfu_0937). Cellobiose was used as the carbon source for the purpose of simulation in all the versions of model to closely mimic the growth condition. Three different approaches (shown in Figure 11) used for building the *T. fusca* model with minimal manual intervention are discussed below along with their comparative statistics.

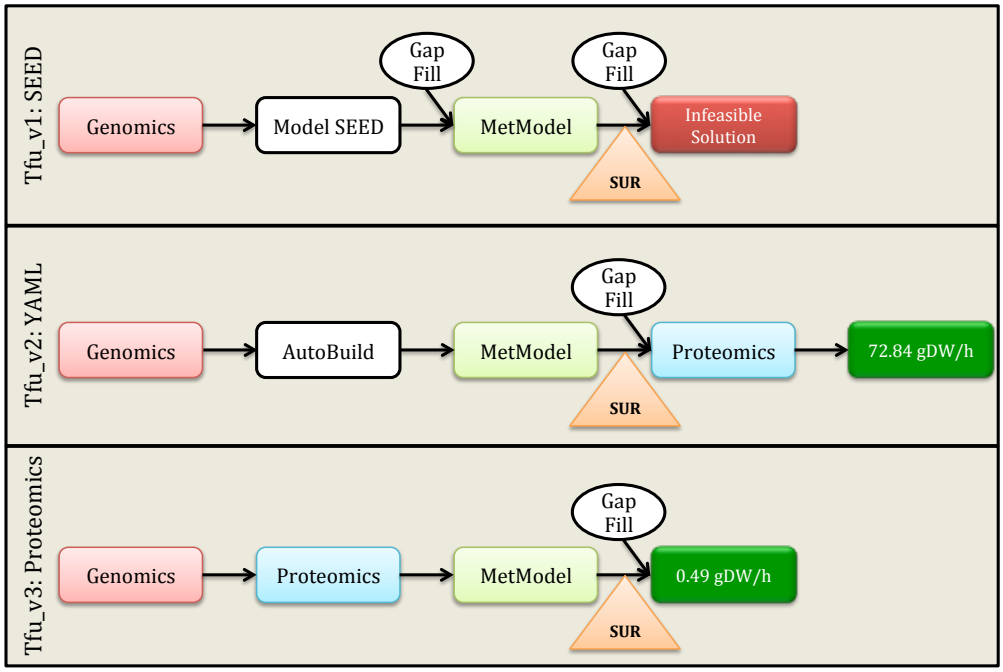


Figure: 11: *Flowchart of the model building step and data incorporation for all the three version of the model. Genomics and Proteomics are the high throughput datasets used for building the models. SUR – Substrate uptake rate for Cellobiose as calculated experimentally was applied as a constraint. Red indicated no solution was obtained when running simulation of SEED model under experimental constraints. Values in the green boxes indicate the growth rates for Tvu_v2 and Tfu_v3.*

2.3.1. Metabolic Reconstruction: Summary and Model Statistics

Tfu_v1: The taxonomy number of *T. fusca* was used to generate a draft model from Model SEED (Henry,C.S., DeJongh,M., et al. 2010, Overbeek,R., Begley,T., et al. 2005). It was then converted to KEGG compound identifiers before running the gap analysis and FBA using the in-house scripts. This version of model comprised of 1302 reactions involving 1213 metabolites and 618 EC numbers. After the gap analysis adds approximately 146 reactions, which primarily include the exchanges reaction (reactions that denote the direct uptake/secretion of the respective metabolite from or to the extra cellular media). SEED Model version calculated the growth rate of 24.25mmoles/gDW/h under the unconstrained substrate uptake rate environment. However, when the experimentally determined substrate uptake rates of Cellobiose (0.25mmoles/gDW/h) were applied to this model it failed to perform with a warning of infeasible solution. This infeasibility was crosschecked and verified by using the Model SEED FBA runs. The model failed to perform under any media formulations (glucose and Cellobiose) tried and tested on Model SEED interface.

Tfu_v2: The second version created by in-house autobuild method as defined in our past publication (Roberts,S.B., Robichaux,J.L., et al. 2009, Roberts,S.B., Gowen,C.M., et al. 2010). This model consists of 1002 reactions involving 584 EC numbers and accounting for 1105 metabolites. Eight out of 48 reactions added in the gap analysis were non-exchange reactions. Applying the experimentally determined constraint of substrate uptake rate for Cellobiose as

0.25mmoles/gDW/h, the optimal biomass growth was 72.84 gDW/h. This growth rate was compared to experimental growth rate of 0.423 gDW/h and proved to be hypothetical and not comparable to biological conditions.

Tfu_v3: The third and the final version of the model is based on the proteomic experimental data generated by our group in collaboration with the Proteomics Core lab facility at University of Manitoba. The detailed characterization of *T. fusca* based on this data is explained in chapter 4 along with the other experimental data. This version of model based on proteomics dataset account for 975 reactions, 1283 metabolites and 257 EC numbers. This model when operated under the constraint of experimental determined substrate uptake rate of 0.25mmoles/gDW/h gave the growth rate of 0.49 gDW/h.

The comparative statistics of three versions of models are summarized in Figure 12 and the detailed model in all three versions is attached as supplementary file (Appendix A).

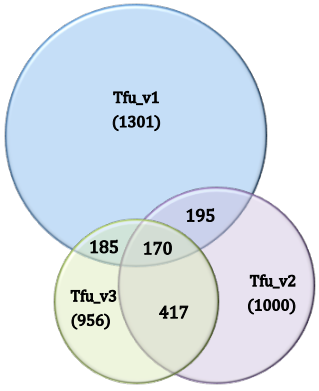


Figure 12: *Summary of three versions of models created in this study: Reaction distribution across the 3 versions is represented in the figure. All three versions had 170 reactions in common. Following was the common reaction across each compared pair of model versions: Tfu_v1:SEED AND Tfu_v2:yaml: 195, Tfu_v2:yaml AND Tfu_v3:Proteomics: 417, Tfu_v1:SEED AND Tfu_v3:Proteomics: 185.*

Both Tfu_v1 and Tfu_v2 are based on the available genomic information on the KEGG and IMG showing the exhaustive genomics coverage. However, Tfu_v1 has a more generalized set of network reactions. To make an exhaustive model it includes approximately 150 transport, source and exchange flux reactions. Tfu_v3, on the other hand, is the proteomics data based model and represents an effort to start from strong experimental evidence. This version of model was built based on proteomics map and thus involves minimal manual validation for gap analysis.

Having determined the Tfu_v3 most closely related to the biological growth rates when grown on Cellobiose, the detailed analysis here after will be done using that version.

As a heterotrophic organism, the basic characteristic traits include utilizing the organic source for carbon to break it down to synthesize other macromolecules such as carbohydrates, amino acids, lipids and nucleotides to sustain and reproduce. Being the origin and central nodes of the metabolic process, carbohydrates and amino acids pathways are also called the Central Metabolism. Thus, our primary goal to characterize the model will be to study the Central Metabolism by comprehending the reactions in all the three versions of the model. To study the individual pathways in carbohydrate and amino acid metabolism, each pathway was contrasted across the reference EC numbers recorded in the KEGG. The summary table is shown in Table 2. At the first glance, all the pathways with the threshold of 20% or above were counted as present/active. This was based on the fact that *E.*

coli's most complete model published in 2011 associates 30% of the gene products (Orth,J.D., Conrad,T.M., et al. 2011).

Table 2: *Summary of individual pathway contrasts between three versions of model: The reference frames selected here is KEGG. Each of these pathways were individually screened to make a call for active or inactive by tracing through the List of EC numbers on the KEGG map. If majority (almost all) of the EC number continuously connecting the pathway were present then the pathways was marked active else inactive*

	REFERENCE	In MODEL					
CARBOHYDRATES METABOLISM	**KEGG**	**Tfu_v1**		**Tfu_v2**		**Tfu_v3**	
Glycolysis / Gluconeogenesis	45	28	62%	22	49%	15	33%
Citrate Cycle (TCA Cycle)	22	15	68%	15	68%	13	59%
Pentose Phosphate Pathway	40	20	50%	15	38%	13	33%
Pentose and Glucuronate Intrconv.	61	10	16%	8	13%	6	10%
Fructose and Mannose Metabolism	65	14	22%	14	22%	5	8%
Galactose Metabolism	38	12	32%	13	34%	8	21%
Starch and Sucrose Metabolism	74	14	19%	14	19%	12	16%
Amino Sugar and Nucleotide Metabolism	108	25	23%	21	19%	15	14%
Pyruvate Metabolism	64	26	41%	17	27%	15	23%
Glyoxylate and Dicarboxylate Metabolism	66	12	18%	11	17%	7	11%
Propanoate Metabolism	47	17	36%	14	30%	12	26%
Butanoate Metabolism	50	17	34%	12	24%	7	14%
C- 5 Branched Diabasic Acid Metabolism	18	3	17%	3	17%	1	6%
Inositol Phosphate Metabolism	43	4	9%	5	12%	4	9%
AMINO ACID METABOLISM							
Ala, Asp and Glu Metabolism	43	21	49%	19	44%	18	42%
Gly, Ser and Thr Metabolism	63	11	17%	13	21%	9	14%
Cys and Met Metabolism	66	8	12%	3	5%	3	5%
Val, Leu and Ile Degradation	35	18	51%	13	37%	16	46%
Val, Leu and Ile Biosynthesis	14	10	71%	10	71%	7	50%
Lys Biosynthesis	30	13	43%	10	33%	8	27%
Lys Degradation	54	7	13%	8	15%	7	13%
Arg and Pro Metabolism	104	32	31%	26	25%	22	21%
His Metabolism	37	12	32%	13	35%	10	27%
Tyr Metabolism	66	11	17%	8	12%	9	14%
Phe Metabolism	70	11	16%	9	13%	9	13%
Trp Metabolism	69	14	20%	14	20%	9	13%
Phe, Tyr and Trp Biosynthesis	37	26	70%	16	43%	16	43%

2.3.2. Tfu_v3: Proteomics Model Reaction Distribution

The growth rate calculated in the Tfu_v3 showed the most realistic outcomes when the Cellobiose uptake rate was applied as constraints. This is the reason for selecting it as a model of choice. The proteomics based model of *T. fusca* account for 216 amino acid reactions and 182 carbohydrates metabolism reactions as illustrated in Figure 13. In the current simulation run performed for the optimization of biomass equation, approximately 110 reactions were operating under significantly high (>100) and low (<-100) fluxes. (The range of flux through reactions was from 0 to 1000; this threshold was selected for the purpose of analysis).

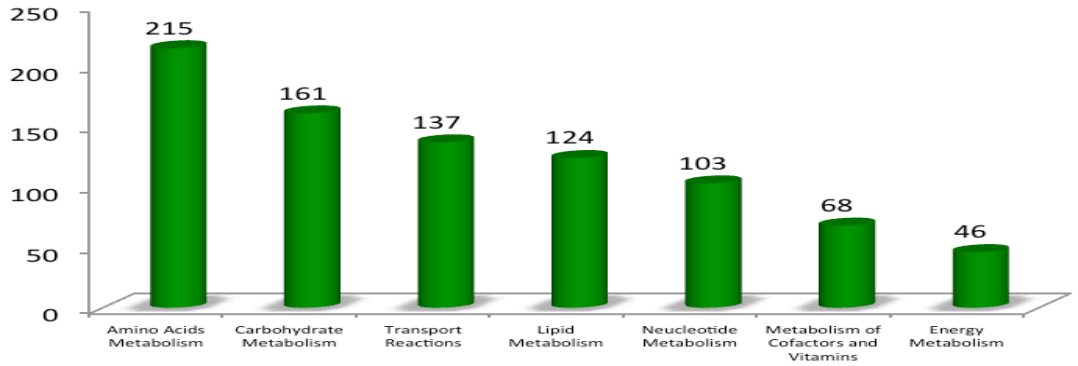


Figure 13: *Major reaction distribution in the proteomics based model comprising total of 975 reactions*

Among these 110 reactions, the majority of the reactions were used in the carbohydrate (37) and amino acids (34) metabolic network. In the carbohydrate metabolism, citric acid cycle or TCA plays a role of an important energy distribution and checkpoint for central metabolism. It account for 11 carbon compounds, all of which play significant role in biosynthesis of complex molecules from glucose or

degradation of other complex molecules for feed into the gluconeogenesis pathway. In the current study, to explain our model, we will be focusing on the seven compounds of TCA cycle that play crucial role of carbon exchange between various pathways in the central metabolism. These intermediates include: Pyruvate (C00022), Acetoacetyl CoA (C00332), Acetylyl CoA (C00024), alpha-Ketoglutarate (C00026), Succinyl CoA (C00091), Fumarate (C00122) and Oxaloacetate (C00036). Studying the reaction flux through these compounds will help us understand the probable activity in amino acid biosynthesis and degradation pathways.

To summarize these nodes in the current proteomics based version of model 60 reactions that were found active (i.e. flux was > 0.01 units). Among these 23 unique reactions, correspond to amino acids network. This indicates the activity around the most of the amino acid – carbohydrate connection nodes as shown in Figure 14.

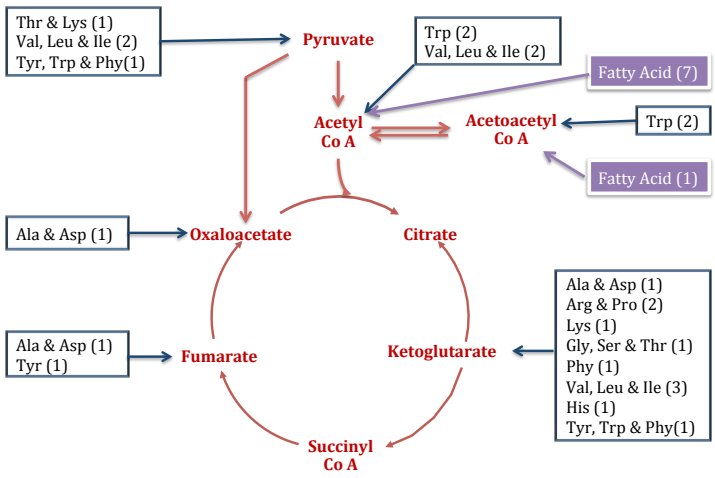


Figure 14: *Summary of carbohydrate and amino acids connection nodes and number of active flux reaction within amino acid pathways. Standard three-letter amino acids code is used to denote the pathway names. The carbohydrate nodes of the central metabolism are highlighted as red and the branching out amino acid pathways are boxed in blue. The purple boxes denote the fatty acids connections from Acetyl Co A and Acetoacetyl Co A. The numbers of reactions for each pathway are represented in the parenthesis*

It was observed that in the carbohydrate-amino acid network connection the majority of reaction (11 out of 23) branch in and out of alpha – ketoglutarate. Acetyl CoA node was more centralize by connecting the amino acids as well as the fatty acid pathways with 8 significantly high flux reactions. The pathway specific details are also illustrated in the Table 2. It was observed that when contrasted with the reaction specific to the biosynthesis or degradation of amino acids, the overall analysis suggests the presence of all but one pathway. There wasn't any significant evidence to prove the presence of Cysteine and Methionine metabolism under the Cellobiose media growth condition.

2.3.3. Comparison of "Model Validation with Data" Vs "Starting from Data"

In past, several attempts have been made to use the model as scaffold and experimental data as the validation evidence (Chandrasekaran,S. and Price,N.D. 2010, Colijn,C., Brandes,A., et al. 2009, Covert,M.W., Knight,E.M., et al. 2004, Lerman,J.A., Hyduke,D.R., et al. 2012, Shlomi,T., Cabili,M.N., et al. 2008). Some of these methods when tried in independent settings failed to perform well and required significant manual curation of the model and modify the method. In the current study, we tried two methods to bring the network model and experimental dataset together to understand and characterize the metabolism of *T. fusca*. For the first approach, the MILP algorithm was used to integrate the proteomics dataset to the model Tfu_v2 (autobuild model). This algorithm aims at optimizing the agreement between the experimental data and the *in silico* model (Shlomi,T.,

Cabili,M.N., et al. 2008). In this context, the experimental information is used as to assign a present or absent call to re-channelize the flux distribution of the network as explained by Gowen et al. (Gowen,C.M. and Fong,S.S. 2010).

Parallel to this, Tfu_v3 was our second approach of using the proteomic data as the preliminary seed point for draft model. Previous method is primarily dependent on the *in silico* information such as genomics data, biochemical literature resource and models of related microorganisms at the initial phase. The later method relies more on the *in vivo* experimental evidence of the functional machinery - proteins. Both the methods vary in terms of the amount of manual validation requirement due to which the Tfu_v2 did not give a reasonable simulation result (72.84 gDW/h). Tfu_v3 provides a more reliable scaffold on which to base the foundation of the model and the Tfu_v2 needs more intense manual curation before this model can be used for simulation and interpretation.

Besides this, another very interesting and significant difference between "Tfu_v2 + MILP" versus "Tfu_v3" was observed in the TCA cycle. The reaction using pyruvate to make oxaloacetate was not found in the autobuild version were as the proteomics version clearly shows its presence (EC 6.4.1.1, Gene ID: Tfu_2557, Tfu_1530, Tfu_0947, Tfu_1228). Besides this, most of the amino acids pathways were fully or partially incomplete in the Tfu_v2. Thus, the flux distribution through the transport reaction was very high to accommodate the metabolic requirement of optimal biomass production. Unlike that, Tfu_v3 showed most of the pathways significantly complete except the Cysteine and Methionine metabolism. Though, the

phenylalanine metabolism was also one of the sparsely populated sub network but the active flux through the reaction involved in the interconversion of phenylalanine to phenylpyruvate guided towards making a present call for this pathway.

2.3.4. Applicability of the Model

The subsystem based analysis of central metabolism and experimental foundation suggests the closer association of Tfu_v3 to the biochemical system of *T. fusca*. Because of the probabilistic nature of metabolic biochemistry and cellular biocomplexity, it is pertinacious to expect a 100% similarity of simulation model to the organism. The most update model of *E. coli* has an account of only for 30% of the gene products in the model (Orth,J.D., Conrad,T.M., et al. 2011). Likewise, this model being the first ever *T. fusca* metabolic network also opens huge scope of pathway-focused review and improvement. Once completely functional these models provide a ground for hypothesizing a target for the further study.

The primary focus of our laboratory is sustainable energy and microbial engineering for industrial application. For this purpose, our target pathways were: butanol and secondary metabolite biosynthesis. The autobuild version (Tfu_v2) incorporates most of the reactions present in the butanoate metabolism however, no active flux was observed through most of them. Tfu_v3 based on experimental dataset confirms approximately 50% of these reactions but fails to establish active flux through these. In 2011 the mutant strain *T. fusca* B6 was designed by Deng et al. (Deng,Y. and Fong,S.S. 2011b) have presented that the addition of adhE2 gene

completes the 1-propanol metabolism. This is a major development in the industrial applicability of this strain. Guided by these results, the quest to better understand our second highly relevant terpenoids backbone pathway is the next target inline.

In contrast to this, the terpenoids backbone pathway was manually incorporated in Tfu_v3 by added seven reactions of mevalonate pathway and nine reactions through non-mevalonate pathway. The simulation run results in production of ispentenyl diphosphate (IPP, C00129) with an active flux of 0.53 mmoles/gDW/h through the mevalonate pathway. IPP is a precursor compound for the family of isoprenoids but it also involves an isomerization reaction between IPP and DMAPP (dimethylalyl pyrophosphate). In this context there was no flux observed in the isomerization reaction. Besides this there was no active flux observed through the DXP pathway. As we know that the production of butanol and isoprenoids branch out of the central metabolism but are not the necessities of primary metabolism, this has led to their exclusion from the current objective function (biomass). In this version, biomass optimization does not target towards elevating any product or pathway. However, this activity of flux through mevalonate pathway has directed our attention towards the experimental characterization and validation of the backbone pathway as a follow-up study.

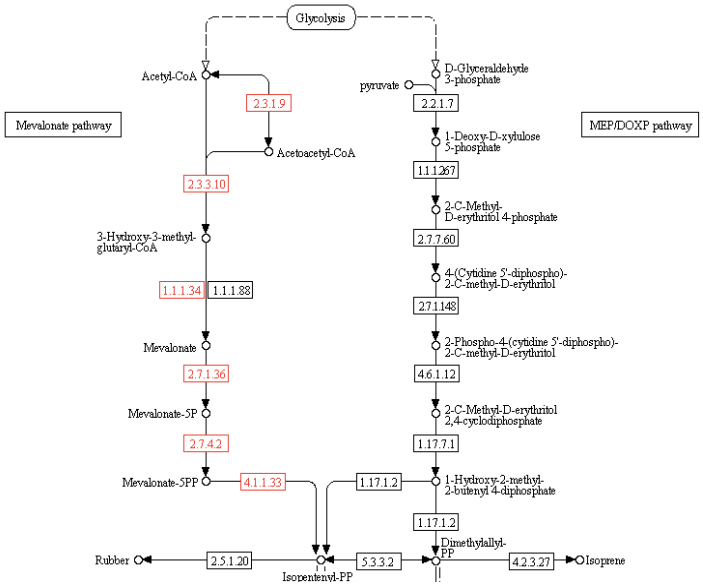


Figure 15: *Depiction of active flux through Mevalonate Pathway in the Terpenoids Backbone Biosynthesis*

2.4. CONCLUSION

The three different methodologies for designing the metabolic model were described in this section. The proteomics based model *i*Tfu1002 was found to mimic the biological growth conditions most closely. It was observed that when Cellobiose uptake rate was constraint as 0.25 mmoles/gDW/h gave the growth rate of 0.48 gDW/h. This was comparable to the experimental growth rate of 0.43 gDW/h. We present here a novel scheme of the model reconstruction based on high throughput experimental data fed at initial draft phase.

Genomics datasets are the most standard high throughput data available at the current stage but it is always a concern to what extent the genomics information is really transcribed and translated into the functional role inside the cell. This may be due to environmental or evolutionary selection process that out of 3195 genes

annotated in the *T. fusca* genome published in 2005, only 3117 translated into proteins coding genes. 1757 of which were associated with predicted functions (Karp,P.D., Riley,M., et al. 2000, Lykidis,A., Mavromatis,K., et al. 2007, Markowitz,V.M., Chen,I.M., et al. 2012).

With the advent of standard genomics information, the genome scale models have become a widely used approach to a systems level understanding of metabolic processes (Durot,M., Bourguignon,P., et al. 2009, Feist,A.M., Herrgard,M.J., et al. Feb 2009, Joyce,A.R. and Palsson,B.Ø. 2007). Each of these models needs to pass through multiple levels of curation and validation based on genome annotation, experimental evidence and (or) biochemical literature study. Knowing that the omics-data can be used to extract biological information, we address the approach of building the model based on the high throughput experimental data. These models contain the scope of integration of genomics, transcriptomics, proteomics, metabolomics and phenomics data. For the current study, proteomics dataset has been used to establish a significantly reliable starting point for the metabolic model reconstruction. This version of model Tfu_v3 is based on functional building blocks that are more closely associated with the phenotypic characteristics when compared to genomics data in the hierarchy.

In a larger context, the modeling approach aims at building link between the molecular and cellular functions. However, it is still hard to find a 100% agreement between the "biology - biochemistry" and "network models - omics data". It is reported that the most updated *E. coli* (Orth,J.D., Conrad,T.M., et al. 2011) model

only associates to 30% of gene products in the model and 1/3 of the gene products are not functionally annotated (Hyduke,D.R., Lewis,N.E., et al. 2013). Irrespective of that, the model-based systems analysis can be useful for developing hypothesis and target for the focused study. In this case we hypothesize the presence of active terpenoids backbone pathway, which will be the focus of our follow up studies using experimental and analytical methods.

Nevertheless, this promising approach suffers with a major limitation to this date - lack of standardized reaction database to build draft model. Due to inconsistency in the labeling of the metabolites (eg: Citrate is almost chemically equivalent to Citric acid; 2-Hydroxy-1,2,3-propanetricarboxylic acid; 2-Hydroxytricarballylic acid and have the same compound identifier on KEGG) it is difficult to assemble a non-redundant reactions database with standard nomenclature. Current systems biology experts are in the quest of cleaning and populating available database with minimal redundancy in the hope of exhaustive coverage of cellular biochemical reactions. Some of the examples are MetRxn and MetaCyc.

CHAPTER 3 – METABOLOMICS PROFILING

3.1. INTRODUCTION

The pillars of the systems biology approach are the high through put dataset viz. genomics, transcriptomics, proteomics and metabolomics. All of the levels in the hierarchy are important in completing the entire puzzle unveiling the complete picture however; the best strategy is to measure the outcome of the systems – metabolites. The metabolite specific information holds the key to the substrate and product relationship and thereby has the capacity to provide an architect for reverse engineering of the strain. The metabolites that are innate to the cellular process can provide the starting point information for efficient pathway engineering. This study of metabolites formed by, or found within the cell or organism is known as Metabolite profiling. The dynamics of this data is not only defined by genetic and environmental factors but also the life stages of the bacteria. As a broad classification, difference between the primary and secondary metabolites is the growth phase when it is produced in the bacteria. The early log phase shows more concentration of primary metabolites, which is utilized for growth, and reproduction of the cells. This is followed by the production of secondary metabolites as the byproducts of the metabolic process. Most of these secondary metabolites are known for their medical and industrial relevance (Citron,C.A., Gleitzmann,J., et al. 2012).

Actinomycetes are known for the production of medically relevant compounds. *T. fusca* belongs to the same family and thus we aim to characterize its cellular systems to better understand the innate production capabilities. This may

be significant for us to streamline the strain engineering protocol. In the previous chapter, we characterized the metabolic process using the systems level modeling based on genomics and proteomic data. In this section, we further explore the macromolecular network by studying the metabolite profile of the bacteria under two different media formulations. The two media conditions used in the current study to conduct comparative analysis are Cellobiose and Avicel. Cellobiose has been studied in past as the inducer of cellulases (Chen,S. and Wilson,D.B. 2007, Deng,Y. and Fong,S.S. 2010b, Deng,Y. and Fong,S.S. 2011a, Spiridonov,N.A. and Wilson,D.B. 1998) thus is used as the reference media condition. Avicel, on the other hand, is a crystalline solid carbon source more closely related to plant waste therefore used for comparative analysis.

Global metabolite profiling experiments attempting to characterize all metabolites of a cellular system involve a huge combinatorial hierarchy of techniques (Wang,Y. and Griffiths,W.J. 2008). Figure 16 shows the compound and technique classification that may be used for targeted or untargeted metabolite profiling. In the current scope, only untargeted metabolite profiling using HPLC/MS TOF in positive polarity was conducted. Using a Methanol:Water:Chlorofom extraction method, the aqueous and non-aqueous layers are separated for 2 different runs: polar and non-polar. The peak and mass data acquired on Agilent Mass Hunter Software from LC-MS was sent to the Omics Discovery Pipeline at Bindley Bioscience Center for deconvolution, alignment, normalization and identification of the compounds (Riley,C.P., Gough,E.S., et al. 2012). The parameters for each step were established after observing the results from each previous step.

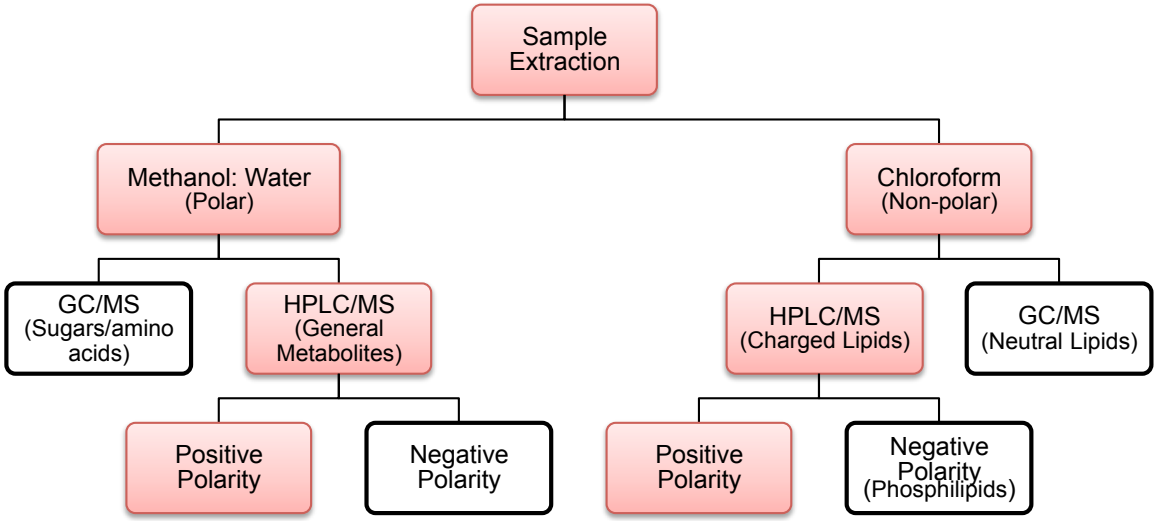


Figure 16: *Metabolite profiling techniques used for the current study is highlighted in red. For both polar and non-polar metabolites, more exhaustive detections is observed in positive polarity mode and thus was the mode of choice in this experiment* (Riley,C.P., Gough,E.S., et al. 2012, Wang,Y. and Griffiths,W.J. 2008)

This analysis detects a subset of polar and non-polar compounds representing general metabolites and lipids, respectively. Technical replicates of *T. fusca* wild type grown on Cellobiose and Avicel. This is the first ever attempt to investigate metabolomics of *T. fusca*. It opens an arena for target-based metabolite profiling to specifically look into the pathways/product of interest that were detected in first screening.

3.2. MATERIALS AND METHODS

3.2.1. Cell Growth

T. fusca YX strain (ATCC BAA-629) cells were grown on Hagerdhal media (ATCC medium: 2382) with Cellobiose and Avicel as the defined carbon source (5.0

gm/L) at 55°C. The two growth conditions resulted in the dry cell weight of 8.4 mg/mL for Cellobiose and 4.5 mg/mL for Avicel growth condition.

3.2.2. Extraction Process

The frozen pellets were re-suspended in 1mL methanol and transferred to glass tubes. Then, 3mL of $CHCl_3$ was added to each tube and sealed with foil to avoid contamination with water. The tubes were incubated for 5 min in sonicator-water bath for cell disruption. To this cell lysate added MeOH:H_2O (3:2) and kept aside for phase separation. This brings the final ratio of solvents MeOH: H_2O: CHCl3 to 4:2:3. The 6mL of polar and 3mL of non-polar phase was separated and kept on speed vacuum overnight. These vials were stored at -80˚C after sealing with parafilm for further detection protocols.

3.2.3. Polar and Non Polar General Metabolites Isolation

The processing of small molecules detection along with the instrumentation conditions are described in Figure 17.

3.2.4. Statistical Analysis Using Omics Discovery Pipeline

The raw data from the Agilent Mass Hunter software was fed to the Omics discovery pipeline developed by Purdue Bindley Biosciences Core Metabolite Care Lab Facility. This pipeline processes the data by performing deconvolution of peaks using XMASS. This preprocessing m/z, intensity and retention time data is fed to XALIGN to align the data from technical replicates to reduce the instrumentation errors. Further, the t-test was conducted to see significant difference from the blank

runs and eliminate the peaks due to solvents and spiked standards (mass of 121.050873 and 922.009798 respectively) (Riley,C.P., Gough,E.S., et al. 2012).

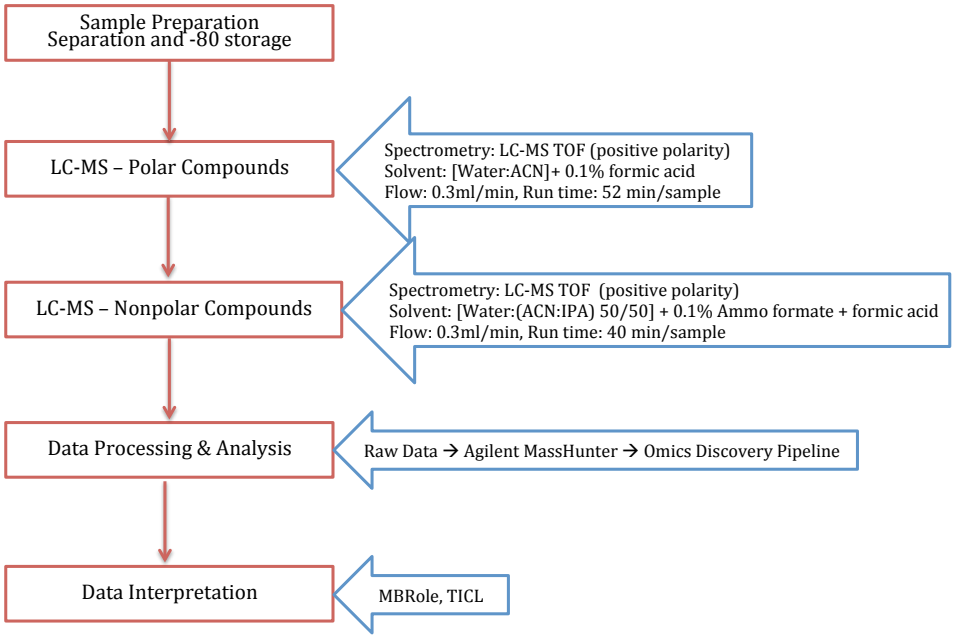


Figure 17: *Flow chart for the method followed for the extraction, isolation and detection of small molecules (general metabolites and lipids)*

3.2.5. Metabolite Identifications and Pathway Association

The identified set of metabolites was then mapped to *T. fusca* pathways using the precompiled compound list on KEGG as a reference. This was done using MBRole (Chagoyen,M. and Pazos,F. 2011), an online compilation of metabolites and pathways.

3.3. RESULTS AND DISCUSSION

The polar and non-polar extracts were run as a separate experiments and the peak data was collected in the form of mzData files by the software Mass Hunter provided by Agilent. These mzData files were processed using Omics Discovery

Pipeline (www.omicsDP.org) provided by Purdue (Riley,C.P., Gough,E.S., et al. 2012). An illustration of retention time plot, spectra data and output of identified compound is shown in Figure 18.

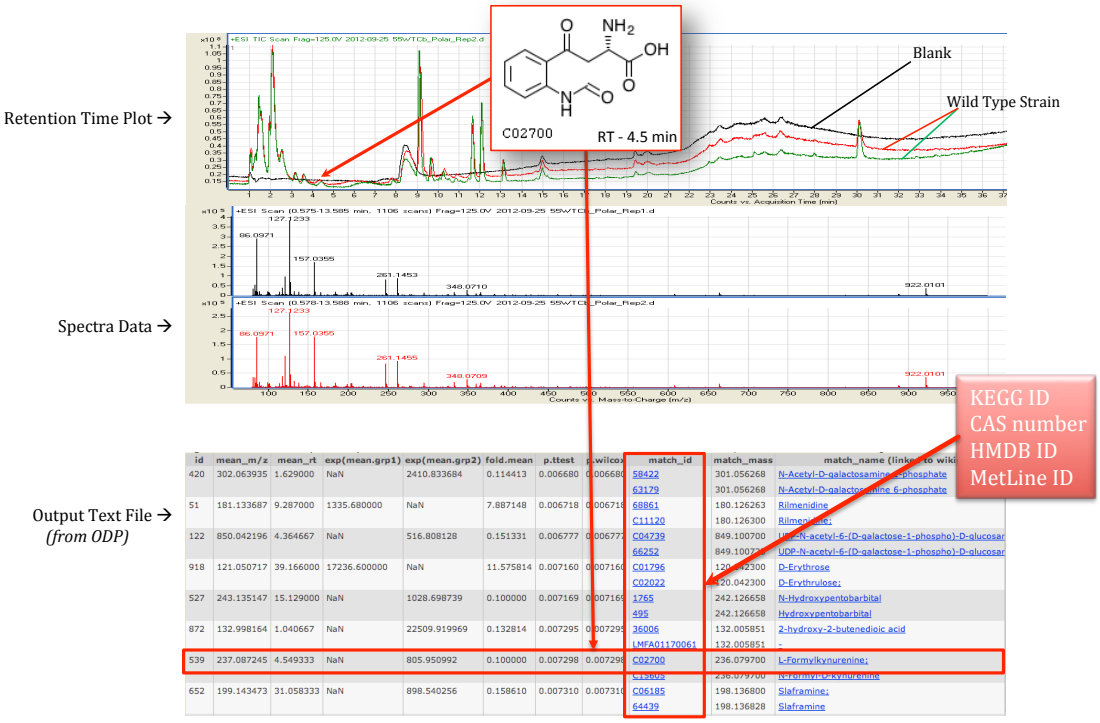


Figure 18: *Illustration of retention time, spectra data peak and sample output file obtained for T. fusca wild type strain grown on Cellobiose growth media*

3.3.1. Coverage Polar and Non-polar Metabolites

All the samples were run with technical replicates and the metabolites detected in both the replicates were used for further processing and analysis. The wild type strain grown on Cellobiose media detected 618-polar and 82-non polar compounds whereas the cells grown on Avicel media detected 402 polar but similar nonpolar compounds. Summary is shown below in Table 3.

Table 3: *Summary of compounds identified in the wild type strain of T. fusca when grown on Cellobiose and Avicel media growth conditions*

	TOTAL DETECTED	POLAR	NON POLAR	IN BOTH
In Cellobiose	667	618	64	15
In Avicel	461	402	82	23

3.3.2. Function Association of the Metabolites

The MBRole (Chagoyen,M. and Pazos,F. 2011) online available software was used for finding the association of the detected metabolites. It provides access to the organism-specific precompiled list of metabolites on KEGG as a reference (Kanehisa,M. and Goto,S. 2000, Kanehisa,M., Goto,S., et al. 2006). The mapping category includes; metabolic pathways, enzyme interactions, biological roles, chemical groups and other interaction (transport associated molecules). The summary of each category is shown in Table 4.

Table 4: *Category distribution for metabolites detected in Cellobiose (green) and Avicel (red) growth condition. The total metabolites detected in Cellobiose were 680 and in Avicel were 461*

Relations Category	Total Relations		Number of Compounds		No Annotation	
Pathways	72	71	191	129	476	332
Enzyme Interactions	299	213	71	45	595	416
Biological Roles	71	63	67	45	600	416
Chemical Groups	62	56	186	123	481	338
Other Interactions	95	74	31	25	636	436

3.3.2.1. In Cellobiose Growth Condition

Out of 680 metabolites detected in the Cellobiose growth conditions, no annotation could be detected for 474 compounds in *T. fusca*. The detected compounds could be broadly classified into macromolecular subcategory 10 sugars,

36 lipids or fatty acids associated molecules, 48 nucleotides, 40 peptides or amino acids molecules, 2 hormone or neurotransmitter like molecules and 9 vitamin molecules were detected in Cellobiose growth condition. Around 81 molecules from the secondary metabolites (or phytochemical compound) as named by KEGG were also identified. The other interaction associated with the transporter (47), reporters (61) and ion channel associated molecules were also identified. The transporter molecules included ABC type, amino acid (arginine, glycine, proline, methionine, arginine/ornithine and glutamate. Among the receptor molecules, we uncovered around 24 glutamate receptors including metabotropic and ionotropic subclass. The ionotropic receptors are the ligand gated non-selective ion channels and metabotropic activates biochemical cascades (Ger,M.F., Rendon,G., et al. 2010). As compared to eukaryotic homologs, the prokaryotic glutamate receptors are less characterized. The detection of 24 compounds from this class opens an arena for further explorations of this family in *T. fusca.* This might also be useful to explain the strong secretome as studied in past (Adav,S.S., Ng,C.S., et al. 2010, Adav,S.S., Ng,C.S., et al. 2011). Compounds associated to cytochrome P450 was another important family of compounds that was observed in the analysis. There were 21 entities similar to CYP1 and CPY2 family mainly. The primary function of this superfamily of proteins is to catalyze the oxidation of lipids, steroids and xenobiotic compounds such as toxic chemicals and drugs (Guengerich,F.P. 2008).

Apart from learning the biological role of the molecules, these detected compounds were also mapped to the metabolic capabilities as pre-compiled by KEGG using the open access online database interface MBRole (Chagoyen,M. and

Pazos,F. 2011). Among these 206 detected compounds, 105 were associated with primary metabolism pathways and 54 belonged to secondary metabolism network. These networks are shown in Figure 19(a) and (b) with compounds highlighted with grey. The maximum metabolites detection associated to a pathway was 38% in oxidative phosphorylation pathway (tfu00190) but maximum compounds associated to nucleotide metabolism were detected (23%) including the pathways 14 from Pyrimidine Metabolism and 21 in Purine Metabolism. Besides that, the major classification of amino acids, carbohydrate and secondary metabolism pathways are shown in Table 5(a).

Table 14: *COG classification based Secondary metabolites associated proteins*

PATHWAY	LOCUS	DESCRIPTION	CB2D	iTRAQ	CB-1D	AV-1D
Cytochrome P450	Tfu_1257	Cytochrome P450 monooxygenase	22.31		18.095	18.075
Cytochrome P450	Tfu_1748	Cytochrome P450-family protein	24.29	0.744	21.5	12.29
Cytochrome P450	Tfu_2976	Cytochrome P450-family protein	21.48	0.739	17.5	17.73
Cytochrome P450	Tfu_2802	Putative cytochrome P450	25.75	1.258	22.67	22.065
Cytochrome P450	Tfu_1747	Putative cytochrome P450	21.61	0.961	16.915	13.995
Cytochrome P450	Tfu_2975	Putative cytochrome P450	19.36	0.862	13.71	15.34
Cytochrome P450	Tfu_2803	Putative cytochrome P450-family protein	21.3	0.87	15.35	17.1
Cytochrome P450	Tfu_2798	Putative DNA-binding protein	15.73			
Carbohydrate Metabolism	Tfu_1298	2-deoxy-D-gluconate 3-dehydrogenase	17.6		13.51	15.16
Ketone Bodies/Butanoate Metabolism	Tfu_0081	3-hydroxybutyrate dehydrogenase	23.95	1.187	11.125	21.285
Fatty Acid Degradation	Tfu_2158	Putative long-chain-fatty-acid-CoA ligase	23.82	0.959	2.53	22.27
Fatty Acids Degradation, Biotin Metabolism	Tfu_1682	3-ketoacyl-(acyl-carrier-protein) reductase	2.33		15.61	16.635
Fatty Acids Degradation, Biotin Metabolism	Tfu_1843	3-oxoacyl-(acyl-carrier-protein) reductase	22.77	1.118	18.5	16.47
Fatty Acids Degradation, Biotin Metabolism	Tfu_1841	Putative 3-ketoacyl-CoA reductase	21.31		16.025	17.51
Fatty Acids Degradation, Biotin Metabolism	Tfu_1976	Putative 3-oxoacyl-ACP synthase II	22.79	0.718	19.515	18.295
Nicotinate & Nicotinamide Metabolism	Tfu_2374	Putative pyrazinamidase / nicotinamidase	19.52			14.58
Secondary Metabolites	Tfu_1300	DitJ-like CoA ligase (AMP forming),(diterpenoid metabolism)	2.78			15.97
Secondary Metabolites	Tfu_1231	Modular polyketide synthase	14.31			
Shikimate Pathway	Tfu_1868	Isochorismatase	16.81			
Shikimate Pathway	Tfu_1872	Isochorismate synthase	17.85			
Siderophores Group Biosynthesis	Tfu_1873	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	14.76			
Siderophores Group Biosynthesis	Tfu_1871	2,3-dihydroxybenzoate-AMP ligase	21.25	0.737	14.555	
Histidine Metabolism	Tfu_0821	Imidazolonepropionase	17.2			
Tyrosine Metabolism	Tfu_0621	5-carboxymethyl-2-hydroxymuconate delta-isomerase	2.92	0.813	16.57	15.3
Tyrosine Metabolism	Tfu_1869	Putative peptide monooxygenase	18.53			
Others	Tfu_0275	Putative short chain dehydrogenase	23.3		18.45	19.325
Others	Tfu_1242	Short chain dehydrogenase	18.48			
Others	Tfu_1279	Short chain dehydrogenase	16.87			
Others	Tfu_1975	Acyl carrier protein	23.95	0.341	12.07	2.45
Others	Tfu_1866	Amino acid adenylation	19.3		13.74	
Others	Tfu_1865	Amino acid adenylation	2.83	0.97	14.72	

Others	Tfu_1267	FrnE protein	16.17	0.636		
Others	Tfu_0080	GAF domain protein	21.11		16.69	18.915
Others	Tfu_0691	Helix-turn-helix, Fis-type	18.97			
Others	Tfu_1795	Helix-turn-helix, Fis-type	14.89			
Others	Tfu_1462	Similar to Acetyl esterase (deacetylase)	21.76	0.85	15.975	16.73
Others	Tfu_1867	Non-ribosomal peptide synthase: Amino acid adenylation	21.64	0.777	16.21	
Others	Tfu_1188	Phenylacetic acid degradation-related protein	2.42	1.83	15.85	
Others	Tfu_2707	Putative acetoin utilization protein	21.16	1.239	15.75	

3.3.2.2. In Avicel Growth Condition

In the Avicel growth condition, 461 compounds were detected but only 330 of which could not be associated to *T. fusca* functional category as defined by KEGG. Following similar pattern of classification, the macromolecular distribution of Avicel media grown strain was: 7 sugar molecules, 21 lipids, 17 nucleotides, 43 peptides (and amino acids) and 6 vitamins. Most of the numbers were lesser as compared to Cellobiose condition analysis except the peptides. The Cellobiose conditions detected 40 peptides which is three less than current set. For the transporter and receptor-associated compounds, the numbers were 43 and 41 respectively. There were 17 cytochrome P450 subfamily proteins and 19 glutamate receptor molecules (ionotropic and metabotropic) identified. One unique entity detected in the Avicel condition was 2-aminoethylphosphonate transporters, which is an ABC-type transporter that helps transport 2-aminoethylphosphonate across the membrane for utilization in bacterial. Bacteria has the capability to use these organophosphates as a source of carbon, energy and phosphorous for growth. These organophosphates are basis of insecticides and herbicides (O'Loughlin,S.N., Graham,R.L., et al. 2006).

Apart from the macromolecular classification, 131 identified compounds were studied for active metabolic role pathways. 71 of them were found to be associated with metabolic process and 31 with secondary metabolism pathway. These networks are shown in Figure 20(a) and (b) with compounds highlighted with grey. The maximum number was found in tfu00300 - Lysine biosynthesis (28%) where 9 out of 32 annotation compounds were identified experimentally. Other detected compounds from carbohydrate, amino acids and secondary metabolism pathway are listed in Table 5(b).

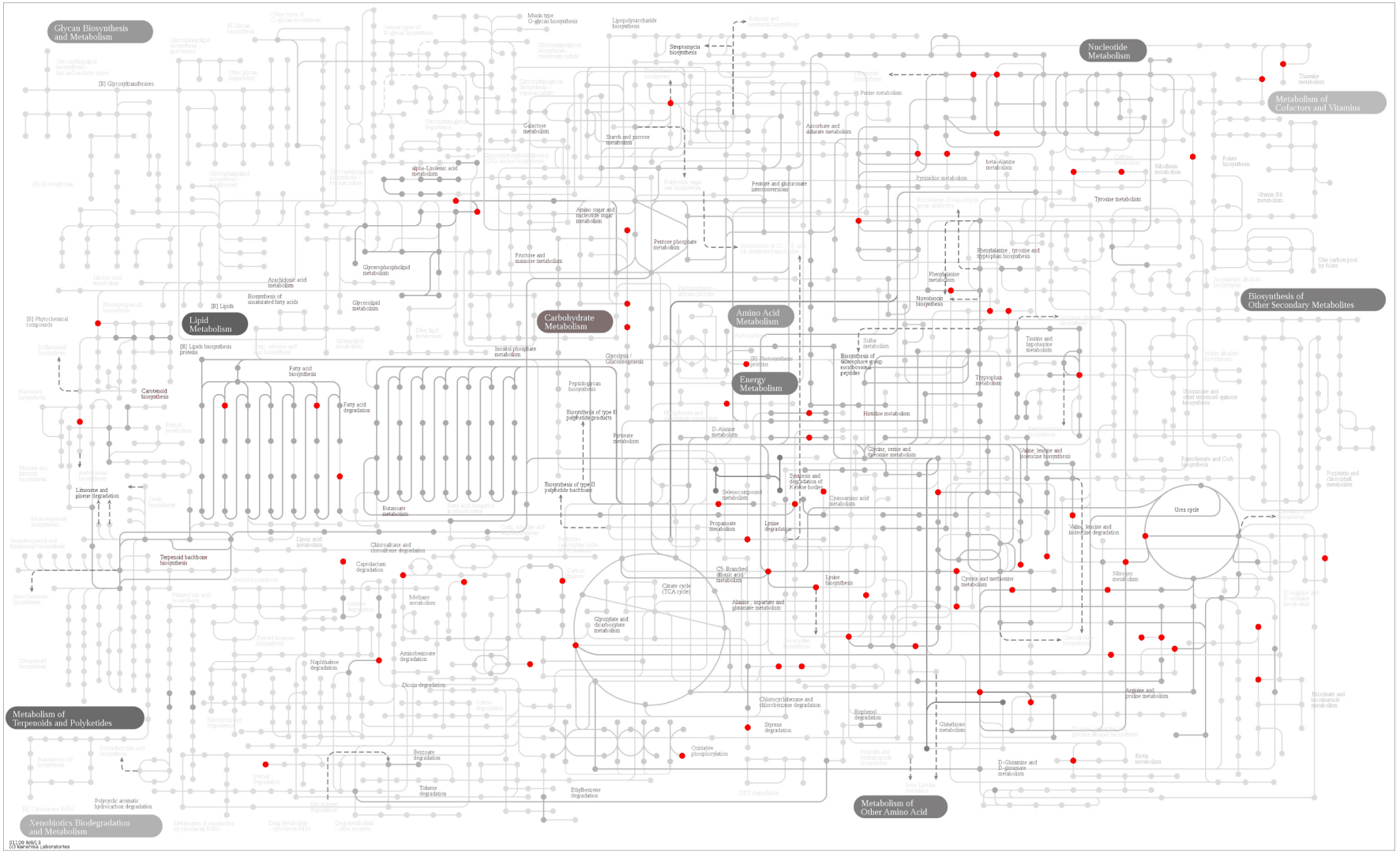


Figure 20(a): *The 71 compounds as detected in Wild type strain grown on Avicel media formulation and mapped to tfu001100, Metabolic Process. The grey dots denote the experimentally detected compounds*(Chagoyen,M. and Pazos,F. 2011, Kanehisa,M. and Goto,S. 2000, Kanehisa,M., Goto,S., et al. 2006)

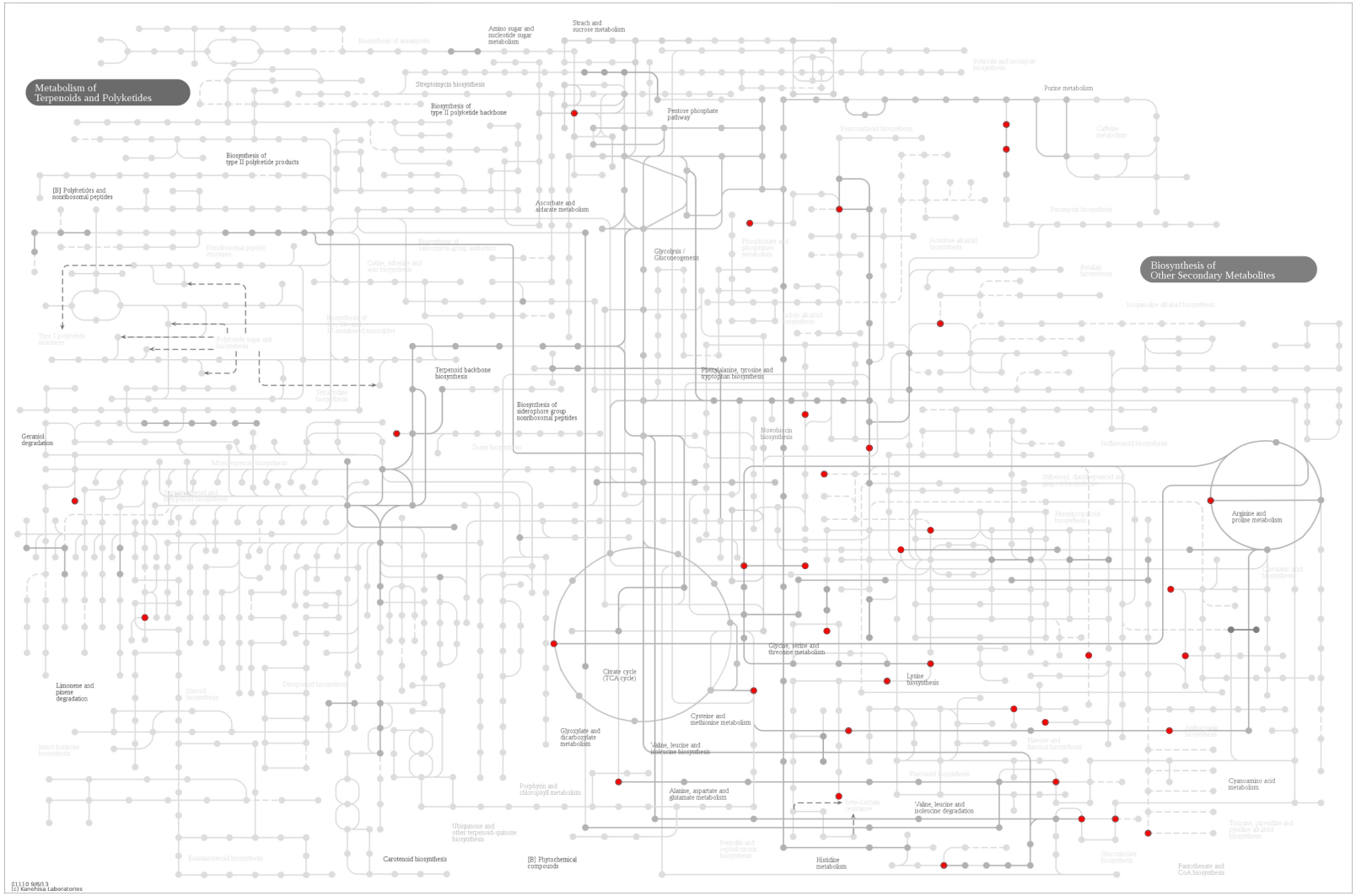


Figure 20(b): *The 31 compounds as detected in Wild type strain grown on Avicel media formulation and mapped to tfu001110, Biosynthesis of Secondary Metabolites. The grey dots denote the experimentally detected compounds* (Chagoyen,M. and Pazos,F. 2011, Kanehisa,M. and Goto,S. 2000, Kanehisa,M., Goto,S., et al. 2006).

TABLE 5(b): *Compounds detected in Amino acids, carbohydrate and secondary metabolism pathways for the Avicel growth condition.*

KEGG PATHWAY ID	PATHWAY	TOTAL	DETECTED	%	COMPOUNDS
AMINO ACIDS METABOLISM					
tfu00300	Lysine biosynthesis	32	9	28.1%	C04421 C03340 C00449 C00049 C12986 C00047 C03871 C00322 C01251
tfu00250	Alanine, aspartate and glutamate metabolism	24	6	25.0%	C00169 C00152 C00049 C00940 C00025 C00122
tfu00330	Arginine and proline metabolism	82	14	17.1%	C03440 C00049 C00122 C00624 C01043 C00025 C18174 C00169 C00327 C00763 C00148 C01250 C00431 C03415
tfu00310	Lysine degradation	47	7	14.9%	C00739 C03656 C03955 C00431 C00322 C00047 C00449
tfu00290	Valine, leucine and isoleucine biosynthesis	28	4	14.3%	C00407 C00188 C00123 C00183
tfu00360	Phenylalanine metabolism	46	6	13.0%	C00811 C05853 C00122 C00166 C02137 C02505
tfu00260	Glycine, serine and threonine metabolism	49	6	12.2%	C00576 C00049 C03283 C00188 C00078 C06231
tfu00280	Valine, leucine and isoleucine degradation	41	4	9.8%	C00183 C00407 C00068 C00123
tfu00340	Histidine metabolism	44	4	9.1%	C00025 C00049 C05575 C05131
tfu00730	Thiamine metabolism	26	2	7.7%	C04327 C00068
tfu00400	Phenylalanine, tyrosine and tryptophan biosynthesis	27	2	7.4%	C00166 C00078
tfu00350	Tyrosine metabolism	76	4	5.3%	C00122 C00483 C17938 C01693
tfu00380	Tryptophan metabolism	81	3	3.7%	C00078 C00322 C05837
tfu00270	Cysteine and methionine metabolism	56	2	3.6%	C00049 C00170
tfu00450	Selenoamino acid metabolism	30	1	3.3%	C05699
CARBOHYDRATE METABOLISM					
tfu00640	Propanoate metabolism	36	5	13.9%	C00183 C00207 C02876 C00894 C05985
tfu00620	Pyruvate metabolism	32	4	12.5%	C03981 C00068 C01251 C03248
tfu00650	Butanoate metabolism	40	4	10.0%	C00025 C01384 C00122 C00068
tfu00020	Citrate cycle (TCA cycle)	20	2	10.0%	C00122 C00068
tfu00660	C5-Branched dibasic acid metabolism	32	2	6.3%	C00025 C02876
tfu00520	Amino sugar and nucleotide sugar metabolism	87	5	5.7%	C00140 C00645 C00029 C00043 C00203
tfu00052	Galactose metabolism	41	2	4.9%	C00029 C00116
tfu00040	Pentose and glucuronate interconversions	53	2	3.8%	C00029 C00085

tfu00010	Glycolysis / Gluconeogenesis	31	1	3.2%	C00068
tfu00030	Pentose phosphate pathway	32	1	3.1%	C01151
tfu00630	Glyoxylate and dicarboxylate metabolism	44	1	2.3%	C00975
tfu00053	Ascorbate and aldarate metabolism	47	1	2.1%	C00029
tfu00500	Starch and sucrose metabolism	50	1	2.0%	C00029
SECONDARY METABOLISM					
tfu00906	Carotenoid biosynthesis	98	5	5.1%	C08583 C08585 C08606 C16280 C15892
tfu00900	Terpenoid backbone biosynthesis	33	1	3.0%	C16521
tfu00401	Novobiocin biosynthesis	37	2	5.4%	C12469 C00148

3.3.2.3. Comparing Cellobiose Vs Avicel

827 unique compounds were detected in both Cellobiose and Avicel growth strains. 301 of were found in both conditions, 366 were unique to Cellobiose and 160 were unique to Avicel growth condition. The pathway association of the compounds in these two conditions has been summarized in Figure 21.

MBRole when maps the compound to the metabolic pathways as per the precompiled compounds list it assigns a score of significance based on the background compounds known for each pathway versus the mapped list. Table 6 summarizes the significantly different pathway along with their compounds that were uniquely detected in each.

Some of the interesting compounds besides the above list that were unique to Cellobiose media conditions were Dihydrostreptomycin 6-phosphate (C01221) from Streptomycin Biosynthesis pathway, Hexadecanoic acid (C00249) of Fatty acid metabolism, Lipoyl-AMP (C16238) of Lipoic Acid and D-Alanine (C00041).

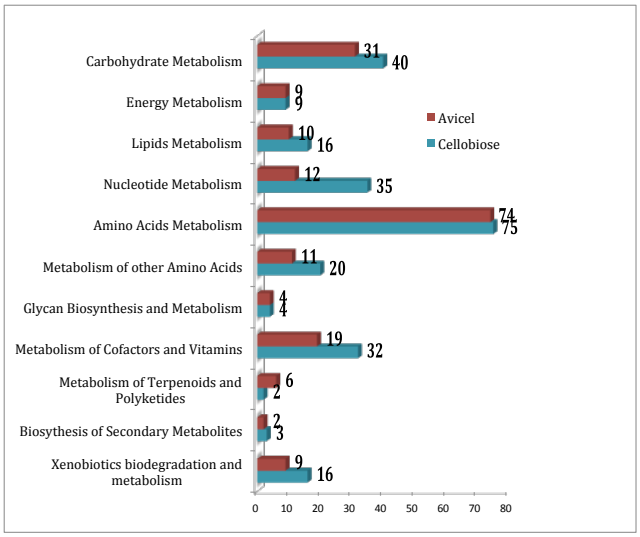


Figure 21: *Distribution of compounds under the metabolic pathways as detected in Cellobiose (blue) and Avicel (red) media condition formulation*

Table 6: *The significantly different pathway detected due to the unique compounds detected in each of the conditions*

KEGG PATHWAY ID	PATHWAY	DETECTED	COMPOUNDS
Unique to Cellobiose			
tfu00230	Purine metabolism	15	C00362 C04376 C00360 C06196 C00130 C00035 C00242 C00655 C00330 C00262 C05515 C03794 C00212 C00048 C00385
tfu00240	Pyrimidine metabolism	8	C00364 C00099 C00112 C00015 C00380 C00055 C02376 C03997
tfu00270	Cysteine and methionine metabolism	7	C00109 C02989 C00041 C00073 C01005 C00021 C01180
tfu00330	Arginine and proline metabolism	6	C00791 C00555 C05931 C00062 C00437 C00048
tfu00450	Selenoamino acid metabolism	5	C05696 C05692 C00041 C05335 C05708
tfu00770	Pantothenate and CoA biosynthesis	4	C00099 C01088 C03492 C00864
tfu00740	Riboflavin metabolism	3	C05775 C00472 C00061
tfu00190	Oxidative phosphorylation	3	C00004 C00061 C00003
Unique to Avicel			
tfu00300	Lysine biosynthesis	5	C00047 C00322 C03340 C00049 C01251
tfu00330	Arginine and proline metabolism	5	C03440 C01043 C00049 C18174 C00327
tfu00906	Carotenoid biosynthesis	5	C16280 C08585 C08606 C15892 C08583
tfu00260	Glycine, serine and threonine metabolism	5	C03283 C06231 C00049 C00188 C00576
tfu02010	ABC transporters	4	C00049 C00047 C03557 C00188
tfu00970	Aminoacyl-tRNA biosynthesis	4	C00188 C00049 C00047 C00152
tfu00340	Histidine metabolism	3	C05575 C05131 C00049
tfu00250	Alanine, aspartate and glutamate metabolism	3	C00152 C00940 C00049
tfu00310	Lysine degradation	3	C00322 C00047 C00739
tfu00910	Nitrogen metabolism	2	C00152 C00049
tfu00641	3-Chloroacrylic acid degradation	2	C16348 C06613

Table 14: *COG classification based Secondary metabolites associated proteins*

PATHWAY	LOCUS	DESCRIPTION	CB2D	iTRAQ	CB-1D	AV-1D
Cytochrome P450	Tfu_1257	Cytochrome P450 monooxygenase	22.31		18.095	18.075
Cytochrome P450	Tfu_1748	Cytochrome P450-family protein	24.29	0.744	21.5	12.29
Cytochrome P450	Tfu_2976	Cytochrome P450-family protein	21.48	0.739	17.5	17.73
Cytochrome P450	Tfu_2802	Putative cytochrome P450	25.75	1.258	22.67	22.065
Cytochrome P450	Tfu_1747	Putative cytochrome P450	21.61	0.961	16.915	13.995
Cytochrome P450	Tfu_2975	Putative cytochrome P450	19.36	0.862	13.71	15.34
Cytochrome P450	Tfu_2803	Putative cytochrome P450-family protein	21.3	0.87	15.35	17.1
Cytochrome P450	Tfu_2798	Putative DNA-binding protein	15.73			
Carbohydrate Metabolism	Tfu_1298	2-deoxy-D-gluconate 3-dehydrogenase	17.6		13.51	15.16
Ketone Bodies/Butanoate Metabolism	Tfu_0081	3-hydroxybutyrate dehydrogenase	23.95	1.187	11.125	21.285
Fatty Acid Degradation	Tfu_2158	Putative long-chain-fatty-acid-CoA ligase	23.82	0.959	2.53	22.27
Fatty Acids Degradation, Biotin Metabolism	Tfu_1682	3-ketoacyl-(acyl-carrier-protein) reductase	2.33		15.61	16.635
Fatty Acids Degradation, Biotin Metabolism	Tfu_1843	3-oxoacyl-(acyl-carrier-protein) reductase	22.77	1.118	18.5	16.47
Fatty Acids Degradation, Biotin Metabolism	Tfu_1841	Putative 3-ketoacyl-CoA reductase	21.31		16.025	17.51
Fatty Acids Degradation, Biotin Metabolism	Tfu_1976	Putative 3-oxoacyl-ACP synthase II	22.79	0.718	19.515	18.295
Nicotinate & Nicotinamide Metabolism	Tfu_2374	Putative pyrazinamidase / nicotinamidase	19.52			14.58
Secondary Metabolites	Tfu_1300	DitJ-like CoA ligase (AMP forming),(diterpenoid metabolism)	2.78			15.97
Secondary Metabolites	Tfu_1231	Modular polyketide synthase	14.31			
Shikimate Pathway	Tfu_1868	Isochorismatase	16.81			
Shikimate Pathway	Tfu_1872	Isochorismate synthase	17.85			
Siderophores Group Biosynthesis	Tfu_1873	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	14.76			
Siderophores Group Biosynthesis	Tfu_1871	2,3-dihydroxybenzoate-AMP ligase	21.25	0.737	14.555	
Histidine Metabolism	Tfu_0821	Imidazolonepropionase	17.2			
Tyrosine Metabolism	Tfu_0621	5-carboxymethyl-2-hydroxymuconate delta-isomerase	2.92	0.813	16.57	15.3
Tyrosine Metabolism	Tfu_1869	Putative peptide monooxygenase	18.53			
Others	Tfu_0275	Putative short chain dehydrogenase	23.3		18.45	19.325
Others	Tfu_1242	Short chain dehydrogenase	18.48			
Others	Tfu_1279	Short chain dehydrogenase	16.87			
Others	Tfu_1975	Acyl carrier protein	23.95	0.341	12.07	2.45
Others	Tfu_1866	Amino acid adenylation	19.3		13.74	

Others	Tfu_1267	FrnE protein	16.17	0.636		
Others	Tfu_0080	GAF domain protein	21.11		16.69	18.915
Others	Tfu_0691	Helix-turn-helix, Fis-type	18.97			
Others	Tfu_1795	Helix-turn-helix, Fis-type	14.89			
Others	Tfu_1462	Similar to Acetyl esterase (deacetylase)	21.76	0.85	15.975	16.73
Others	Tfu_1867	Non-ribosomal peptide synthase: Amino acid adenylation	21.64	0.777	16.21	
Others	Tfu_1188	Phenylacetic acid degradation-related protein	2.42	1.83	15.85	
Others	Tfu_2707	Putative acetoin utilization protein	21.16	1.239	15.75	

5.3.4. Metabolites Detected

The global metabolites detection was done for the general metabolites and mapped to the metabolic pathway of *T. fusca* using MBRole. As per the KEGG's compilation of tfu01110 Biosynthesis of Secondary Metabolites there were total of 1038 compounds in list. This compilation includes the intermediates and the final products. When metabolomics data of the wild type strain grown on Cellobiose and Avicel was mapped to this list only 63 hits for obtained which included both intermediates and 21 natural products. To find of the missing nodes of the pre-compiled tfu01110 list the metabolomics data was mapped to the list of all the natural products (total 2480). This gave an interesting list of 88 secondary metabolites (shown in Figure 33). This breaks down into a total of alkaloids (41), terpenoids (25), phenylpropanoids (8), amino acids related compounds (8), polyketides (4), flavonoids (4) and fatty acids related compounds (2). The details of these subcategories can be seen in Table 15. The list of compounds can be obtained from Appendix G.

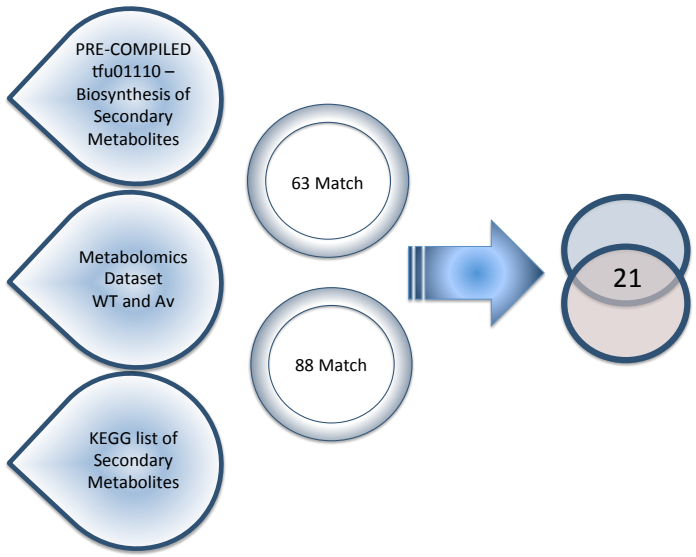


Figure 33: *Comparison of match with pre-compiles list of T. fusca computationally compiled by KEGG*

One of the most interesting finding from this level of data was detection of hemiterpenoid – Isoprene. Past study have shown that both gram positive and gram negative bacterial possess the capability to produce Isoprene (Kuzma,J., Nemecek-Marshall,M., et al. 1995). A comparative study between *Bacillus sp.*, *Micrococcus, Rhodococcus, E. coli, Pseudomonas* and *Agrobacterium* was conducted and concluded that Bacillus ranks highest among all in the production of Isoprene. The study illustrated the capability of gram-positive bacteria to produce this industrially significant product - Isoprene. In our metabolomics analysis for *T. fusca* we propose that this actinomycete also possess similar characteristics. The biological role of this compound as defined by Sharkey et al in 2007 (Sharkey,T.D., Wiberley,A.E., et al. 2008) as protection against the temperature stress (~40°C). This might be useful to understand the mechanism of thermostability in *T. fusca.*

Table 15: *Distribution of Secondary Metabolites as detected in each of the growth conditions*

	BOTH	Cb	Av	TOTAL
Alkaloids	21	17	3	41
Alkaloids derived by amination reactions	6	1	1	8
Alkaloids derived from lysine	2	4		6
Alkaloids derived from nicotinic acid	2	2		4
Alkaloids derived from ornithine	7	1	1	9
Alkaloids derived from tryptophan and anthranilic acid	1	3	1	5
Alkaloids derived from tyrosine	3	3		6
Others		3		3
Amino acid related compounds	1	2	1	4
Betalains	1	2	1	4
Fatty acids related compounds		2		2
Fatty acids		2		2
Flavonoids		1	1	2
Flavonoids		1	1	2
Phenylpropanoids	3	4	1	8
Coumarins	1	2	1	4

Lignans	1	2		3
Monolignols	1			1
Polyketides	4			4
Others	2			2
Pyrones	2			2
Terpenoids	6	12	7	25
Carotenoids and apocarotenoids			3	3
Diterpenoids (C20)		4	1	5
Hemiterpenoids (C5)	1			1
Monoterpenoids (C10)	2	2	1	5
Sesquiterpenoids (C15)	3	3	1	7
Steroids		3		3
Triterpenoids (C30)			1	1
Others	2			2
Others	1			1
Tannins and galloyl derivatives	1			1
Grand Total	37	38	13	88

5.4. CONCLUSIONS

To summarize the finding of this case study it was observed that TBB pathway was alternating between both mevalonate and non-mevalonate pathways. Besides providing the evidence for the complete TBB within the strain, alternating between the mevalonate and non-mevalonate pathway it was also concluded that *T. fusca* could be cultured for the production of an important industrial product. Isoprene is the monomeric unit for the huge family of Isoprenoids, thus hold importance in pharmaceutical industry, perfumes, incense, flavoring, spices, and varnishes.

T. fusca was found to be a biofuel producing strain after the genetic modification protocol for this strain was established by Deng & Fong. With this systems level characterization of secondary metabolites, it can be suggested as a

highly useful, robust and inexpensive strain for industrial application. However, this opens an arena for the scale up and optimization study to successfully launch this strain in industrially significant microbes.

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Appendix - A - Tfu_v1 - SEED Model Without Constraints

ID	Flux	Pathways	ECs	Reversible	Name	Equation	SEED ID
R_rxn00986	0	.	.	TRUE	PropanoateCoA ligase (	[c] : C00002 + C00080 + C00163 <==> C00013 + C05983	rxn00986
R_SRC_C00458#_c	0.29243	SourceFlux	.	FALSE	. source flux	C00458#[b] --> C00458#[c]	
R_rxn00985	0	.	.	TRUE	ATPacetate phosphotra	[c] : C00002 + C00080 + C00163 <==> C00008 + C02876	rxn00985
R_ESC_C01936_e	0	EscapeFlux	.	FALSE	. escape flux	C01936[e] --> C01936[b]	
R_rxn03638	0	.	.	FALSE	Acetyl-CoAD-glucosami	[c] : C00024 + C06156 --> C00010 + C00080 + C04501	rxn03638
R_rxn00988	0	.	.	FALSE	AcetoacetateCoA ligase	[c] : C00002 + C00010 + C00080 + C00164 --> C00013 + C00020 + C00332	rxn00988
R_rxn00331	0	.	.	TRUE	(3S)-3-Carboxy-3-hydr	[c] : C04348 <==> C00024 + C00048	rxn00331
R_rxn00330	0	.	.	TRUE	L-Malate glyoxylate-lya	[c] : C00010 + C00080 + C00711 <==> C00001 + C00024 + C00048	rxn00330
R_rxn01352	0	.	.	FALSE	dGTP triphosphohydrol	[c] : C00001 + C00286 --> C00080 + C00330 + C00536	rxn01352
R_rxn01353	0	.	.	TRUE	ATPnucleoside-diphosp	[c] : C00002 + C00361 <==> C00008 + C00286	rxn01353
R_rxn05116	0	.	.	FALSE	rxn05116	[c] : C00080 + C07335 --> C00011 + C11638	rxn05116
R_o2t	0	Transport Databas	.	FALSE	o2transport	C00007[e] --> C00007[c]	rxn05468
R_rxn00337	0	.	.	TRUE	ATPL-aspartate 4-phos	[c] : C00002 + C00049 + C00080 <==> C00008 + C03082	rxn00337
R_rxn03908	0	.	.	TRUE	ATP 4-(Cytidine 5'-diph	[c] : C00002 + C11435 <==> C00008 + C11436	rxn03908
R_rxn01358	-1000	.	.	TRUE	inosineorthophosphate	[c] : C00009 + C00080 + C00294 <==> C00262 + C00620	rxn01358
R_rxn00338	0	.	.	FALSE	L-aspartate oxidase	[c] : C00007 + C00049 --> C00027 + C00080 + C05840	rxn00338
R_rxn03904	0	.	.	TRUE	UDPMurAc(oyl-L-Ala-D	[c] : C17556 + C04882 <==> C00105 + C05897	rxn03904
R_rxn03903	0	.	.	TRUE	UDPMurAc(oyl-L-Ala-D	[c] : C17556 + C04702 <==> C00105 + C04851	rxn03903
R_rxn03901	0	.	.	FALSE	Undecaprenyl-diphosph	[c] : C00001 + C04574 --> C00009 + C00080 + C17556	rxn03901
R_rxn08818	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15363 <==> C00080 + C00623 + C06424	rxn08818
R_rxn08819	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15362 <==> C00080 + C00623 + cpd15298	rxn08819
R_rxn05459	0	.	.	TRUE	stearyl-ACP[acyl-carrie	[c] : C00010 + cpd11573 <==> C00412 + C00229	rxn05459
R_rxn05458	0	.	.	TRUE	hexadecanoyl-ACP[acyl	[c] : C00010 + C05764 <==> C00154 + C00229	rxn05458
R_rxn00506	0	.	.	FALSE	AcetaldehydeNAD+ oxi	[c] : C00001 + C00003 + C00084 --> C00004 + C00033 + 2 C00080	rxn00506
R_rxn05024	0	.	.	FALSE	rxn05024	[c] : C00080 + C03160 --> C00001 + C15547	rxn05024
R_mant	0	Transport Databas	.	FALSE	mantransport	C00936[e] --> C00936[c]	rxn12997
R_rxn00973	-1000	.	.	TRUE	citrate hydro-lyase	[c] : C00158 <==> C00311	rxn00973
R_rxn08811	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15319 <==> C00080 + C03274 + C06424	rxn08811
R_rxn08812	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15320 <==> C00080 + C03274 + cpd15298	rxn08812
R_rxn08813	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15321 <==> C00080 + C00249 + C03274	rxn08813
R_rxn05457	0	.	.	TRUE	tetradecanoyl-ACP[acyl	[c] : C00010 + C05761 <==> C02593 + C00229	rxn05457
R_rxn05456	0	.	.	TRUE	14-methyl-pentadecanc	[c] : C00010 + cpd11569 <==> cpd11441 + C00229	rxn05456
R_rxn08816	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15324 <==> C00080 + C03274 + cpd15269	rxn08816
R_rxn05454	0	.	.	TRUE	15-methyl-hexa-decanc	[c] : C00010 + cpd11544 <==> cpd11432 + C00229	rxn05454
R_rxn00872	-1000	.	.	TRUE	Butanoyl-CoAoxygen 2-	[c] : C00016 + C00136 <==> C00877 + C01352	rxn00872
R_rxn10264	0	.	.	TRUE	isohexadecanoyl-CDPdi	[c] : C00623 + cpd15688 <==> C00055 + cpd15721	rxn10264
R_rxn10262	0	.	.	TRUE	isopentadecanoyl-CDPd	[c] : C00623 + cpd15686 <==> C00055 + cpd15719	rxn10262
R_rxn10263	0	.	.	TRUE	anteisopentadecanoyl-(	[c] : C00623 + cpd15687 <==> C00055 + cpd15720	rxn10263
R_rxn10260	0	.	.	TRUE	anteisoheptadecanoyl-(	[c] : C00623 + cpd15684 <==> C00055 + cpd15717	rxn10260
R_rxn10261	0	.	.	TRUE	isotetradecanoyl-CDPdi	[c] : C00623 + cpd15685 <==> C00055 + cpd15718	rxn10261
R_rxn10341	0	.	.	TRUE	anteisopentadecanoyl-c	[c] : 2 cpd15726 <==> C00116 + cpd15798	rxn10341
R_rxn10340	0	.	.	TRUE	isopentadecanoyl-cardi	[c] : 2 cpd15725 <==> C00116 + cpd15797	rxn10340

R_SRC_C00243_e	0	SourceFlux	.	FALSE	. source flux	C00243[b] --> C00243[e]	
R_rxn10342	0	.	.	TRUE	isohexadecanoyl-cardio	[c] : 2 cpd15727 <==> C00116 + cpd15799	rxn10342
R_SRC_C00007_e	0	SourceFlux	.	FALSE	. source flux	C00007[b] --> C00007[e]	
R_rxn02911	0	.	.	TRUE	(S)-3-Hydroxydodecano	[c] : C05262 <==> C00001 + C03221	rxn02911
R_rxn08976	0	.	.	FALSE	NADH dehydrogenase (	[c] : C00004 + C00080 + C05818 --> C00003 + C19847	rxn08976
R_rxn03446	0	.	.	FALSE	O-Phospho-4-hydroxy-I	[c] : C00001 + C06055 --> C00009 + C00080 + C06056	rxn03446
R_rxn01791	0	.	.	FALSE	(R)-Pantoatebeta-alanir	[c] : C00002 + C00099 + C00522 --> C00013 + C00020 + C00864	rxn01791
R_rxn03445	0	.	.	TRUE	O-Phospho-4-hydroxy-I	[c] : C00026 + C06055 <==> C00025 + C06054	rxn03445
R_rxn08975	0	.	.	FALSE	NADH dehydrogenase (	[c] : C00004 + C00080 + C17569 --> C00003 + C00390	rxn08975
R_rxn12851	0	.	.	FALSE	Gly-Try ABC transporte	C00001[c] + C00002[c] + cpd15606[e] --> C00008[c] + C00009[c] + cpd156	rxn12851
R_rxn01799	0	.	.	TRUE	deoxyuridineorthophos	[c] : C00009 + C00080 + C00526 <==> C00106 + C00672	rxn01799
R_rxn05735	0	.	.	TRUE	aldehyde dehydrogenas	[c] : C00001 + C00003 + C06735 <==> C00004 + C00037 + 2 C00080	rxn05735
R_rxn08711	0	.	.	TRUE	heptosyltransferase II (	[c] : C06398 + cpd15485 <==> C00008 + cpd15484	rxn08711
R_rxn02916	0	.	.	FALSE	6-Amino-2-oxohexanoa	[c] : C03239 --> C00001 + C00080 + C04092	rxn02916
R_urit	0	Transport Databas	.	FALSE	uritransport	C00299[e] --> C00299[c]	rxn10987
R_SRC_C11458_e	0	SourceFlux	.	FALSE	. source flux	C11458[b] --> C11458[e]	
R_rxn08820	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15355 <==> C00080 + C00623 + C00249	rxn08820
R_rxn12636	0	.	.	TRUE	aminopeptidase	[c] : C00001 + C00080 + cpd11590 <==> C00041 + C00073	rxn12636
R_rxn01740	0	.	.	TRUE	ShikimateNADP+ 5-oxid	[c] : C00006 + C00493 <==> C00005 + C00080 + C02637	rxn01740
R_SRC_gly_DASH_gl	0	SourceFlux	.	FALSE	. source flux	gly-glu-L[b] --> gly-glu-L[e]	
R_rxn01226	-1000	.	.	TRUE	Guanosine ribohydrolas	[c] : C00001 + C00387 <==> C00121 + C00242	rxn01226
R_biomass_target	24.8941	BiomassObjective	.	FALSE	BiomassRxn	[c] : 34.7964804614 C00001# + 40.1701382876 C00002# + 0.00780937124549 C000	
R_rxn04384	0	.	.	TRUE	adenosylcobyric acid(R	[c] : C00002 + C04122 + C06507 <==> C00008 + C00009 + 2 C00080 + C06	rxn04384
R_rxn04385	0	.	.	FALSE	L-threonine-O-3-phosp	[c] : C00080 + C12147 --> C00011 + C04122	rxn04385
R_rxn05239	0	.	.	FALSE	adenosine 3',5'-bisphos	[c] : C00053 + C00342 --> C00054 + C00094 + C00343	rxn05239
R_rxn00022	0	.	.	TRUE	alpha-D-Glucoside gluc	[c] : C00001 + C00208 <==> 2 C00267	rxn00022
R_rxn00612	1000	.	.	TRUE	sn-Glycerol-3-phosphat	[c] : C00006 + C00623 <==> C00005 + C00080 + C00111	rxn00612
R_rxn09203	0	.	.	TRUE	Phosphatidylserine dec	[c] : 2 C00080 + cpd15558 <==> C00011 + cpd15534	rxn09203
R_rxn00029	0	.	.	FALSE	5-Aminolevulinate hydr	[c] : 2 C00430 --> 2 C00001 + C00080 + C00931	rxn00029
R_SRC_C00305_e	0	SourceFlux	.	FALSE	. source flux	C00305[b] --> C00305[e]	
R_rxn03974	0	.	.	FALSE	FMNH2NAD+ oxidoredu	[c] : C00004 + C00061 + C00080 --> C00003 + C01847	rxn03974
R_rxn03975	0	.	.	FALSE	FMNH2NADP+ oxidore	[c] : C00005 + C00061 + C00080 --> C00006 + C01847	rxn03975
R_rxn05336	0	.	.	TRUE	(3R)-3-Hydroxypalmito	[c] : C00006 + C04633 <==> C00005 + C00080 + C05762	rxn05336
R_rxn05337	0	.	.	TRUE	(3R)-3-Hydroxyhexano	[c] : C00006 + C05747 <==> C00005 + C00080 + C05746	rxn05337
R_zymstt	0	Transport Databas	.	FALSE	zymsttransport	C05437[e] --> C05437[c]	rxn09649
R_folt	0	Transport Databas	.	FALSE	foltransport	C00504[e] --> C00504[c]	.
R_rxn02320	0	.	.	TRUE	5-Amino-2-oxopentano	[c] : C00026 + C01100 <==> C00025 + C01267	rxn02320
R_ptrct	0	Transport Databas	.	FALSE	ptrctransport	C00134[e] --> C00134[c]	.
R_rxn05338	0	.	.	TRUE	(3R)-3-Hydroxydecano	[c] : C00006 + C04619 <==> C00005 + C00080 + C05753	rxn05338
R_rxn05339	0	.	.	TRUE	(3R)-3-Hydroxybutano	[c] : C00006 + C04618 <==> C00005 + C00080 + C05744	rxn05339
R_rxn09562	1000	.	.	TRUE	guanylate kinase (GMP(	[c] : C00131 + C00144 <==> C00035 + C00206	rxn09562
R_SRC_C00078#_c	1.37309	SourceFlux	.	FALSE	. source flux	C00078#[b] --> C00078#[c]	
R_rxn01069	0	.	.	FALSE	O-Phospho-L-homoseri	[c] : C00001 + C01102 --> C00009 + C00080 + C00188	rxn01069
R_rxn03909	0	.	.	FALSE	1-Deoxy-D-xylulose-5-p	[c] : C00022 + C00080 + C00118 --> C00011 + C11437	rxn03909
R_ESC_C19331_e	0	EscapeFlux	.	FALSE	. escape flux	C19331[e] --> C19331[b]	
R_ESC_C01419_e	0	EscapeFlux	.	FALSE	. escape flux	C01419[e] --> C01419[b]	
R_rxn09200	0	.	.	TRUE	Phosphatidylserine dec	[c] : 2 C00080 + cpd15555 <==> C00011 + cpd15531	rxn09200

R_rxn02889	0	.	.	TRUE	3-Methylcrotonoyl-CoA	[c] : C00002 + C01353 + C03069 <==> C00008 + C00009 + C00080 + C0323	rxn02889
R_lac_Dt	0	Transport Databas	.	TRUE	lac-Dtransport	C00256[c] <==> C00256[e]	.
R_rxn00336	0	.	.	TRUE	Isocitrate glyoxylate-lya	[c] : C00311 <==> C00042 + C00048	rxn00336
R_SRC_C00076#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00076#[b] --> C00076#[c]	
R_ca2t	0	Transport Databas	.	FALSE	ca2transport	C00076[e] --> C00076[c]	.
R_pro_Lt	0	Transport Databas	.	FALSE	pro-Ltransport	C00148[e] --> C00148[c]	rxn10945
R_mn2t	0	Transport Databas	.	FALSE	mn2transport	C00034[e] --> C00034[c]	.
R_rxn03907	0	.	.	TRUE	CTP 2-C-Methyl-D-eryth	[c] : C00063 + C11434 <==> C00013 + C11435	rxn03907
R_rxn01974	0	.	.	TRUE	LL-2,6-Diaminoheptane	[c] : C00666 <==> C00680	rxn01974
R_SRC_C00038#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00038#[b] --> C00038#[c]	
R_ESC_C00719_e	0	EscapeFlux	.	FALSE	. escape flux	C00719[e] --> C00719[b]	
R_retinolt	0	Transport Databas	.	FALSE	retinoltransport	C00473[e] --> C00473[c]	.
R_SRC_Gly_DASH_L	0	SourceFlux	.	FALSE	. source flux	Gly-Leu[b] --> Gly-Leu[e]	
R_rxn08291	-1000	.	.	TRUE	D-Amino acid dehydrog	[c] : C00001 + C00016 + C00133 <==> C01342 + C00022 + C01352	rxn08291
R_rxn07589	0	.	.	TRUE	rxn07589	[c] : C00019 + C16244 <==> C00011 + C00021 + C11545	rxn07589
R_rxn07588	0	.	.	TRUE	rxn07588	[c] : C00019 + C11543 <==> C00021 + C00080 + C16244	rxn07588
R_rxn00159	0	.	.	FALSE	(S)-MalateNADP+ oxido	[c] : C00003 + C00711 --> C00004 + C00011 + C00022	rxn00159
R_rxn00650	0	.	.	TRUE	membrane alanyl amino	[c] : C00001 + C01419 <==> C00037 + C00097	rxn00650
R_ESC_gly_DASH_as	0	EscapeFlux	.	FALSE	. escape flux	gly-asn-L[e] --> gly-asn-L[b]	
R_rxn00151	-500	.	.	TRUE	ATPpyruvate,orthophos	[c] : C00002 + C00009 + C00022 + C00080 <==> C00013 + C00020 + C0007	rxn00151
R_ESC_C02989_e	0	EscapeFlux	.	FALSE	. escape flux	C02989[e] --> C02989[b]	
R_rxn08841	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15339 <==> C00080 + C00249 + C01233	rxn08841
R_avite1t	0	Transport Databas	.	FALSE	avite1transport	avite1[e] --> avite1[c]	.
R_ESC_Ala_DASH_H	0	EscapeFlux	.	FALSE	. escape flux	Ala-His[e] --> Ala-His[b]	
R_rxn05939	1000	.	.	TRUE	2-oxoglutarate synthase	[c] : C00011 + C00080 + C00091 + C00138 <==> C00010 + C00026 + C0013	rxn05939
R_rxn05248	0	.	.	FALSE	FACOAL150(anteiso)	[c] : C00002 + C00010 + C00080 + cpd11438 --> C00013 + C00020 + cpd11	rxn05248
R_rxn05249	0	.	.	FALSE	FACOAL150(ISO)	[c] : C00002 + C00010 + C00080 + cpd11436 --> C00013 + C00020 + cpd11	rxn05249
R_rxn05527	0	.	.	TRUE	cytosine transport in vi	C00080[e] + C00380[e] <==> C00080[c] + C00380[c]	rxn05527
R_succt	1000	Transport Databas	.	TRUE	succtransport	C00042[c] <==> C00042[e]	.
R_rxn05466	-1000	.	.	TRUE	Ammonia transport via	C01342[e] <==> C01342[c]	rxn05466
R_SRC_C00698#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00698#[b] --> C00698#[c]	
R_SRC_C00061_e	0	SourceFlux	.	FALSE	. source flux	C00061[b] --> C00061[e]	
R_rxn05247	0	.	.	FALSE	FACOAL140(ISO)	[c] : C00002 + C00010 + C00080 + C00638 --> C00013 + C00020 + cpd1143	rxn05247
R_ESC_C00183_e	0	EscapeFlux	.	FALSE	. escape flux	C00183[e] --> C00183[b]	
R_rxn05467	-1000	.	.	TRUE	CO2 transport via diffus	C00011[e] <==> C00011[c]	rxn05467
R_rxn10094	0	.	.	FALSE	S-adenosylmethione2-d	[c] : C00019 + C05818 --> C00021 + C00080 + C00828	rxn10094
R_rxn00931	-1000	.	.	TRUE	L-ProlineNADP+ 5-oxid	[c] : C00006 + C00148 <==> C00005 + C00080 + C03912	rxn00931
R_rxn05464	0	.	.	FALSE	trans-Octodec-2-enoyl-	[c] : C00004 + C00080 + cpd11572 --> C00003 + cpd11573	rxn05464
R_rxn00503	0	.	.	TRUE	L-1-Pyrroline-5-carbox	[c] : 2 C00001 + C00003 + C03912 <==> C00004 + C00025 + C00080	rxn00503
R_rxn11544	0	.	.	TRUE	Hydrogenobyrinate = H	[c] : C00001 + 2 C00002 + 2 C00064 + C06399 <==> 2 C00008 + C00013 + 2	rxn11544
R_rxn11545	0	.	.	TRUE	Precorrin 3A + Oxygen	[c] : 0.5 C00007 + C05772 <==> C06406	rxn11545
R_lys_Lt	0	Transport Databas	.	FALSE	lys-Ltransport	C00047[e] --> C00047[c]	rxn10834
R_rxn08844	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15342 <==> C00080 + C01233 + cpd15269	rxn08844
R_ESC_C00042_e	1000	EscapeFlux	.	FALSE	. escape flux	C00042[e] --> C00042[b]	
R_rxn05957	0	.	.	TRUE	O-Succinyl-L-homoserin	[c] : C00297 + C01118 <==> C00042 + C00080 + C05330	rxn05957
R_rxn05426	0	.	.	TRUE	12-methyl-3-oxo-tridec	[c] : C00005 + C00080 + cpd11562 <==> C00006 + cpd11563	rxn05426
R_rxn00501	0	.	.	TRUE	3-OxopropanoateNAD+	[c] : C00003 + C00010 + C00222 <==> C00004 + C00011 + C00024	rxn00501

R_ESC_C00009#_c	995.57	EscapeFlux	.	FALSE	. escape flux	C00009#[c] --> C00009#[b]	
R_rxn00737	0	.	.	FALSE	L-threonine ammonia-l	[c] : C00188 --> C01342 + C00109	rxn00737
R_rxn03892	0	.	.	TRUE	PPTT	[c] : C00129 + C04217 <==> C00013 + C01230	rxn03892
R_rxn08849	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15347 <==> C00080 + C03274 + cpd15237	rxn08849
R_SRC_ala_DASH_L_	0	SourceFlux	.	FALSE	. source flux	ala-L-glu-L[b] --> ala-L-glu-L[e]	
R_SRC_C00059#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00059#[b] --> C00059#[c]	
R_rxn01673	0	.	.	TRUE	ATPnucleoside-diphosp	[c] : C00002 + C00705 <==> C00008 + C00458	rxn01673
R_rxn01672	0	.	.	FALSE	dCTP aminohydrolase	[c] : C00001 + C00080 + C00458 --> C01342 + C00460	rxn01672
R_rxn10232	0	.	.	TRUE	isoheptadecanoyl-phos	[c] : 2 C00080 + cpd15689 <==> C00011 + cpd15695	rxn10232
R_ESC_C00120_e	0	EscapeFlux	.	FALSE	. escape flux	C00120[e] --> C00120[b]	
R_SRC_C00286#_c	0.29243	SourceFlux	.	FALSE	. source flux	C00286#[b] --> C00286#[c]	
R_rxn01678	1000	.	.	TRUE	ATPnucleoside-diphosp	[c] : C00002 + C01346 <==> C00008 + C00460	rxn01678
R_rxn08527	1000	.	.	TRUE	fumarate reductase	[c] : C00122 + C05819 <==> C00042 + C00828	rxn08527
R_rxn09208	0	.	.	FALSE	Phosphatidylserine syn	[c] : C00716 + cpd15419 --> C00055 + C00080 + cpd15555	rxn09208
R_rxn02342	0	.	.	TRUE	2-(alpha-Hydroxyethyl)	[c] : C15972 + C05125 <==> C00068 + C16255	rxn02342
R_rxn08810	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15318 <==> C00080 + C02679 + C03274	rxn08810
R_SRC_met_DASH_l	0	SourceFlux	.	FALSE	. source flux	met-L-ala-L[b] --> met-L-ala-L[e]	
R_rxn02341	0	.	.	FALSE	N-[(R)-4'-Phosphopant	[c] : C00080 + C04352 --> C00011 + C01134	rxn02341
R_SRC_ala_DASH_L_	0	SourceFlux	.	FALSE	. source flux	ala-L-asp-L[b] --> ala-L-asp-L[e]	
R_rxn08669	0	.	.	TRUE	Glycerophosphodiester	[c] : C00001 + C03274 <==> C00623 + C00116	rxn08669
R_SRC_C19331_e	0	SourceFlux	.	FALSE	. source flux	C19331[b] --> C19331[e]	
R_rxn05452	0	.	.	TRUE	14-methyl-hexa-decano	[c] : C00010 + cpd11519 <==> cpd11434 + C00229	rxn05452
R_rxn00493	0	.	.	TRUE	L-Phenylalanine2-oxog	[c] : C00026 + C00079 <==> C00025 + C00166	rxn00493
R_rxn00615	1000	.	.	TRUE	ATPglycerol 3-phospho	[c] : C00002 + C00116 <==> C00008 + C00623	rxn00615
R_rxn05451	0	.	.	TRUE	12-methyl-tetra-decano	[c] : C00010 + cpd11515 <==> cpd11439 + C00229	rxn05451
R_SRC_C00114_e	0	SourceFlux	.	FALSE	. source flux	C00114[b] --> C00114[e]	
R_rxn00953	0	.	.	TRUE	L-Serine hydro-lyase (a	[c] : C00716 + C05330 <==> C00001 + C00542	rxn00953
R_ESC_C15998_e	0	EscapeFlux	.	FALSE	. escape flux	C15998[e] --> C15998[b]	
R_rxn05029	0	.	.	TRUE	ATPcobinamide Cobeta	[c] : C00002 + C05774 <==> C00536 + C06508	rxn05029
R_rxn00379	1000	.	.	TRUE	ATPsulfate adenylyltrar	[c] : C00002 + C00059 + C00080 <==> C00013 + C00224	rxn00379
R_rxn08814	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15322 <==> C00080 + C03274 + cpd15237	rxn08814
R_btnt	0	Transport Databas	.	FALSE	btntransport	C00120[e] --> C00120[c]	.
R_SRC_Ala_DASH_H	0	SourceFlux	.	FALSE	. source flux	Ala-His[b] --> Ala-His[e]	
R_rxn08815	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15323 <==> C00080 + C01530 + C03274	rxn08815
R_lctst	0	Transport Databas	.	FALSE	lctstransport	C00243[e] --> C00243[c]	.
R_rxn00533	0	.	.	TRUE	Acetyl-CoAcarbon-dioxi	[c] : C00002 + C00024 + C01353 <==> C00008 + C00009 + C00080 + C0008	rxn00533
R_rxn05385	0	.	.	TRUE	5-methyl-3-oxo-hexano	[c] : C00005 + C00080 + cpd11521 <==> C00006 + cpd11522	rxn05385
R_rxn05384	0	.	.	FALSE	3-methylbutanoyl-ACPr	[c] : C00080 + C01209 + cpd11520 --> C00011 + C00229 + cpd11521	rxn05384
R_rxn05383	0	.	.	TRUE	3-methylbutanoyl-CoA[	[c] : C02939 + C00229 <==> C00010 + cpd11520	rxn05383
R_rxn05455	0	.	.	TRUE	12-methyl-tridecanoyl-	[c] : C00010 + cpd11565 <==> cpd11435 + C00229	rxn05455
R_rxn00548	0	.	.	FALSE	D-Fructose-6-phosphat	[c] : C00009 + C00080 + C05345 --> C00001 + C00227 + C00279	rxn00548
R_rxn00549	0	.	.	FALSE	D-Fructose-1,6-bisphos	[c] : C00001 + C00354 --> C00009 + C00080 + C05345	rxn00549
R_rxn09211	0	.	.	FALSE	Phosphatidylserine syn	[c] : C00716 + cpd15420 --> C00055 + C00080 + cpd15558	rxn09211
R_rxn00547	-250	.	.	TRUE	ATPD-fructose 6-phosp	[c] : C00002 + C10906 <==> C00008 + C05345	rxn00547
R_rxn05064	0	.	.	TRUE	carbamate hydro-lyase	[c] : 2 C00080 + C01563 <==> C00011 + C01342	rxn05064
R_rxn00545	750	.	.	TRUE	ATPD-fructose-6-phosp	[c] : C00002 + C05345 <==> C00008 + C00354	rxn00545
R_rxn00278	1000	.	.	TRUE	L-AlanineNAD+ oxidore	[c] : C00001 + C00003 + C00041 <==> C00004 + C01342 + C00022 + C0008	rxn00278

R_rxn00543	0	.	.	TRUE	EthanolNAD+ oxidored	[c] : C00003 + C00469 <==> C00004 + C00080 + C00084	rxn00543
R_rxn05389	0	.	.	TRUE	7-methyl-3-oxo-octanoy	[c] : C00005 + C00080 + cpd11525 <==> C00006 + cpd11526	rxn05389
R_rxn05388	0	.	.	FALSE	5-methyl-hexanoyl-ACP	[c] : C00080 + C01209 + cpd11524 --> C00011 + C00229 + cpd11525	rxn05388
R_rxn05417	0	.	.	FALSE	6-methyl-heptanoyl-AC	[c] : C00080 + C01209 + cpd11553 --> C00011 + C00229 + cpd11554	rxn05417
R_rxn00420	0	.	.	FALSE	L-O-Phosphoserine pho	[c] : C00001 + C01005 --> C00009 + C00716 + C00080	rxn00420
R_rxn05414	0	.	.	TRUE	6-methyl-3-oxo-heptan	[c] : C00005 + C00080 + cpd11550 <==> C00006 + cpd11551	rxn05414
R_rxn05145	0	.	.	TRUE	Orthophosphate-ABC tr	C00001[c] + C00002[c] + C00009[e] <==> C00008[c] + 2 C00009[c] + C000	rxn05145
R_rxn05144	0	.	.	FALSE	rxn05144	[c] : C00064 + C00118 + C00199 --> 3 C00001 + C00009 + C00018 + C0002	rxn05144
R_rxn00838	0	.	.	FALSE	IMPL-aspartate ligase (	[c] : C00044 + C00049 + C00130 --> C00009 + C00035 + 2 C00080 + C0379	rxn00838
R_rxn05410	0	.	.	TRUE	4-methyl-3-oxo-pentan	[c] : C00005 + C00080 + cpd11546 <==> C00006 + cpd11547	rxn05410
R_rxn00836	0	.	.	TRUE	IMPpyrophosphate pho	[c] : C00013 + C00130 <==> C00119 + C00262	rxn00836
R_rxn00781	500	.	.	TRUE	D-Glyceraldehyde-3-ph	[c] : C00003 + C00009 + C00118 <==> C00004 + C00236	rxn00781
R_rxn00834	0	.	.	TRUE	IMPNAD+ oxidoreducta	[c] : C00001 + C00003 + C00130 <==> C00004 + C00080 + C00655	rxn00834
R_SRC_C00073#_c	3.71771	SourceFlux	.	FALSE	. source flux	C00073#[b] --> C00073#[c]	
R_rxn00832	0	.	.	TRUE	IMP 1,2-hydrolase (dec	[c] : C00001 + C00130 <==> C04734	rxn00832
R_rxn00785	0	.	.	TRUE	D-Fructose 6-phosphat	[c] : C05345 + C00118 <==> C00231 + C00279	rxn00785
R_rxn00830	-1000	.	.	TRUE	Isopentenyl-diphospha	[c] : C00129 <==> C00235	rxn00830
R_rxn00938	0	.	.	FALSE	Nicotinamide amidohyd	[c] : C00001 + C00153 --> C01342 + C00253	rxn00938
R_rxn02167	0	.	.	TRUE	(S)-3-Hydroxybutanoyl	[c] : C01144 <==> C00001 + C00877	rxn02167
R_rxn10307	0	.	.	TRUE	palmitoyl-lipoteichoic a	[c] : 24 C00043 + cpd15746 <==> 24 C00015 + cpd15764	rxn10307
R_xyltt	0	Transport Databas	.	FALSE	xylttransport	C00379[e] --> C00379[c]	rxn09651
R_SRC_C00123#_c	10.92	SourceFlux	.	FALSE	. source flux	C00123#[b] --> C00123#[c]	
R_rxn02160	0	.	.	FALSE	L-Histidinol-phosphate	[c] : C00001 + C01100 --> C00009 + C00080 + C00860	rxn02160
R_ESC_C00245_e	0	EscapeFlux	.	FALSE	. escape flux	C00245[e] --> C00245[b]	
R_rxn05181	0	.	.	FALSE	Betaine-ABC transport	C00001[c] + C00002[c] + C00719[e] --> C00008[c] + C00009[c] + C00080[c	rxn05181
R_rxn03068	1000	.	.	TRUE	(R)-2,3-Dihydroxy-3-m	[c] : C00006 + C04039 <==> C00005 + C00080 + C04181	rxn03068
R_rxn10308	0	.	.	TRUE	myristoyl-lipoteichoic a	[c] : 24 C00043 + cpd15747 <==> 24 C00015 + cpd15765	rxn10308
R_ile_Lt	0	Transport Databas	.	FALSE	ile-Ltransport	C00407[e] --> C00407[c]	rxn10933
R_rxn05401	0	.	.	TRUE	13-methyl-3-oxo-tetra-	[c] : C00005 + C00080 + cpd11537 <==> C00006 + cpd11538	rxn05401
R_rxn01453	1000	.	.	TRUE	(R)-3-Hydroxybutanoyl	[c] : C00006 + C03561 <==> C00005 + C00080 + C00332	rxn01453
R_rxn05183	0	.	.	FALSE	D-Methionine-ABC tran	C00001[c] + C00002[c] + C00855[e] --> C00008[c] + C00009[c] + C00080[c	rxn05183
R_rxn01451	-1000	.	.	TRUE	(S)-3-Hydroxybutanoyl	[c] : C00003 + C01144 <==> C00004 + C00080 + C00332	rxn01451
R_rxn01519	1000	.	.	FALSE	dUTP nucleotidohydrol	[c] : C00001 + C00460 --> C00013 + C00365	rxn01519
R_rxn00775	0	.	.	FALSE	ADPribose ribophosphc	[c] : C00001 + C00301 --> C00020 + C03736	rxn00775
R_rxn01517	1000	.	.	TRUE	ATPdTMP phosphotran	[c] : C00002 + C00365 <==> C00008 + C01346	rxn01517
R_rxn00184	-1000	.	.	TRUE	L-GlutamateNADP+ oxi	[c] : C00001 + C00006 + C00025 <==> C00005 + C01342 + C00026 + C0008	rxn00184
R_rxn01512	1000	.	.	TRUE	ATPnucleoside-diphosp	[c] : C00002 + C00363 <==> C00008 + C00459	rxn01512
R_rxn01513	0	.	.	TRUE	ATPdTMP phosphotran	[c] : C00002 + C00364 <==> C00008 + C00363	rxn01513
R_rxn01459	-1000	.	.	TRUE	4-Aminobutyraldehyde	[c] : C00001 + C00006 + C00555 <==> C00005 + 2 C00080 + C00334	rxn01459
R_rxn08194	0	.	.	TRUE	cob(I)alamin adenosylt	[c] : C00002 + C00853 <==> C00194 + C00536	rxn08194
R_rxn01265	0	.	.	TRUE	Nicotinate D-ribonucleo	[c] : C00013 + C01185 <==> C00080 + C00119 + C00253	rxn01265
R_rxn01303	0	.	.	FALSE	Acetyl-CoAL-homoserin	[c] : C00024 + C00263 --> C00010 + C01077	rxn01303
R_rxn01302	1000	.	.	TRUE	L-HomoserineNADP+ o	[c] : C00006 + C00263 <==> C00005 + C00080 + C00441	rxn01302
R_rxn01301	-1000	.	.	TRUE	L-HomoserineNAD+ oxi	[c] : C00003 + C00263 <==> C00004 + C00080 + C00441	rxn01301
R_rxn01300	0	.	.	TRUE	ATPL-homoserine O-ph	[c] : C00002 + C00263 <==> C00008 + C01102	rxn01300
R_ESC_C00114_e	0	EscapeFlux	.	FALSE	. escape flux	C00114[e] --> C00114[b]	
R_rxn03004	0	.	.	TRUE	10-Formyltetrahydrofo	[c] : C00234 + C03838 <==> C00080 + C00101 + C04376	rxn03004

R_rxn03248	0	.	.	TRUE	Hexanoyl-CoAacetyl-Co	[c] : C00024 + C05270 <==> C00010 + C05267	rxn03248
R_rxn03249	0	.	.	TRUE	(S)-Hydroxyhexanoyl-C	[c] : C00003 + C05268 <==> C00004 + C00080 + C05269	rxn03249
R_SRC_C01551_e	0	SourceFlux	.	FALSE	. source flux	C01551[b] --> C01551[e]	
R_rxn03933	0	.	.	TRUE	UDP-N-acetylglucosami	[c] : C00043 + C04851 <==> C00015 + C05893	rxn03933
R_rxn05667	0	.	.	TRUE	Urea transport via facili	C00086[e] <==> C00086[c]	rxn05667
R_rxn03240	0	.	.	TRUE	(S)-3-Hydroxyhexadeca	[c] : C05258 <==> C00001 + C05272	rxn03240
R_rxn03241	0	.	.	TRUE	(S)-3-Hydroxytetradeca	[c] : C05260 <==> C00001 + C05273	rxn03241
R_rxn03242	0	.	.	TRUE	(S)-3-Hydroxydodecano	[c] : C00003 + C05262 <==> C00004 + C00080 + C05263	rxn03242
R_rxn03243	0	.	.	TRUE	Decanoyl-CoAacetyl-Co	[c] : C00024 + C05274 <==> C00010 + C05263	rxn03243
R_rxn03244	0	.	.	TRUE	(S)-Hydroxydecanoyl-C	[c] : C00003 + C05264 <==> C00004 + C00080 + C05265	rxn03244
R_rxn03245	0	.	.	TRUE	(S)-Hydroxydecanoyl-C	[c] : C05264 <==> C00001 + C05275	rxn03245
R_rxn03246	0	.	.	TRUE	(S)-Hydroxyoctanoyl-Co	[c] : C00003 + C05266 <==> C00004 + C00080 + C05267	rxn03246
R_rxn03247	0	.	.	TRUE	(S)-Hydroxyoctanoyl-Co	[c] : C05266 <==> C00001 + C05276	rxn03247
R_rxn08843	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15341 <==> C00080 + C01233 + C01530	rxn08843
R_rxn08842	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15340 <==> C00080 + C01233 + cpd15237	rxn08842
R_rxn05460	0	.	.	FALSE	3-Oxooctodecanoyl-ACI	[c] : C00080 + C05764 + C01209 --> C00011 + C00229 + cpd11570	rxn05460
R_rxn08840	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15338 <==> C00080 + C01233 + cpd15298	rxn08840
R_guat	0	Transport Databas	.	FALSE	guatransport	C00242[e] --> C00242[c]	rxn10142
R_rxn08846	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15344 <==> C00080 + C03274 + C06424	rxn08846
R_rxn08845	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15343 <==> C00080 + C02679 + C03274	rxn08845
R_rxn05465	0	.	.	TRUE	malonyl-ACP[acyl-carri	[c] : C00083 + C00229 <==> C00010 + C01209	rxn05465
R_rxn10231	0	.	.	FALSE	isohexadecanoyl-CDPdi	[c] : C00716 + cpd15688 --> C00055 + C00080 + cpd15694	rxn10231
R_rxn10230	0	.	.	FALSE	anteisopentadecanoyl-C	[c] : C00716 + cpd15687 --> C00055 + C00080 + cpd15693	rxn10230
R_rxn05468	0	.	.	TRUE	O2 transport via diffusi	C00007[e] <==> C00007[c]	rxn05468
R_rxn08848	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15346 <==> C00080 + C00249 + C03274	rxn08848
R_rxn10235	0	.	.	TRUE	isopentadecanoyl-phos	[c] : 2 C00080 + cpd15692 <==> C00011 + cpd15698	rxn10235
R_rxn10234	0	.	.	TRUE	isotetradecanoyl-phosp	[c] : 2 C00080 + cpd15691 <==> C00011 + cpd15697	rxn10234
R_rxn10237	0	.	.	TRUE	isohexadecanoyl-phosp	[c] : 2 C00080 + cpd15694 <==> C00011 + cpd15700	rxn10237
R_rxn10236	0	.	.	TRUE	anteisopentadecanoyl-p	[c] : 2 C00080 + cpd15693 <==> C00011 + cpd15699	rxn10236
R_rxn03419	0	.	.	TRUE	Formamidopyrimidine	[c] : C00001 + C05922 <==> C00058 + C00080 + C05923	rxn03419
R_rxn02831	0	.	.	FALSE	O-SuccinylbenzoateCoA	[c] : C00002 + C00010 + C00080 + C02730 --> C00013 + C00020 + C03160	rxn02831
R_rxn02832	0	.	.	FALSE	O-succinylbenzoate-CoA	[c] : C05817 --> C00001 + C02730	rxn02832
R_rxn02834	0	.	.	FALSE	Phosphoribosyl-ATP py	[c] : C00001 + C02739 --> C00013 + C02741	rxn02834
R_rxn02835	0	.	.	TRUE	1-(5-phospho-D-ribosyl	[c] : C00001 + C02741 <==> C04896	rxn02835
R_glc_Dt	1000	Transport Databas	.	FALSE	glc-Dtransport	C00267[e] --> C00267[c]	rxn09679
R_ESC_C03688#_c	0.19441	EscapeFlux	.	FALSE	. escape flux	C03688#[c] --> C03688#[b]	
R_rxn05682	0	.	.	TRUE	allantoin transport in vi	C00080[e] + C01551[e] <==> C00080[c] + C01551[c]	rxn05682
R_rxn05372	0	.	.	TRUE	10-methyl-3-oxo-doded	[c] : C00005 + C00080 + cpd11508 <==> C00006 + cpd11509	rxn05372
R_rxn08333	0	.	.	FALSE	1,4-dihydroxy-2-naphtl	[c] : C00080 + C03657 + C04146 --> C00011 + C00013 + C19847	rxn08333
R_rxn08335	0	.	.	FALSE	dihydoorotic acid dehyd	[c] : C00337 + C17569 --> C00295 + C00390	rxn08335
R_rxn02376	1000	.	.	TRUE	3-Carboxy-1-hydroxypr	[c] : C15972 + C05381 <==> C00068 + C16254	rxn02376
R_rxn08336	0	.	.	FALSE	dihydroorotic acid (me	[c] : C00337 + C00828 --> C00295 + C05819	rxn08336
R_rxn00692	0	.	.	TRUE	5,10-Methylenetetrahyd	[c] : C00001 + C00037 + C00143 <==> C00716 + C00101	rxn00692
R_rxn00693	0	.	.	TRUE	5-Methyltetrahydrofola	[c] : C05330 + C00440 <==> C00073 + C00101	rxn00693
R_rxn00691	0	.	.	FALSE	10-Formyltetrahydrofo	[c] : C00001 + C00234 --> C00058 + C00080 + C00101	rxn00691
R_SRC_C14819_e	0	SourceFlux	.	FALSE	. source flux	C14819[b] --> C14819[e]	
R_rxn01044	0	.	.	TRUE	D-Xylose ketol-isomera	[c] : C01394 <==> C00310	rxn01044

R_pyrt	0	Transport Databas	.	TRUE	pyrtransport	C00022[c] <==> C00022[e]	.
R_fe2t	0	Transport Databas	.	FALSE	fe2transport	C14818[e] --> C14818[c]	rxn10963
R_rxn00117	0	.	.	TRUE	ATPnucleoside-diphosp	[c] : C00002 + C00015 <==> C00008 + C00075	rxn00117
R_rxn00058	0	.	.	TRUE	Ferrocytochrome-coxyg	[c] : C00007 + 4 C00080 + 4 C01071 <==> 2 C00001 + 4 C01070	rxn00058
R_ESC_ala_DASH_L_	0	EscapeFlux	.	FALSE	. escape flux	ala-L-Thr-L[e] --> ala-L-Thr-L[b]	
R_rxn00056	0	.	.	TRUE	Fe(II)oxygen oxidoredu	[c] : C00007 + 4 C00080 + 4 C14818 <==> 2 C00001 + 4 C14819	rxn00056
R_rxn03841	0	.	.	FALSE	4-amino-4-deoxychoris	[c] : C11355 --> C00022 + C00080 + C00568	rxn03841
R_rxn00119	0	.	.	TRUE	ATPnucleoside-phosph	[c] : C00002 + C00105 <==> C00008 + C00015	rxn00119
R_zn2t	0	Transport Databas	.	FALSE	zn2transport	C00038[e] --> C00038[c]	.
R_rxn05561	-500	.	.	TRUE	fumarate transport in/c	C00080[e] + C00122[e] <==> C00080[c] + C00122[c]	rxn05561
R_rxn03482	1000	.	.	TRUE	Salicin 6-phosphate glu	[c] : C00001 + C06188 <==> C01172 + C02323	rxn03482
R_rxn05368	0	.	.	TRUE	8-methyl-3-oxo-decano	[c] : C00005 + C00080 + cpd11504 <==> C00006 + cpd11505	rxn05368
R_SRC_C00238#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00238#[b] --> C00238#[c]	
R_rxn03481	0	.	.	TRUE	Arbutin 6-phosphate gl	[c] : C00001 + C06187 <==> C02389 + C01172	rxn03481
R_rxn06493	0	.	.	TRUE	dihydrolipoylproteinNA	[c] : C00003 + C02972 <==> C00004 + C00080 + C02051	rxn06493
R_SRC_C11459_e	0	SourceFlux	.	FALSE	. source flux	C11459[b] --> C11459[e]	
R_rxn05360	0	.	.	TRUE	4-methyl-3-oxo-hexano	[c] : C00005 + C00080 + cpd11496 <==> C00006 + cpd11497	rxn05360
R_rxn05363	0	.	.	FALSE	4-methyl-hexanoyl-ACP	[c] : C00080 + C01209 + cpd11499 --> C00011 + C00229 + cpd11500	rxn05363
R_rxn05364	0	.	.	TRUE	6-methyl-3-oxo-octanoy	[c] : C00005 + C00080 + cpd11500 <==> C00006 + cpd11501	rxn05364
R_rxn05367	0	.	.	FALSE	6-methyl-octanoyl-ACP	[c] : C00080 + C01209 + cpd11503 --> C00011 + C00229 + cpd11504	rxn05367
R_rxn05209	-1000	.	.	TRUE	Proton sodium antiport	C00080[c] + C01330[e] <==> C00080[e] + C01330[c]	rxn05209
R_rxn04133	0	.	.	FALSE	rxn04133	[c] : C00001 + C11821 --> C00011 + C01551	rxn04133
R_rxn04132	0	.	.	FALSE	rxn04132	[c] : C00001 + C11821 --> C00011 + C02348	rxn04132
R_rxn00763	-750	.	.	TRUE	GlycerolNAD+ oxidored	[c] : C00003 + C00116 <==> C00004 + C00080 + C00577	rxn00763
R_ala_Lt	0	Transport Databas	.	FALSE	ala-Ltransport	C00041[e] --> C00041[c]	rxn10921
R_ESC_C00001_e	500	EscapeFlux	.	FALSE	. escape flux	C00001[e] --> C00001[b]	
R_rxn04674	0	.	.	FALSE	rxn04674	[c] : C00019 + C13309 --> C00021 + C00080 + C02059	rxn04674
R_ESC_C00122_e	0	EscapeFlux	.	FALSE	. escape flux	C00122[e] --> C00122[b]	
R_rxn01637	1000	.	.	TRUE	N2-Acetyl-L-ornithine2	[c] : C00026 + C00437 <==> C00025 + C01250	rxn01637
R_rxn01636	-1000	.	.	TRUE	N2-Acetyl-L-ornithineL	[c] : C00025 + C00437 <==> C00077 + C00624	rxn01636
R_rxn01634	0	.	.	FALSE	5-Dehydro-4-deoxy-D-g	[c] : C00080 + C00679 --> C00001 + C00011 + C00433	rxn01634
R_SRC_C00044#_c	5.20539	SourceFlux	.	FALSE	. source flux	C00044#[b] --> C00044#[c]	
R_rxn00609	0	.	.	TRUE	1L-myo-Inositol-1-phos	[c] : C01177 <==> C00668	rxn00609
R_rxn00608	0	.	.	TRUE	6-Phospho-beta-D-gluc	[c] : C00001 + C04534 <==> C00267 + C00668	rxn00608
R_rxn02465	1000	.	.	TRUE	N-Acetyl-L-glutamate-5	[c] : C00006 + C00009 + C01250 <==> C00005 + C04133	rxn02465
R_ESC_C00148_e	0	EscapeFlux	.	FALSE	. escape flux	C00148[e] --> C00148[b]	
R_rxn03194	0	.	.	TRUE	(S)-2-Aceto-2-hydroxyb	[c] : C00109 + C05125 <==> C00068 + C00659	rxn03194
R_rxn02304	0	.	.	TRUE	Protoporphyrinogen-IX	[c] : 3 C00007 + 2 C01079 <==> 6 C00001 + 2 C02191	rxn02304
R_rxn02305	0	.	.	TRUE	2-Methyl-4-amino-5-hy	[c] : C00080 + C04327 + C04752 <==> C00013 + C01081	rxn02305
R_rxn00605	0	.	.	TRUE	UDPglucoseD-glucose-6	[c] : C00029 + C00668 <==> C00015 + C00689	rxn00605
R_rxn02303	0	.	.	TRUE	Coproporphyrinogenox	[c] : C00007 + 2 C00080 + C03263 <==> 2 C00001 + 2 C00011 + C01079	rxn02303
R_rxn01739	0	.	.	TRUE	ATPshikimate 3-phosph	[c] : C00002 + C00493 <==> C00008 + C03175	rxn01739
R_rxn02264	0	.	.	TRUE	Hydroxymethylbilane h	[c] : C01024 <==> C00001 + C01051	rxn02264
R_rxn04048	0	.	.	TRUE	cobalt-precorrin-4 meth	[c] : C00019 + C11540 <==> C00021 + C11541	rxn04048
R_rxn04047	0	.	.	TRUE	precorrin-3B C17-meth	[c] : C00019 + C11539 <==> C00021 + C00080 + C11540	rxn04047
R_rxn02268	0	.	.	FALSE	(S)-2-methylbutanoyl-C	[c] : C00007 + 2 C01033 --> 2 C00001 + 2 C03345	rxn02268
R_rxn01280	500	.	.	TRUE	(R)-GlycerateNAD+ oxic	[c] : C00003 + C00258 <==> C00004 + C00080 + C01146	rxn01280

R_rxn01281	-500	.	.	TRUE	(R)-GlycerateNADP+ ox	[c] : C00006 + C00258 <==> C00005 + C00080 + C01146	rxn01281
R_rxn01286	-1000	.	.	TRUE	D-GlyceraldehydeNAD+	[c] : C00001 + C00003 + C00577 <==> C00004 + 2 C00080 + C00258	rxn01286
R_rxn05517	0	.	.	TRUE	cadminum transport ou	C00080[e] + C00238[e] + C01413[c] <==> C00080[c] + C00238[c] + C0141	rxn05517
R_amett	0	Transport Databas	.	FALSE	amettransport	C00019[e] --> C00019[c]	.
R_rxn00237	-1000	.	.	TRUE	ATPnucleoside-diphosp	[c] : C00002 + C00035 <==> C00008 + C00044	rxn00237
R_ESC_C00059_e	0	EscapeFlux	.	FALSE	. escape flux	C00059[e] --> C00059[b]	
R_rxn00239	-1000	.	.	TRUE	ATP(d)GMP phosphotra	[c] : C00002 + C00144 <==> C00008 + C00035	rxn00239
R_4abzt	0	Transport Databas	.	FALSE	4abztransport	C00568[e] --> C00568[c]	.
R_SRC_C00148#_c	5.36283	SourceFlux	.	FALSE	. source flux	C00148#[b] --> C00148#[c]	
R_rxn02484	0	.	.	TRUE	ATP4-amino-5-hydroxy	[c] : C00002 + C01279 <==> C00008 + C04556	rxn02484
R_inostt	0	Transport Databas	.	FALSE	inosttransport	C00137[e] --> C00137[c]	.
R_rxn10289	0	.	.	TRUE	palmitoyl-lipoteichoic a	[c] : 24 C00513 + cpd15728 <==> 24 C00055 + cpd15746	rxn10289
R_rxn01199	0	.	.	TRUE	ATPD-xylulose 5-phosp	[c] : C00002 + C00310 <==> C00008 + C00231	rxn01199
R_ESC_C00855_e	0	EscapeFlux	.	FALSE	. escape flux	C00855[e] --> C00855[b]	
R_rxn02004	0	.	.	FALSE	Trehalose-6-phosphate	[c] : C00001 + C00689 --> C00009 + C00080 + C01083	rxn02004
R_SRC_C00038_e	0	SourceFlux	.	FALSE	. source flux	C00038[b] --> C00038[e]	
R_SRC_C00082#_c	3.34205	SourceFlux	.	FALSE	. source flux	C00082#[b] --> C00082#[c]	
R_rxn12008	0	.	.	TRUE	rxn12008	[c] : C00013 + C04146 <==> C00129 + C04216	rxn12008
R_rxn00467	-1000	.	.	TRUE	L-Ornithine2-oxo-acid a	[c] : C00026 + C00077 <==> C00025 + C01165	rxn00467
R_rxn09310	0	.	.	FALSE	thiazole phosphate synt	[c] : C00002 + C00082 + C00097 + C11437 --> C00001 + C00011 + C00013	rxn09310
R_SRC_C00064#_c	6.37322	SourceFlux	.	FALSE	. source flux	C00064#[b] --> C00064#[c]	
R_rxn01123	0	.	.	TRUE	ATP2-dehydro-3-deoxy	[c] : C00002 + C00204 <==> C00008 + C04442	rxn01123
R_rxn01121	0	.	.	FALSE	D-gluconate hydro-lyas	[c] : C00257 --> C00001 + C00204	rxn01121
R_rxn00747	-500	.	.	TRUE	D-Glyceraldehyde-3-ph	[c] : C00118 <==> C00111	rxn00747
R_rxn01127	0	.	.	TRUE	ATPAMP phosphotrans	[c] : C00002 + C00360 <==> C00008 + C00206	rxn01127
R_acaldt	0	Transport Databas	.	FALSE	acaldtransport	C00084[c] --> C00084[e]	.
R_rxn00742	0	.	.	FALSE	L-Cystathionine Lystein	[c] : C00001 + C00542 --> C01342 + C00097 + C00109	rxn00742
R_rxn01642	0	.	.	FALSE	4-imidazolone-5-propa	[c] : C00001 + C03680 --> C00439	rxn01642
R_arab_Dt	0	Transport Databas	.	FALSE	arab-Dtransport	C00216[e] --> C00216[c]	rxn05499
R_rxn03147	0	.	.	TRUE	1-(5-Phosphoribosyl)-5	[c] : C00002 + C00049 + C04751 <==> C00008 + C00009 + 2 C00080 + C04	rxn03147
R_rxn01647	0	.	.	TRUE	Nicotinate D-ribonucleo	[c] : C00009 + C05841 <==> C00253 + C00620	rxn01647
R_rxn01644	0	.	.	FALSE	L-Aspartate-4-semialde	[c] : C00022 + C00441 --> 2 C00001 + C00080 + C03340	rxn01644
R_ESC_C00380_e	0	EscapeFlux	.	FALSE	. escape flux	C00380[e] --> C00380[b]	
R_rxn10199	0	.	.	TRUE	Peptidoglycan subunit s	[c] : C05898 + cpd15666 <==> C04574 + cpd15665	rxn10199
R_na1t	1000	Transport Databas	.	FALSE	na1transport	C01330[e] --> C01330[c]	rxn10899
R_SRC_C00002#_c	1000	SourceFlux	.	FALSE	. source flux	C00002#[b] --> C00002#[c]	
R_SRC_C00013_e	0	SourceFlux	.	FALSE	. source flux	C00013[b] --> C00013[e]	
R_rxn10192	0	.	.	TRUE	CDP-glycerolpoly(glyce	[c] : 45 C00513 + C04881 <==> 45 C00055 + cpd15661	rxn10192
R_ESC_C00007_e	0	EscapeFlux	.	FALSE	. escape flux	C00007[e] --> C00007[b]	
R_rxn02008	0	.	.	FALSE	UDP-N-acetylmuramoy	[c] : C00002 + C00217 + C01212 --> C00008 + C00009 + C00080 + C00692	rxn02008
R_ESC_gly_DASH_pr	0	EscapeFlux	.	FALSE	. escape flux	gly-pro-L[e] --> gly-pro-L[b]	
R_a_D_glucoset	750	Transport Databas	.	FALSE	a-D-glucosetransport	C00267[e] --> C00267[c]	
R_rxn00991	0	.	.	TRUE	(S)-3-Hydroxy-3-methy	[c] : C00356 <==> C00024 + C00164	rxn00991
R_rxn10571	0	.	.	FALSE	magnesium transport v	C00001[c] + C00002[c] + C00305[e] --> C00008[c] + C00009[c] + C00080[c	rxn10571
R_urat	1000	Transport Databas	.	FALSE	uratransport	C00106[e] --> C00106[c]	rxn10993
R_SRC_Ala_DASH_G	0	SourceFlux	.	FALSE	. source flux	Ala-Gln[b] --> Ala-Gln[e]	
R_SRC_C01330_e	0	SourceFlux	.	FALSE	. source flux	C01330[b] --> C01330[e]	

R_fmnt	0	Transport Databas	.	FALSE	fmntransport	C00061[e] --> C00061[c]	.
R_rxn00305	1000	.	.	FALSE	GTPoxaloacetate carbox	[c] : C00036 + C00044 + C00080 --> C00011 + C00035 + C00074	rxn00305
R_SRC_C00123_e	0	SourceFlux	.	FALSE	. source flux	C00123[b] --> C00123[e]	
R_rxn00300	0	.	.	FALSE	GTP 7,8-8,9-dihydrolas	[c] : 3 C00001 + C00044 --> C00013 + C00058 + C00080 + C01304	rxn00300
R_rxn00302	0	.	.	FALSE	GTP 7,8-8,9-dihydrolas	[c] : C00001 + C00044 --> C05922	rxn00302
R_rxn00303	0	.	.	TRUE	ATPGTP 3'-pyrophosph	[c] : C00002 + C00044 <==> C00020 + C04494	rxn00303
R_rxn04954	-1000	.	.	TRUE	5-methyltetrahydrofola	[c] : C00003 + C00440 <==> C00004 + C00080 + C00143	rxn04954
R_SRC_C01936_e	0	SourceFlux	.	FALSE	. source flux	C01936[b] --> C01936[e]	
R_rxn00525	0	.	.	FALSE	L-arogenateNAD+ oxido	[c] : C00003 + C00826 --> C00004 + C00011 + C00082	rxn00525
R_rxn00020	0	.	.	TRUE	beta-D-Glucoside glucol	[c] : C00001 + C00185 <==> 2 C00221	rxn00020
R_rxn05031	0	.	.	TRUE	prephytoene diphospha	[c] : C03427 <==> C00013 + C05413	rxn05031
R_spmdt	0	Transport Databas	.	FALSE	spmdtransport	C00315[e] --> C00315[c]	.
R_gsnt	0	Transport Databas	.	FALSE	gsntransport	C00387[e] --> C00387[c]	rxn10897
R_rxn00515	0	.	.	TRUE	ATPnucleoside-diphosp	[c] : C00002 + C00104 <==> C00008 + C00081	rxn00515
R_ESC_gly_DASH_gl	0	EscapeFlux	.	FALSE	. escape flux	gly-glu-L[e] --> gly-glu-L[b]	
R_rxn08809	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + C04438 <==> C00080 + C01233 + cpd15269	rxn08809
R_rxn05429	0	.	.	FALSE	12-methyl-tridecanoyl-	[c] : C00080 + C01209 + cpd11565 --> C00011 + C00229 + cpd11566	rxn05429
R_rxn05039	0	.	.	FALSE	pyrimidine phosphatase	[c] : C00001 + C04454 --> C00009 + C00080 + C04732	rxn05039
R_rxn00907	0	.	.	TRUE	5,10-methylenetetrahyd	[c] : C00006 + C00143 <==> C00005 + C00445	rxn00907
R_rxn08805	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15315 <==> C00080 + C01233 + cpd15298	rxn08805
R_rxn08804	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15314 <==> C00080 + C01233 + C06424	rxn08804
R_rxn00902	0	.	.	TRUE	3-Carboxy-3-hydroxy-4	[c] : C00010 + C00080 + C02504 <==> C00001 + C00024 + C00141	rxn00902
R_rxn00903	0	.	.	TRUE	L-Valine2-oxoglutarate	[c] : C00026 + C00183 <==> C00025 + C00141	rxn00903
R_rxn08801	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15329 <==> C00080 + C00623 + C01530	rxn08801
R_rxn05421	0	.	.	FALSE	8-methyl-nonanoyl-ACP	[c] : C00080 + C01209 + cpd11557 --> C00011 + C00229 + cpd11558	rxn05421
R_rxn00863	0	.	.	TRUE	L-HistidinalNAD+ oxido	[c] : C00001 + C00003 + C01929 <==> C00004 + 2 C00080 + C00135	rxn00863
R_rxn08025	0	.	.	TRUE	Arbutin 6-phosphate gl	[c] : C00001 + C06187 <==> C00668 + C02389	rxn08025
R_rxn00868	1000	.	.	TRUE	Butanoyl-CoA(acceptor	[c] : C00003 + C00136 <==> C00004 + C00080 + C00877	rxn00868
R_SRC_C00259_e	0	SourceFlux	.	FALSE	. source flux	C00259[b] --> C00259[e]	
R_gln_Lt	0	Transport Databas	.	FALSE	gln-Ltransport	C00064[e] --> C00064[c]	rxn10928
R_rxn01258	0	.	.	TRUE	Chorismate hydroxymu	[c] : C00251 <==> C00885	rxn01258
R_cytdt	0	Transport Databas	.	FALSE	cytdtransport	cytd[e] --> cytd[c]	.
R_SRC_C00097#_c	2.21508	SourceFlux	.	FALSE	. source flux	C00097#[b] --> C00097#[c]	
R_ESC_C00076_e	0	EscapeFlux	.	FALSE	. escape flux	C00076[e] --> C00076[b]	
R_rxn01466	0	.	.	FALSE	Geranyl-diphosphateiso	[c] : C00129 + C00341 --> C00013 + C00448	rxn01466
R_rxn05233	0	.	.	TRUE	Ribonucleotide reducta	[c] : C00035 + C00342 <==> C00001 + C00361 + C00343	rxn05233
R_rxn05256	0	.	.	FALSE	APSPTi	[c] : C00224 + C00342 --> C00020 + C00094 + C00343	rxn05256
R_rxn01465	0	.	.	TRUE	(S)-Dihydroorotate ami	[c] : C00001 + C00337 <==> C00080 + C00438	rxn01465
R_rxn08821	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15354 <==> C00080 + C00623 + cpd15237	rxn08821
R_rxn03512	0	.	.	TRUE	Precorrin 8X 11,12-met	[c] : C00080 + C06408 <==> C06399	rxn03512
R_rxn03513	0	.	.	TRUE	S-Adenosyl-L-methioni	[c] : C00019 + C06406 <==> C00021 + 2 C00080 + C06407	rxn03513
R_rxn01545	1000	.	.	TRUE	Xanthosine ribohydrola	[c] : C00001 + C01762 <==> C00121 + C00385	rxn01545
R_rxn01544	0	.	.	TRUE	XMPpyrophosphate pho	[c] : C00013 + C00655 <==> C00119 + C00385	rxn01544
R_rxn01548	1000	.	.	TRUE	guanosineorthophosph	[c] : C00009 + C00080 + C00387 <==> C00242 + C00620	rxn01548
R_rxn06510	0	.	.	TRUE	Lauroyl-CoAacetyl-CoA	[c] : C00024 + C01832 <==> C00010 + C05261	rxn06510
R_rxn00016	0	.	.	TRUE	Hexosaminidase	[c] : C00001 + C01674 <==> 2 C00140	rxn00016
R_rxn01332	0	.	.	FALSE	PhosphoenolpyruvateD	[c] : C00001 + C00074 + C00279 --> C00009 + C00080 + C04691	rxn01332

R_rxn01333	1000	.	.	TRUE	Sedoheptulose-7-phosp	[c] : C00118 + C05382 <==> C05345 + C00279	rxn01333
R_rxn01331	0	.	.	TRUE	D-erythrose 4-phospha	[c] : C00001 + C00003 + C00279 <==> C00004 + 2 C00080 + C03393	rxn01331
R_rxn01334	-1000	.	.	TRUE	Sedoheptulose 1,7-bisp	[c] : C00447 <==> C00111 + C00279	rxn01334
R_rxn00394	0	.	.	TRUE	L-Arginine amidinohyd	[c] : C00001 + C00062 <==> C00077 + C00086	rxn00394
R_rxn01537	0	.	.	TRUE	Thiamin hydrolase	[c] : C00001 + C00378 <==> C00080 + C01279 + C04294	rxn01537
R_rxn09448	0	.	.	FALSE	fatty-acid--CoA ligase (c	[c] : C00002 + C00010 + C00080 + cpd15269 --> C00013 + C00020 + cpd15	rxn09448
R_rxn05447	0	.	.	FALSE	8-methyl-trans-non-2-e	[c] : C00004 + C00080 + cpd11556 --> C00003 + cpd11557	rxn05447
R_rxn05325	0	.	.	TRUE	Octanoyl-[acyl-carrier p	[c] : C00003 + C05752 <==> C00004 + C00080 + C05751	rxn05325
R_rxn05324	0	.	.	TRUE	Dodecanoyl-[acyl-carrie	[c] : C00003 + C05223 <==> C00004 + C00080 + C05758	rxn05324
R_rxn05327	0	.	.	TRUE	Decanoyl-[acyl-carrier p	[c] : C00003 + C05755 <==> C00004 + C00080 + C05754	rxn05327
R_rxn05326	0	.	.	TRUE	Hexanoyl-[acyl-carrier p	[c] : C00003 + C05749 <==> C00004 + C00080 + C05748	rxn05326
R_rxn08793	1000	.	.	FALSE	L-Lactate dehydrogenas	[c] : C00186 + C00828 --> C00022 + C05819	rxn08793
R_rxn08792	1000	.	.	TRUE	L-Lactate dehydrogenas	[c] : C00186 + C17569 <==> C00022 + C00390	rxn08792
R_rxn05323	0	.	.	TRUE	Tetradecanoyl-[acyl-car	[c] : C00003 + C05761 <==> C00004 + C00080 + C05760	rxn05323
R_rxn05322	0	.	.	TRUE	Butyryl-[acyl-carrier pr	[c] : C00003 + C05745 <==> C00004 + C00080 + C04246	rxn05322
R_rxn10474	0	.	.	TRUE	cobalt transport in/out	C00175[c] <==> C00175[e]	rxn10474
R_rxn10473	-1000	.	.	TRUE	chlorideion transport o	C00698[e] <==> C00698[c]	rxn10473
R_rxn05328	0	.	.	TRUE	Hexadecanoyl-[acyl-car	[c] : C00003 + C05764 <==> C00004 + C00080 + C05763	rxn05328
R_rxn08799	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15327 <==> C00080 + C00623 + C00249	rxn08799
R_rxn08798	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15330 <==> C00080 + C00623 + cpd15298	rxn08798
R_SRC_C14818_e	0	SourceFlux	.	FALSE	. source flux	C14818[b] --> C14818[e]	
R_rxn02945	0	.	.	FALSE	prephytoene diphospha	[c] : C03427 --> C00013 + C05421	rxn02945
R_rxn02949	0	.	.	TRUE	(S)-3-Hydroxyisobutyry	[c] : C00001 + C03460 <==> C06000	rxn02949
R_SRC_gly_DASH_pr	0	SourceFlux	.	FALSE	. source flux	gly-pro-L[b] --> gly-pro-L[e]	
R_rxn02866	0	.	.	TRUE	3-Methylbutanoyl-CoA(	[c] : C00016 + C02939 <==> C01352 + C03069	rxn02866
R_SRC_C00006#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00006#[b] --> C00006#[c]	
R_SRC_C00459#_c	0.29243	SourceFlux	.	FALSE	. source flux	C00459#[b] --> C00459#[c]	
R_ESC_Gly_DASH_M	0	EscapeFlux	.	FALSE	. escape flux	Gly-Met[e] --> Gly-Met[b]	
R_rxn08470	0	.	.	FALSE	FMNH2-dependent mor	[c] : C00007 + C01847 + cpd11596 --> C00001 + C00061 + C00094 + C0141	rxn08470
R_rxn08471	0	.	.	FALSE	FMNH2-dependent mor	[c] : C00007 + C01847 + C14179 --> C00001 + C00048 + C00061 + C00094	rxn08471
R_nact	0	Transport Databas	.	FALSE	nactransport	C11486[e] --> C11486[c]	rxn05623
R_rxn03239	0	.	.	TRUE	(S)-3-Hydroxyhexadeca	[c] : C00003 + C05258 <==> C00004 + C00080 + C05259	rxn03239
R_rxn09992	-1000	.	.	TRUE	Salicin 6-phosphate glu	[c] : C00001 + C06188 <==> C00668 + C02323	rxn09992
R_rxn00641	0	.	.	TRUE	GTPalpha-D-mannose-1	[c] : C00044 + C00636 <==> C00013 + C00096	rxn00641
R_rxn08851	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15349 <==> C00080 + C03274 + cpd15269	rxn08851
R_rxn08822	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15358 <==> C00080 + C00623 + C01530	rxn08822
R_rxn00649	0	.	.	TRUE	O3-Acetyl-L-serine acet	[c] : C00297 + C00979 <==> C00033 + C00080 + C00097	rxn00649
R_rxn00161	500	.	.	FALSE	(S)-MalateNADP+ oxido	[c] : C00006 + C00711 --> C00005 + C00011 + C00022	rxn00161
R_rxn06600	0	.	.	TRUE	S-aminomethyldihydro	[c] : C00101 + C01242 <==> C01342 + C00143 + C02972	rxn06600
R_xant	0	Transport Databas	.	FALSE	xantransport	C00385[e] --> C00385[c]	rxn09652
R_ESC_Gly_DASH_Le	0	EscapeFlux	.	FALSE	. escape flux	Gly-Leu[e] --> Gly-Leu[b]	
R_rxn05555	0	.	.	FALSE	iron (II) transport via A	C00001[c] + C00002[c] + C14818[e] --> C00008[c] + C00009[c] + C00080[c	rxn05555
R_rxn01930	0	.	.	FALSE	3-Hydroxy-L-kynurenin	[c] : C00001 + C03227 --> C00041 + C00080 + C00632	rxn01930
R_rxn09177	0	.	.	FALSE	phosphopantothenate-c	[c] : C00063 + C00097 + C03492 --> C00013 + C00055 + C04352	rxn09177
R_rxn05251	0	.	.	FALSE	FACOAL170(anteiso)	[c] : C00002 + C00010 + C00080 + cpd11433 --> C00013 + C00020 + cpd11	rxn05251
R_rxn05250	0	.	.	FALSE	FACOAL160(ISO)	[c] : C00002 + C00010 + C00080 + cpd11440 --> C00013 + C00020 + cpd11	rxn05250
R_rxn05252	0	.	.	FALSE	FACOAL170(ISO)	[c] : C00002 + C00010 + C00080 + C00638 --> C00013 + C00020 + cpd1143	rxn05252

R_rxn04673	0	.	.	FALSE	rxn04673	[c] : C03657 + C05427 --> C00011 + C00013 + C00080 + C13309	rxn04673
R_ESC_C01413_e	0	EscapeFlux	.	FALSE	. escape flux	C01413[e] --> C01413[b]	
R_rxn00897	0	.	.	TRUE	N-Acyl-D-glucosamine 2	[c] : C00140 <==> C00645	rxn00897
R_rxn09296	0	.	.	FALSE	hydrogen peroxide redu	[c] : C00027 + C00342 --> 2 C00001 + C00343	rxn09296
R_thft	0	Transport Databas	.	FALSE	thftransport	C00101[e] --> C00101[c]	.
R_rxn10309	0	.	.	TRUE	stearoyl-lipoteichoic ac	[c] : 24 C00043 + cpd15748 <==> 24 C00015 + cpd15766	rxn10309
R_rxn09198	0	.	.	TRUE	Phosphatidylserine dec	[c] : 2 C00080 + cpd15553 <==> C00011 + cpd15529	rxn09198
R_rxn09199	0	.	.	TRUE	Phosphatidylserine dec	[c] : 2 C00080 + cpd15554 <==> C00011 + cpd15530	rxn09199
R_rxn02898	0	.	.	FALSE	O-Succinylbenzoyl-CoA	[c] : C03160 --> C00010 + C03657	rxn02898
R_rxn00707	0	.	.	TRUE	ITPcytidine 5'-phospho	[c] : C00081 + C00475 <==> C00055 + C00104	rxn00707
R_ESC_ala_DASH_L_	0	EscapeFlux	.	FALSE	. escape flux	ala-L-glu-L[e] --> ala-L-glu-L[b]	
R_rxn06077	0	.	.	TRUE	L-methionineoxidized-t	[c] : C00001 + C00073 + C00343 <==> C02989 + C00342	rxn06077
R_pnto_Rt	0	Transport Databas	.	FALSE	pnto-Rtransport	C00864[e] --> C00864[c]	.
R_rxn09197	0	.	.	TRUE	Phosphatidylserine dec	[c] : 2 C00080 + cpd15552 <==> C00011 + cpd15528	rxn09197
R_thymt	0	Transport Databas	.	FALSE	thymtransport	C00178[e] --> C00178[c]	.
R_rxn06078	0	.	.	TRUE	O-Acetyl-L-homoserine	[c] : C05529 + C01077 + C00342 <==> C00033 + C00094 + C05330 + C0034	rxn06078
R_rxn02897	0	.	.	TRUE	Nicotinate-nucleotidedi	[c] : C01185 + C03114 <==> C00080 + C00253 + C04778	rxn02897
R_rxn02895	0	.	.	TRUE	5-Phospho-D-ribosylam	[c] : C00002 + C00037 + C03090 <==> C00008 + C00009 + C00080 + C0383	rxn02895
R_rxn01603	0	.	.	FALSE	7,8-dihydropteroateL-g	[c] : C00002 + C00025 + C00921 --> C00008 + C00009 + C00080 + C00415	rxn01603
R_ESC_Gly_DASH_Cy	0	EscapeFlux	.	FALSE	. escape flux	Gly-Cys[e] --> Gly-Cys[b]	
R_SRC_C00255#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00255#[b] --> C00255#[c]	
R_SRC_C00070#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00070#[b] --> C00070#[c]	
R_rxn08088	0	.	.	FALSE	1-octadecanoyl-sn-glyc	[c] : cpd15268 + cpd15329 --> C00229 + cpd15526	rxn08088
R_rxn06075	0	.	.	TRUE	2'-Deoxyuridine 5'-diph	[c] : C00001 + C01346 + C00343 <==> C00015 + C00342	rxn06075
R_rxn06076	0	.	.	TRUE	2'-Deoxycytidine dipho	[c] : C00001 + C00705 + C00343 <==> C00112 + C00342	rxn06076
R_csnt	0	Transport Databas	.	FALSE	csntransport	C00380[e] --> C00380[c]	.
R_rxn08087	0	.	.	FALSE	1-hexadec-7-enoyl-sn-g	[c] : C04364 + cpd15326 --> C00229 + cpd15525	rxn08087
R_rxn10229	0	.	.	FALSE	isopentadecanoyl-CDPd	[c] : C00716 + cpd15686 --> C00055 + C00080 + cpd15692	rxn10229
R_rxn06777	0	.	.	TRUE	(S)-3-Hydroxytetradeca	[c] : C00003 + C05260 <==> C00004 + C00080 + C05261	rxn06777
R_SRC_C00378_e	0	SourceFlux	.	FALSE	. source flux	C00378[b] --> C00378[e]	
R_rxn06672	0	.	.	TRUE	biotin-carboxyl-carrier-	[c] : C00002 + C01353 + C06250 <==> C00008 + C00009 + C00080 + C0441	rxn06672
R_rxn03884	0	.	.	TRUE	2-dehydro-3-deoxy-D-g	[c] : C04442 <==> C00022 + C00118	rxn03884
R_rxn09450	0	.	.	FALSE	fatty-acid--CoA ligase (l	[c] : C00002 + C00010 + C00080 + cpd15237 --> C00013 + C00020 + C0527	rxn09450
R_SRC_C00380_e	0	SourceFlux	.	FALSE	. source flux	C00380[b] --> C00380[e]	
R_rxn03087	0	.	.	TRUE	N-Succinyl-L-2,6-diamin	[c] : C00026 + C04421 <==> C00025 + C04462	rxn03087
R_rxn03084	0	.	.	FALSE	5'-Phosphoribosylform	[c] : C00001 + C00002 + C00064 + C04376 --> C00008 + C00009 + C00025	rxn03084
R_SRC_Gly_DASH_G	0	SourceFlux	.	FALSE	. source flux	Gly-Gln[b] --> Gly-Gln[e]	
R_rxn00346	0	.	.	FALSE	L-Aspartate 1-carboxy-l	[c] : C00049 + C00080 --> C00011 + C00099	rxn00346
R_ESC_C00034_e	0	EscapeFlux	.	FALSE	. escape flux	C00034[e] --> C00034[b]	
R_ht	0	Transport Databas	.	FALSE	htransport	C00080[c] --> C00080[e]	.
R_rxn00260	0	.	.	TRUE	L-Aspartate2-oxoglutar	[c] : C00026 + C00049 <==> C00025 + C00036	rxn00260
R_rxn00611	0	.	.	TRUE	sn-Glycerol-3-phosphat	[c] : C00003 + C00623 <==> C00004 + C00080 + C00111	rxn00611
R_ESC_C00238_e	0	EscapeFlux	.	FALSE	. escape flux	C00238[e] --> C00238[b]	
R_rxn06979	0	.	.	TRUE	rxn06979	[c] : 2 C00001 + 2 C00002 + 2 C00064 + C05773 <==> 2 C00008 + 2 C0000	rxn06979
R_rxn02359	0	.	.	TRUE	trans-4-Hydroxy-L-prol	[c] : C00016 + C01157 <==> C01352 + C04281	rxn02359
R_SRC_C00034#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00034#[b] --> C00034#[c]	
R_rxn00559	0	.	.	TRUE	D-Mannose-6-phosphat	[c] : C00275 <==> C05345	rxn00559

R_rxn00558	1000	.	.	TRUE	D-Glucose-6-phosphate	[c] : C00668 <==> C05345	rxn00558
R_his_Lt	0	Transport Databas	.	FALSE	his-Ltransport	C00135[e] --> C00135[c]	rxn10932
R_rxn00555	0	.	.	TRUE	L-GlutamineD-fructose-	[c] : C00064 + C05345 <==> C00025 + C00352	rxn00555
R_SRC_C00175#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00175#[b] --> C00175#[c]	
R_rib_Dt	0	Transport Databas	.	FALSE	rib-Dtransport	C00121[e] --> C00121[c]	.
R_SRC_C00011_e	0	SourceFlux	.	FALSE	. source flux	C00011[b] --> C00011[e]	
R_SRC_ala_DASH_L_	0	SourceFlux	.	FALSE	. source flux	ala-L-Thr-L[b] --> ala-L-Thr-L[e]	
R_rxn00414	0	.	.	FALSE	Carbon-dioxideL-glutar	[c] : C00001 + 2 C00002 + C00064 + C01353 --> 2 C00008 + C00009 + C00(	rxn00414
R_rxn10339	0	.	.	TRUE	isotetradecanoyl-cardio	[c] : 2 cpd15724 <==> C00116 + cpd15796	rxn10339
R_rxn05177	0	.	.	FALSE	Thiamin-ABC transport	C00001[c] + C00002[c] + C00378[e] --> C00008[c] + C00009[c] + C00080[c	rxn05177
R_vitd2t	0	Transport Databas	.	FALSE	vitd2transport	vitd2[e] --> vitd2[c]	.
R_rxn00412	1000	.	.	FALSE	UTPammonia ligase(AD	[c] : C00001 + C00002 + C00064 + C00075 --> C00008 + C00009 + C00025	rxn00412
R_rxn05173	0	.	.	FALSE	L-Arabinose-ABC transp	C00001[c] + C00002[c] + C00259[e] --> C00008[c] + C00009[c] + C00080[c	rxn05173
R_rxn10226	0	.	.	FALSE	isoheptadecanoyl-CDPd	[c] : C00716 + cpd15683 --> C00055 + C00080 + cpd15689	rxn10226
R_rxn00827	0	.	.	FALSE	CTPN-acylneuraminate	[c] : C00063 + C00270 --> C00013 + C00128	rxn00827
R_rxn02680	0	.	.	TRUE	Octanoyl-CoAacetyl-Co/	[c] : C00024 + C01944 <==> C00010 + C05265	rxn02680
R_rxn01116	0	.	.	TRUE	D-Ribulose-5-phosphat	[c] : C00199 <==> C00231	rxn01116
R_rxn00792	0	.	.	FALSE	BiotinCoA ligase (AMP-	[c] : C00013 + C05921 --> C00002 + C00080 + C00120	rxn00792
R_rxn00791	0	.	.	TRUE	N-(5-Phospho-D-ribosy	[c] : C00013 + C04302 <==> C00108 + C00119	rxn00791
R_rxn01115	0	.	.	FALSE	6-Phospho-D-gluconate	[c] : C00006 + C00345 --> C00005 + C00011 + C00199	rxn01115
R_cholt	0	Transport Databas	.	FALSE	choltransport	C00114[e] --> C00114[c]	.
R_ESC_C00009_e	0	EscapeFlux	.	FALSE	. escape flux	C00009[e] --> C00009[b]	
R_lac_Lt	0	Transport Databas	.	TRUE	lac-Ltransport	C00186[c] <==> C00186[e]	.
R_rxn03174	0	.	.	FALSE	2-Amino-4-hydroxy-6-(	[c] : C06148 --> C00001 + C04895	rxn03174
R_rxn03175	0	.	.	TRUE	N-(5'-Phospho-D-ribosy	[c] : C04896 <==> C04916	rxn03175
R_rxn11650	0	.	.	TRUE	cob(II)yrinic acid-a,c-di	[c] : C01847 + 2 C06504 <==> C00061 + 2 C00080 + 2 C06505	rxn11650
R_ESC_Gly_DASH_Pl	0	EscapeFlux	.	FALSE	. escape flux	Gly-Phe[e] --> Gly-Phe[b]	
R_rxn10447	0	.	.	FALSE	calcium transport via A	C00001[c] + C00002[c] + C00076[e] --> C00008[c] + C00009[c] + C00076[c	rxn10447
R_cd2t	0	Transport Databas	.	FALSE	cd2transport	C01413[e] --> C01413[c]	.
R_rxn00602	0	.	.	TRUE	(R)-2-Methyl-3-oxopro	[c] : C01213 <==> C00091	rxn00602
R_rxn00199	0	.	.	FALSE	OxalosuccinateNADP+ (	[c] : C00080 + C05379 --> C00011 + C00026	rxn00199
R_SRC_C00698_e	0	SourceFlux	.	FALSE	. source flux	C00698[b] --> C00698[e]	
R_ESC_C11458_e	0	EscapeFlux	.	FALSE	. escape flux	C11458[e] --> C11458[b]	
R_mal_Lt	0	Transport Databas	.	TRUE	mal-Ltransport	C00711[c] <==> C00711[e]	.
R_rxn00196	0	.	.	TRUE	2,5-dioxopentanoateNA	[c] : C00001 + C00006 + C00433 <==> C00005 + C00026 + 2 C00080	rxn00196
R_rxn00269	0	.	.	FALSE	Aminoacetic acidoxyger	[c] : C00001 + C00007 + C00037 --> C01342 + C00027 + C00048	rxn00269
R_rxn00193	0	.	.	TRUE	L-Glutamate racemase	[c] : C00025 <==> C00217	rxn00193
R_rxn00604	-1000	.	.	TRUE	D-Glucose-6-phosphate	[c] : C00006 + C00668 <==> C00005 + C00080 + C01236	rxn00604
R_SRC_C00076_e	0	SourceFlux	.	FALSE	. source flux	C00076[b] --> C00076[e]	
R_rxn01275	0	.	.	TRUE	ATPD-Gluconate 6-phos	[c] : C00002 + C00257 <==> C00008 + C00345	rxn01275
R_fumt	-1000	Transport Databas	.	TRUE	fumtransport	C00122[c] <==> C00122[e]	.
R_ESC_C00175_e	0	EscapeFlux	.	FALSE	. escape flux	C00175[e] --> C00175[b]	
R_rxn01270	0	.	.	TRUE	L-Aspartate2-oxoglutar	[c] : C00036 + C00826 <==> C00049 + C00254	rxn01270
R_rxn05287	0	.	.	TRUE	GGTT	[c] : C00129 + C00353 <==> C00013 + C04217	rxn05287
R_rxn00392	0	.	.	TRUE	ATPriboflavin 5'-phosp	[c] : C00002 + C00255 <==> C00008 + C00061	rxn00392
R_rxn10122	-1000	.	.	TRUE	NADH dehydrogenase (	C00004[c] + 4.5 C00080[c] + C17569[c] <==> C00003[c] + 3.5 C00080[e] +	rxn10122
R_ESC_C00407_e	0	EscapeFlux	.	FALSE	. escape flux	C00407[e] --> C00407[b]	

R_thr_Lt	0	Transport Databas	.	FALSE	thr-Ltransport	C00188[e] --> C00188[c]	rxn10898
R_rxn05444	0	.	.	FALSE	15-methyl-trans-hexa-d	[c] : C00004 + C00080 + cpd11543 --> C00003 + cpd11544	rxn05444
R_rxn01073	0	.	.	TRUE	sn-Glycero-3-phosphoe	[c] : C00001 + C01233 <==> C00623 + C00189	rxn01073
R_rxn00295	0	.	.	TRUE	UDP-N-acetyl-D-glucosa	[c] : C00043 <==> C00203	rxn00295
R_rxn05453	0	.	.	TRUE	13-methyl-tetra-decanc	[c] : C00010 + cpd11540 <==> cpd11437 + C00229	rxn05453
R_rxn03080	0	.	.	TRUE	6,7-Dimethyl-8-(1-D-rib	[c] : C04732 + C15556 <==> 2 C00001 + C00009 + C00080 + C04332	rxn03080
R_rxn05445	0	.	.	FALSE	4-methyl-trans-pent-2-	[c] : C00004 + C00080 + cpd11548 --> C00003 + cpd11549	rxn05445
R_asn_Lt	0	Transport Databas	.	FALSE	asn-Ltransport	C00152[e] --> C00152[c]	rxn05220
R_rxn05446	0	.	.	FALSE	6-methyl-trans-hept-2-	[c] : C00004 + C00080 + cpd11552 --> C00003 + cpd11553	rxn05446
R_rxn03250	0	.	.	TRUE	(S)-Hydroxyhexanoyl-C	[c] : C05268 <==> C00001 + C05271	rxn03250
R_rxn00898	0	.	.	FALSE	2,3-Dihydroxy-3-methy	[c] : C04039 --> C00001 + C00141	rxn00898
R_rxn04456	0	.	.	FALSE	rxn04456	[c] : C00080 + C12248 --> C00011 + C01551	rxn04456
R_rxn04457	0	.	.	FALSE	rxn04457	[c] : C00080 + C12248 --> C00011 + C02348	rxn04457
R_rxn10208	0	.	.	FALSE	isopentadecanoyl-glyce	[c] : C00623 + cpd11437 --> C00010 + cpd15674	rxn10208
R_rxn10209	0	.	.	FALSE	anteisopentadecanoyl-g	[c] : C00623 + cpd11439 --> C00010 + cpd15675	rxn10209
R_rxn00262	1000	.	.	FALSE	L-Aspartic acidoxygen c	[c] : C00001 + C00007 + C00049 --> C01342 + C00027 + C00036	rxn00262
R_rxn10204	0	.	.	FALSE	stearoyl-glycerol-3-pho	[c] : C00623 + C00412 --> C00010 + cpd15329	rxn10204
R_rxn10205	0	.	.	FALSE	isoheptadecanoyl-glyce	[c] : C00623 + cpd11432 --> C00010 + cpd15671	rxn10205
R_rxn10206	0	.	.	FALSE	anteisoheptadecanoyl-g	[c] : C00623 + cpd11434 --> C00010 + cpd15672	rxn10206
R_rxn02774	0	.	.	TRUE	S-Adenosyl-L-methionii	[c] : C00003 + C02463 <==> C00004 + C00080 + C05778	rxn02774
R_rxn00776	0	.	.	TRUE	Uracil hydro-lyase (add	[c] : C00106 + C03736 <==> C00001 + C01168	rxn00776
R_rxn10202	0	.	.	FALSE	palmitoyl-glycerol-3-ph	[c] : C00623 + C00154 --> C00010 + cpd15327	rxn10202
R_rxn10203	0	.	.	FALSE	myristoyl-glycerol-3-ph	[c] : C00623 + C02593 --> C00010 + cpd15331	rxn10203
R_ser_Lt	0	Transport Databas	.	FALSE	ser-Ltransport	C00716[e] --> C00716[c]	rxn10999
R_SRC_C00305#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00305#[b] --> C00305#[c]	
R_rxn08308	0	.	.	TRUE	CDP-diacylglycerol synt	[c] : C00063 + cpd15523 <==> C00013 + cpd15422	rxn08308
R_rxn10215	0	.	.	FALSE	anteisoheptadecanoyl-1	[c] : cpd11434 + cpd15672 --> C00010 + cpd15678	rxn10215
R_rxn00947	0	.	.	FALSE	PalmitateCoA ligase (AM	[c] : C00002 + C00010 + C00080 + C00249 --> C00013 + C00020 + C00154	rxn00947
R_rxn00974	1000	.	.	TRUE	citrate hydro-lyase	[c] : C00158 <==> C00001 + C00417	rxn00974
R_rxn08306	0	.	.	TRUE	CDP-diacylglycerol synt	[c] : C00063 + cpd15521 <==> C00013 + cpd15417	rxn08306
R_rxn05443	0	.	.	FALSE	13-methyl-trans-tetra-d	[c] : C00004 + C00080 + cpd11539 --> C00003 + cpd11540	rxn05443
R_SRC_Gly_DASH_C	0	SourceFlux	.	FALSE	. source flux	Gly-Cys[b] --> Gly-Cys[e]	
R_rxn03421	0	.	.	TRUE	GTP 7,8-8,9-dihydrolase	[c] : C05923 <==> C06148	rxn03421
R_rxn03407	0	.	.	FALSE	Undecaprenyl-diphosph	[c] : C00002 + C01342 + C05893 --> C00008 + C00009 + C00080 + C05894	rxn03407
R_SRC_L_DASH_alar	0	SourceFlux	.	FALSE	. source flux	L-alanylglycine[b] --> L-alanylglycine[e]	
R_rxn00527	0	.	.	TRUE	L-Tyrosine2-oxoglutara	[c] : C00026 + C00082 <==> C00025 + C01179	rxn00527
R_thmt	0	Transport Databas	.	FALSE	thmtransport	C00378[e] --> C00378[c]	rxn11006
R_rxn01434	-1000	.	.	TRUE	L-CitrullineL-aspartate	[c] : C00002 + C00049 + C00327 <==> C00013 + C00020 + C03406	rxn01434
R_rxn01437	0	.	.	TRUE	N-Formyl-L-kynurenine	[c] : C00001 + C02700 <==> C00058 + C00080 + C00328	rxn01437
R_rxn04046	0	.	.	TRUE	S-adenosyl-L-methionir	[c] : C00019 + C11538 <==> C00021 + C00080 + C11539	rxn04046
R_rxn00689	0	.	.	FALSE	TetrahydrofolateL-gluta	[c] : C00002 + C00025 + C00101 --> C00008 + C00009 + C00080 + C03541	rxn00689
R_SRC_C00047#_c	8.30332	SourceFlux	.	FALSE	. source flux	C00047#[b] --> C00047#[c]	
R_rxn00122	0	.	.	FALSE	ATPFMN adenylyltrans	[c] : C00002 + C00061 --> C00013 + C00016	rxn00122
R_rxn10233	0	.	.	TRUE	anteisoheptadecanoyl-g	[c] : 2 C00080 + cpd15690 <==> C00011 + cpd15696	rxn10233
R_rxn00126	0	.	.	TRUE	ATPL-methione S-adeno	[c] : C00001 + C00002 + C00073 <==> C00009 + C00013 + C00019	rxn00126
R_rxn03108	0	.	.	TRUE	ATP4-amino-2-methyl-	[c] : C00002 + C04556 <==> C00008 + C04752	rxn03108
R_rxn01972	0	.	.	TRUE	N6-Acetyl-LL-2,6-diami	[c] : C00001 + C04390 <==> C00033 + C00666	rxn01972

R_rxn01973	0	.	.	TRUE	N-Succinyl-LL-2,6-diam	[c] : C00001 + C04421 <==> C00042 + C00666	rxn01973
R_rxn05596	0	.	.	TRUE	potassium transport ou	C00080[e] + C00238[c] <==> C00080[c] + C00238[e]	rxn05596
R_rxn01975	1000	.	.	TRUE	beta-D-Glucose-6-phos	[c] : C00006 + C01172 <==> C00005 + C00080 + C01236	rxn01975
R_etoht	0	Transport Databas	.	FALSE	etohtransport	C00469[c] --> C00469[e]	.
R_rxn01977	-1000	.	.	TRUE	alpha-D-Glucose 6-phos	[c] : C00668 <==> C01172	rxn01977
R_rxn00883	0	.	.	FALSE	1D-myo-Inositol 3-phos	[c] : C00001 + C04006 --> C00009 + C00080 + C00137	rxn00883
R_rxn05598	0	.	.	FALSE	Lactose transport out v	C00001[c] + C00002[c] + C00243[e] --> C00008[c] + C00009[c] + C00080[c	rxn05598
R_rxn00048	0	.	.	FALSE	6,7-Dimethyl-8-(1-D-rib	[c] : 2 C04332 --> C00255 + C04732	rxn00048
R_rxn05449	0	.	.	FALSE	12-methyl-trans-tridec-	[c] : C00004 + C00080 + cpd11564 --> C00003 + cpd11565	rxn05449
R_rxn03491	0	.	.	TRUE	S-Adenosyl-L-methioni	[c] : 2 C00019 + C06319 <==> C00011 + 2 C00021 + 2 C00080 + C06408	rxn03491
R_rxn00915	0	.	.	TRUE	GMPpyrophosphate pho	[c] : C00013 + C00144 <==> C00119 + C00242	rxn00915
R_rxn10334	0	.	.	TRUE	palmitoyl-cardiolipin sy	[c] : 2 cpd15538 <==> C00116 + cpd15791	rxn10334
R_xyl_Dt	0	Transport Databas	.	FALSE	xyl-Dtransport	C01394[e] --> C01394[c]	rxn09650
R_rxn05358	0	.	.	TRUE	2-methylbutanoyl-CoA[	[c] : C01033 + C00229 <==> C00010 + cpd11495	rxn05358
R_rxn05359	0	.	.	FALSE	4-methyl-3-oxo-hexano	[c] : C00080 + C01209 + cpd11495 --> C00011 + C00229 + cpd11496	rxn05359
R_rxn05434	0	.	.	FALSE	6-methyl-trans-oct-2-e	[c] : C00004 + C00080 + cpd11502 --> C00003 + cpd11503	rxn05434
R_rxn05193	0	.	.	FALSE	Butyro-betaine ABC tra	C00001[c] + C00002[c] + C11459[e] --> C00008[c] + C00009[c] + C00080[c	rxn05193
R_rxn05608	0	.	.	FALSE	Maltotriose transport v	C00001[c] + C00002[c] + C01835[e] --> C00008[c] + C00009[c] + C00080[c	rxn05608
R_rxn05409	0	.	.	FALSE	2-methylpropionyl-ACP	[c] : C00080 + C01209 + cpd11545 --> C00011 + C00229 + cpd11546	rxn05409
R_rxn05350	0	.	.	FALSE	hexanoyl-[acyl-carrier p	[c] : C00080 + C05749 + C01209 --> C00011 + C05750 + C00229	rxn05350
R_rxn00917	0	.	.	FALSE	Xanthosine-5'-phospha	[c] : C00001 + C00002 + C00064 + C00655 --> C00013 + C00020 + C00025	rxn00917
R_kt	0	Transport Databas	.	FALSE	ktransport	C00238[e] --> C00238[c]	rxn05206
R_ESC_C00123_e	0	EscapeFlux	.	FALSE	. escape flux	C00123[e] --> C00123[b]	
R_rxn01851	1000	.	.	TRUE	4-aminobutanalNAD+ 1	[c] : C00001 + C00003 + C00555 <==> C00004 + 2 C00080 + C00334	rxn01851
R_SRC_C00855_e	0	SourceFlux	.	FALSE	. source flux	C00855[b] --> C00855[e]	
R_ergstt	0	Transport Databas	.	FALSE	ergsttransport	C01694[e] --> C01694[c]	rxn09684
R_rxn04020	0	.	.	TRUE	trehalose 6-phosphatep	[c] : C00009 + C00080 + C00689 <==> C00668 + C00663	rxn04020
R_rxn01859	0	.	.	TRUE	Deoxyadenosineorthop	[c] : C00009 + C00080 + C00559 <==> C00147 + C00672	rxn01859
R_rxn01858	0	.	.	TRUE	Deoxyadenosine amino	[c] : C00001 + C00080 + C00559 <==> C01342 + C05512	rxn01858
R_rxn01996	0	.	.	TRUE	(R)-2-Methyl-3-oxopro	[c] : C01213 <==> C00683	rxn01996
R_rxn01997	0	.	.	TRUE	dTDPglucose 4,6-hydro	[c] : C00842 <==> C00001 + C11907	rxn01997
R_rxn02914	0	.	.	TRUE	3-Phosphoserine2-oxog	[c] : C00026 + C01005 <==> C00025 + C03232	rxn02914
R_rxn08546	0	.	.	FALSE	glycerol-3-phosphate a	[c] : C00623 + C05223 --> C00229 + cpd15325	rxn08546
R_rxn08547	0	.	.	FALSE	glycerol-3-phosphate a	[c] : C00623 + C05761 --> C00229 + cpd15331	rxn08547
R_hco3t	0	Transport Databas	.	TRUE	hco3transport	C01353[c] <==> C01353[e]	.
R_rxn02339	0	.	.	TRUE	4-Hydroxy-L-glutamate	[c] : C00026 + C03079 <==> C00025 + C05946	rxn02339
R_SRC_Gly_DASH_T	0	SourceFlux	.	FALSE	. source flux	Gly-Tyr[b] --> Gly-Tyr[e]	
R_sprmt	0	Transport Databas	.	FALSE	sprmtransport	C00750[e] --> C00750[c]	rxn09659
R_rxn00800	0	.	.	TRUE	N6-(1,2-Dicarboxyethyl	[c] : C03794 <==> C00020 + C00122	rxn00800
R_rxn08548	0	.	.	FALSE	glycerol-3-phosphate a	[c] : C00623 + C05760 --> C00229 + cpd15330	rxn08548
R_rxn08549	0	.	.	FALSE	glycerol-3-phosphate a	[c] : C00623 + cpd15277 --> C00229 + cpd15327	rxn08549
R_rxn10113	0	.	.	FALSE	cytochrome oxidase bo	0.5 C00007[c] + 2.5 C00080[c] + C00390[c] --> C00001[c] + 2.5 C00080[e]	rxn10113
R_uratet	0	Transport Databas	.	FALSE	uratetransport	C00366[e] --> C00366[c]	.
R_rxn01489	0	.	.	TRUE	Geranylgeranyl-diphosp	[c] : 2 C00353 <==> C00013 + C03427	rxn01489
R_rxn10118	0	.	.	FALSE	hydrogenase (ubiquino	2 C00080[c] + C00282[c] + C17569[c] --> 2 C00080[e] + C00390[c]	rxn10118
R_rxn02314	0	.	.	TRUE	ATPD-tagatose-6-phosp	[c] : C00002 + C01097 <==> C00008 + C03785	rxn02314
R_rxn01486	0	.	.	FALSE	trans,trans-Farnesyl-di	[c] : C00129 + C00448 --> C00013 + C00353	rxn01486

R_rxn05902	0	.	.	TRUE	Hydrogen-sulfideferred	[c] : 3 C00001 + C00297 + 3 C00139 <==> 7 C00080 + C00094 + 3 C00138	rxn05902
R_rxn01480	0	.	.	TRUE	3-Hydroxy-2-methylpro	[c] : C00003 + C06001 <==> C00004 + C00080 + C00349	rxn01480
R_rxn06591	0	.	.	TRUE	L-glutamate-semialdeh	[c] : C00005 + C00080 + C02987 <==> C00006 + C03741 + C01641	rxn06591
R_rxn02312	0	.	.	TRUE	S-Adenosyl-L-methioni	[c] : C00019 + C01092 <==> C01037 + C04425	rxn02312
R_rxn01299	1000	.	.	TRUE	Inosine ribohydrolase	[c] : C00001 + C00294 <==> C00121 + C00262	rxn01299
R_rxn10806	0	.	.	FALSE	cytochrome oxidase bd	0.5 C00007[c] + 2 C00080[c] + C05819[c] --> C00001[c] + 2 C00080[e] + C0	rxn10806
R_ESC_C00008#_c	995.765	EscapeFlux	.	FALSE	. escape flux	C00008#[c] --> C00008#[b]	
R_rxn01291	0	.	.	TRUE	L-ArabitolNADP+ 1-oxi	[c] : C00006 + C00532 <==> C00005 + C00080 + C00259	rxn01291
R_SRC_C00034_e	0	SourceFlux	.	FALSE	. source flux	C00034[b] --> C00034[e]	
R_rxn03062	0	.	.	TRUE	3-IsopropylmalateNAD-	[c] : C00003 + C04411 <==> C00004 + C00080 + C04236	rxn03062
R_rxn05504	0	.	.	FALSE	arsenobetaine transpor	C00001[c] + C00002[c] + C19331[e] --> C00008[c] + C00009[c] + C00080[c	rxn05504
R_rxn00227	0	.	.	FALSE	Acetyl phosphate phosp	[c] : C00001 + C00227 --> C00009 + C00033 + 2 C00080	rxn00227
R_rxn10338	0	.	.	TRUE	anteisoheptadecanoyl-c	[c] : 2 cpd15723 <==> C00116 + cpd15795	rxn10338
R_rxn00225	0	.	.	TRUE	ATPacetate phosphotra	[c] : C00002 + C00033 + C00080 <==> C00008 + C00227	rxn00225
R_rxn00224	0	.	.	TRUE	Protoporphyrin ferro-ly	[c] : C02191 + C14818 <==> C00032 + 2 C00080	rxn00224
R_rxn00223	-250	.	.	TRUE	xylose isomerase	[c] : C00267 <==> C10906	rxn00223
R_rxn00222	0	.	.	TRUE	1,4-beta-D-Glucan gluc	[c] : C00001 + C00185 <==> 2 C00267	rxn00222
R_rxn05175	0	.	.	FALSE	Spermidine-ABC transp	C00001[c] + C00002[c] + C00315[e] --> C00008[c] + C00009[c] + C00080[c	rxn05175
R_SRC_C01342_e	0	SourceFlux	.	FALSE	. source flux	C01342[b] --> C01342[e]	
R_ESC_C00086_e	0	EscapeFlux	.	FALSE	. escape flux	C00086[e] --> C00086[b]	
R_rxn09108	0	.	.	TRUE	Phosphatidylglycerol sy	[c] : C00623 + cpd15417 <==> C00055 + cpd15542	rxn09108
R_rxn06937	0	.	.	FALSE	L-GlutamatetRNA(Glu)	[c] : C00002 + C00025 + C00080 + C01641 --> C00013 + C00020 + C02987	rxn06937
R_rxn00758	0	.	.	TRUE	sn-Glycero-3-phosphoc	[c] : C00001 + C00670 <==> C00623 + C00114	rxn00758
R_h2ot	-1000	Transport Databas	.	TRUE	h2otransport	C00001[c] <==> C00001[e]	.
R_rxn00459	-500	.	.	TRUE	2-Phospho-D-glycerate	[c] : C00631 <==> C00001 + C00074	rxn00459
R_galt	0	Transport Databas	.	FALSE	galtransport	C00124[e] --> C00124[c]	rxn10911
R_ESC_ala_DASH_L_	0	EscapeFlux	.	FALSE	. escape flux	ala-L-asp-L[e] --> ala-L-asp-L[b]	
R_fe3t	0	Transport Databas	.	FALSE	fe3transport	C14819[e] --> C14819[c]	rxn05292
R_rxn10126	-1000	.	.	TRUE	succinate dehyrdogenas	[c] : C01352 + C17569 <==> C00016 + C00390	rxn10126
R_rxn00799	500	.	.	TRUE	(S)-Malate hydro-lyase	[c] : C00711 <==> C00001 + C00122	rxn00799
R_rxn03031	0	.	.	TRUE	Succinyl-CoA2,3,4,5-tet	[c] : C00001 + C00091 + C03972 <==> C00010 + C04462	rxn03031
R_rxn03136	0	.	.	TRUE	1-(5'-Phosphoribosyl)-5	[c] : C04823 <==> C00122 + C04677	rxn03136
R_rxn03137	0	.	.	TRUE	10-Formyltetrahydrofo	[c] : C00234 + C04677 <==> C00101 + C04734	rxn03137
R_rxn01653	0	.	.	FALSE	5-Formyltetrahydrofola	[c] : C00002 + C03479 --> C00008 + C00009 + C00445	rxn01653
R_rxn03135	0	.	.	FALSE	Imidazole-glycerol-3-ph	[c] : C00064 + C04916 --> C00025 + C00080 + C04666 + C04677	rxn03135
R_tcyntt	0	Transport Databas	.	FALSE	tcynttransport	C01755[e] --> C01755[c]	.
R_rxn06023	0	.	.	TRUE	CoAapo-[acyl-carrier-pr	[c] : C00010 + C03688 <==> C00054 + C00229	rxn06023
R_SRC_C02989_e	0	SourceFlux	.	FALSE	. source flux	C02989[b] --> C02989[e]	
R_pydxnt	0	Transport Databas	.	FALSE	pydxntransport	C00314[e] --> C00314[c]	rxn13097
R_rxn10067	0	.	.	FALSE	FMN-dependent monoo	[c] : C00007 + C01847 + cpd11578 --> C00001 + C00061 + C00094 + C0237	rxn10067
R_rxn10060	1000	.	.	TRUE	NAD kinase (dTTP)	[c] : C00003 + C00459 <==> C00006 + C00363	rxn10060
R_rxn00060	0	.	.	FALSE	Porphobilinogen ammo	[c] : C00001 + 4 C00931 --> 4 C01342 + C01024	rxn00060
R_ESC_C00070_e	0	EscapeFlux	.	FALSE	. escape flux	C00070[e] --> C00070[b]	
R_SRC_Gly_DASH_M	0	SourceFlux	.	FALSE	. source flux	Gly-Met[b] --> Gly-Met[e]	
R_rxn05937	-1000	.	.	TRUE	FerredoxinNADP+ oxid	[c] : C00006 + C00080 + C00138 <==> C00005 + C00139	rxn05937
R_rxn08971	0	.	.	FALSE	NADH dehydrogenase (	[c] : C00004 + C00080 + C00828 --> C00003 + C05819	
R_rxn05380	0	.	.	TRUE	14-methyl-3-oxo-hexa-(	[c] : C00005 + C00080 + cpd11516 <==> C00006 + cpd11517	rxn05380

R_SRC_gly_DASH_as	0	SourceFlux	.	FALSE	. source flux	gly-asp-L[b] --> gly-asp-L[e]	
R_rxn00062	0	.	.	FALSE	ATP phosphohydrolase	[c] : C00001 + C00002 --> C00008 + C00009 + C00080	rxn00062
R_rxn08089	0	.	.	FALSE	1-octadec-7-enoyl-sn-g	[c] : C01203 + cpd15328 --> C00229 + cpd15527	rxn08089
R_rxn00097	-1000	.	.	TRUE	ATPAMP phosphotrans	[c] : C00002 + C00020 <==> 2 C00008	rxn00097
R_rxn00313	0	.	.	FALSE	meso-2,6-Diaminohepta	[c] : C00080 + C00680 --> C00011 + C00047	rxn00313
R_rxn08086	0	.	.	FALSE	1-hexadecanoyl-sn-glyc	[c] : cpd15277 + cpd15327 --> C00229 + cpd15524	rxn08086
R_rxn08085	0	.	.	FALSE	1-tetradec-7-enoyl-sn-g	[c] : C05760 + cpd15330 --> C00229 + cpd15523	rxn08085
R_rxn08084	0	.	.	FALSE	1-tetradecanoyl-sn-glyc	[c] : C05761 + cpd15331 --> C00229 + cpd15522	rxn08084
R_rxn08083	0	.	.	FALSE	1-tetradecanoyl-sn-glyc	[c] : C05223 + cpd15325 --> C00229 + cpd15521	rxn08083
R_leu_Lt	0	Transport Databas	.	FALSE	leu-Ltransport	C00123[e] --> C00123[c]	rxn11003
R_rxn12510	0	.	.	TRUE	ATPpantothenate 4'-ph	[c] : C00002 + C00864 <==> C00008 + C03492	rxn12510
R_rxn10335	0	.	.	TRUE	myristoyl-cardiolipin sy	[c] : 2 cpd15536 <==> C00116 + cpd15792	rxn10335
R_ESC_C01551_e	0	EscapeFlux	.	FALSE	. escape flux	C01551[e] --> C01551[b]	
R_rxn00251	-1000	.	.	TRUE	Orthophosphateoxaloac	[c] : C00009 + C00036 + 2 C00080 <==> C00001 + C00011 + C00074	rxn00251
R_rxn00256	0	.	.	TRUE	Citrate oxaloacetate-lya	[c] : C00010 + C00080 + C00158 <==> C00001 + C00024 + C00036	rxn00256
R_rxn10336	0	.	.	TRUE	stearoyl-cardiolipin syn	[c] : 2 cpd15540 <==> C00116 + cpd15793	rxn10336
R_rxn01484	0	.	.	TRUE	N-Acetyl-D-glucosamin	[c] : C00001 + C00357 <==> C00033 + C00352	rxn01484
R_ESC_C01342_e	0	EscapeFlux	.	FALSE	. escape flux	C01342[e] --> C01342[b]	
R_rxn00790	0	.	.	TRUE	5-Phosphoribosylamine	[c] : C00013 + C00025 + C03090 <==> C00001 + C00064 + C00119	rxn00790
R_rxn02175	0	.	.	TRUE	ATPpantetheine-4'-pho	[c] : C00002 + C01134 <==> C00013 + C00882	rxn02175
R_rxn00526	0	.	.	FALSE	L-arogenateNAD+ oxid	[c] : C00006 + C00826 --> C00005 + C00011 + C00082	rxn00526
R_rxn04413	-1000	.	.	TRUE	rxn04413	[c] : C00044 + C06508 <==> C00035 + C00080 + C06509	rxn04413
R_rxn05439	0	.	.	FALSE	5-methyl-trans-hex-2-e	[c] : C00004 + C00080 + cpd11523 --> C00003 + cpd11524	rxn05439
R_rxn05438	0	.	.	FALSE	14-methyl-trans-hexa-d	[c] : C00004 + C00080 + cpd11518 --> C00003 + cpd11519	rxn05438
R_rxn05435	0	.	.	FALSE	8-methyl-trans-dec-2-e	[c] : C00004 + C00080 + cpd11506 --> C00003 + cpd11507	rxn05435
R_rxn00461	0	.	.	TRUE	PhosphoenolpyruvateU	[c] : C00043 + C00074 <==> C00009 + C00080 + C04631	rxn00461
R_rxn05437	0	.	.	FALSE	12-methyl-trans-tetra-d	[c] : C00004 + C00080 + cpd11514 --> C00003 + cpd11515	rxn05437
R_rxn05436	0	.	.	FALSE	10-methyl-trans-dodec	[c] : C00004 + C00080 + cpd11510 --> C00003 + cpd11511	rxn05436
R_rxn00910	1000	.	.	TRUE	5-methyltetrahydrofola	[c] : C00006 + C00440 <==> C00005 + C00080 + C00143	rxn00910
R_rxn05433	0	.	.	FALSE	4-methyl-trans-hex-2-e	[c] : C00004 + C00080 + cpd11498 --> C00003 + cpd11499	rxn05433
R_rxn00912	0	.	.	TRUE	5,10-Methylenetetrahyd	[c] : C00001 + C00141 + C00143 <==> C00101 + C00966	rxn00912
R_SRC_C04574#_c	2.30212	SourceFlux	.	FALSE	. source flux	C04574#[b] --> C04574#[c]	
R_met_Lt	0	Transport Databas	.	FALSE	met-Ltransport	C00073[e] --> C00073[c]	rxn10976
R_rxn00851	0	.	.	TRUE	D-AlanineD-Alanine liga	[c] : C00002 + 2 C00133 <==> C00008 + C00009 + C00080 + C00993	rxn00851
R_ESC_Gly_DASH_G	0	EscapeFlux	.	FALSE	. escape flux	Gly-Gln[e] --> Gly-Gln[b]	
R_nmnt	0	Transport Databas	.	FALSE	nmntransport	C00455[e] --> C00455[c]	rxn10181
R_rxn00858	0	.	.	TRUE	Agmatine amidinohydr	[c] : C00001 + C00179 <==> C00086 + C00134	rxn00858
R_asp_Lt	0	Transport Databas	.	FALSE	asp-Ltransport	C00049[e] --> C00049[c]	rxn10906
R_SRC_C00719_e	0	SourceFlux	.	FALSE	. source flux	C00719[b] --> C00719[e]	
R_SRC_Gly_DASH_P	0	SourceFlux	.	FALSE	. source flux	Gly-Phe[b] --> Gly-Phe[e]	
R_rxn00744	-250	.	.	TRUE	ATPglycerone phospho	[c] : C00002 + C00184 <==> C00008 + C00111	rxn00744
R_orott	0	Transport Databas	.	TRUE	orottransport	C00295[c] <==> C00295[e]	.
R_rxn02504	0	.	.	TRUE	2-Amino-4-hydroxy-6-(	[c] : C04874 <==> C00266 + C01300	rxn02504
R_rxn05413	0	.	.	FALSE	4-methyl-pentanoyl-AC	[c] : C00080 + C01209 + cpd11549 --> C00011 + C00229 + cpd11550	rxn05413
R_ESC_Ala_DASH_G	0	EscapeFlux	.	FALSE	. escape flux	Ala-Gln[e] --> Ala-Gln[b]	
R_rxn01790	0	.	.	TRUE	(R)-PantoateNADP+ 2-(	[c] : C00006 + C00522 <==> C00005 + C00080 + C00966	rxn01790
R_rxn01476	0	.	.	TRUE	6-Phospho-D-glucono-1	[c] : C00001 + C01236 <==> C00080 + C00345	rxn01476

R_rxn01575	0	.	.	TRUE	L-Isoleucine2-oxoglutar	[c] : C00026 + C00407 <==> C00025 + C03465	rxn01575
R_rxn01649	-1000	.	.	TRUE	Xanthosineorthophospl	[c] : C00009 + C00080 + C01762 <==> C00385 + C00620	rxn01649
R_SRC_cpd17041#_	24.8941	SourceFlux	.	FALSE	. source flux	cpd17041#[b] --> cpd17041#[c]	
R_ESC_C14818_e	0	EscapeFlux	.	FALSE	. escape flux	C14818[e] --> C14818[b]	
R_ESC_C11459_e	0	EscapeFlux	.	FALSE	. escape flux	C11459[e] --> C11459[b]	
R_rxn00006	500	.	.	FALSE	hydrogen-peroxidehydı	[c] : 2 C00027 --> 2 C00001 + C00007	rxn00006
R_rxn00002	0	.	.	FALSE	Urea-1-carboxylate ami	[c] : C00001 + 3 C00080 + C01010 --> 2 C00011 + 2 C01342	rxn00002
R_rxn00001	0	.	.	FALSE	Pyrophosphate phosph	[c] : C00001 + C00013 --> 2 C00009 + 2 C00080	rxn00001
R_rxn01241	1000	.	.	TRUE	DihydrolipoamideNAD-	[c] : C00003 + C00579 <==> C00004 + C00080 + C15972	rxn01241
R_rxn05319	-500	.	.	TRUE	H2Ot5	C00001[e] <==> C00001[c]	rxn05319
R_rxn01388	-1000	.	.	TRUE	isocitrate hydro-lyase	[c] : C00311 <==> C00001 + C00417	rxn01388
R_rxn03958	0	.	.	TRUE	1-Deoxy-D-xylulose-5-p	[c] : C00006 + C11434 <==> C00005 + C00080 + C11437	rxn03958
R_SRC_C00073_e	0	SourceFlux	.	FALSE	. source flux	C00073[b] --> C00073[e]	
R_ESC_C00936_e	0	EscapeFlux	.	FALSE	. escape flux	C00936[e] --> C00936[b]	
R_co2t	-500	Transport Databas	.	TRUE	co2transport	C00011[c] <==> C00011[e]	.
R_rxn01329	0	.	.	TRUE	D-Mannose 6-phosphat	[c] : C00275 <==> C00636	rxn01329
R_rxn00102	0	.	.	TRUE	Carbonic acid hydro-lya	[c] : C00080 + C01353 <==> C00001 + C00011	rxn00102
R_rxn05312	-1000	.	.	TRUE	PIt6	C00009[e] + C00080[e] <==> C00009[c] + C00080[c]	rxn05312
R_rxn05315	0	.	.	TRUE	ZN2t4	C00038[c] + C00080[e] + C00238[e] <==> C00038[e] + C00080[c] + C0023	rxn05315
R_SRC_C00315_e	0	SourceFlux	.	FALSE	. source flux	C00315[b] --> C00315[e]	
R_rxn05442	0	.	.	FALSE	11-methyl-trans-dodec	[c] : C00004 + C00080 + cpd11535 --> C00003 + cpd11536	rxn05442
R_st	0	Transport Databas	.	FALSE	stransport	C00087[e] --> C00087[c]	rxn10605
R_SRC_C00135#_c	2.30576	SourceFlux	.	FALSE	. source flux	C00135#[b] --> C00135#[c]	
R_rxn10481	0	.	.	FALSE	Copper transport via AI	C00001[c] + C00002[c] + C00070[e] --> C00008[c] + C00009[c] + C00070[e	rxn10481
R_SRC_C00049#_c	5.84212	SourceFlux	.	FALSE	. source flux	C00049#[b] --> C00049#[c]	
R_rxn01643	0	.	.	TRUE	L-Aspartate-4-semialde	[c] : C00006 + C00009 + C00441 <==> C00005 + C03082	rxn01643
R_rxn05375	0	.	.	FALSE	10-methyl-dodecanoyl-	[c] : C00080 + C01209 + cpd11511 --> C00011 + C00229 + cpd11512	rxn05375
R_fort	0	Transport Databas	.	FALSE	fortransport	C00058[c] --> C00058[e]	.
R_rxn09112	0	.	.	TRUE	Phosphatidylglycerol sy	[c] : C00623 + cpd15418 <==> C00055 + cpd15546	rxn09112
R_rxn09113	0	.	.	TRUE	Phosphatidylglycerol sy	[c] : C00623 + cpd15421 <==> C00055 + cpd15547	rxn09113
R_rxn09110	0	.	.	TRUE	Phosphatidylglycerol sy	[c] : C00623 + cpd15422 <==> C00055 + cpd15544	rxn09110
R_rxn09111	0	.	.	TRUE	Phosphatidylglycerol sy	[c] : C00623 + cpd15419 <==> C00055 + cpd15545	rxn09111
R_rxn12848	0	.	.	FALSE	Gly-Cys ABC transporte	C00001[c] + C00002[c] + cpd15603[e] --> C00008[c] + C00009[c] + cpd156	rxn12848
R_rxn12849	0	.	.	FALSE	Gly-Leu ABC transporte	C00001[c] + C00002[c] + cpd15604[e] --> C00008[c] + C00009[c] + cpd156	rxn12849
R_rxn09114	0	.	.	TRUE	Phosphatidylglycerol sy	[c] : C00623 + cpd15420 <==> C00055 + cpd15548	rxn09114
R_rxn12844	0	.	.	TRUE	Gly-Cys aminopeptidase	[c] : C00001 + cpd15603 <==> C00037 + C00097	rxn12844
R_rxn01646	0	.	.	TRUE	N-Ribosylnicotinamide(	[c] : C00009 + C03150 <==> C00153 + C00620	rxn01646
R_rxn12846	0	.	.	TRUE	Gly-Phe aminopeptidas	[c] : C00001 + cpd15605 <==> C00037 + C00079	rxn12846
R_rxn12847	0	.	.	TRUE	Gly-Try aminopeptidase	[c] : C00001 + cpd15606 <==> C00037 + C00082	rxn12847
R_rxn01682	1000	.	.	TRUE	(1S,2R)-1-C-(indol-3-yl	[c] : C03506 <==> C00118 + C00463	rxn01682
R_SRC_C00070_e	0	SourceFlux	.	FALSE	. source flux	C00070[b] --> C00070[e]	
R_rxn02811	0	.	.	TRUE	3-Isopropylmalate hydı	[c] : C04411 <==> C00001 + C02631	rxn02811
R_rxn08467	0	.	.	FALSE	FMNH2-dependent mor	[c] : C00007 + C01847 + C05123 --> C00001 + C00061 + C00094 + C00266	rxn08467
R_inst	0	Transport Databas	.	FALSE	instransport	C00294[e] --> C00294[c]	.
R_rxn12639	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11587 <==> C00041 + C00064	rxn12639
R_rxn12638	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11588 <==> C00037 + C00080 + C00148	rxn12638
R_rxn12637	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11589 <==> C00037 + C00049	rxn12637

R_rxn00671	0	.	.	TRUE	2-Methyl-3-oxopropand	[c] : C00003 + C00010 + C00349 <==> C00004 + C00011 + C00100	rxn00671
R_rxn12635	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11591 <==> C00037 + C00073	rxn12635
R_rxn12634	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11592 <==> C00025 + C00037	rxn12634
R_rxn12633	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11593 <==> C00041 + C00049	rxn12633
R_rxn08468	0	.	.	FALSE	FMNH2-dependent mor	[c] : C00007 + C01847 + C11145 --> C00001 + C00061 + C00067 + C00094	rxn08468
R_rxn00676	0	.	.	TRUE	Propanoyl-CoAacetyl-C	[c] : C00024 + C00100 <==> C00010 + C03344	rxn00676
R_ESC_C00305_e	0	EscapeFlux	.	FALSE	. escape flux	C00305[e] --> C00305[b]	
R_rxn05611	-1000	.	.	TRUE	D-mannose transport in	C00080[e] + C00936[e] <==> C00080[c] + C00936[c]	rxn05611
R_rxn02212	0	.	.	FALSE	2-Dehydro-3-deoxy-D-a	[c] : C04691 --> C00009 + C00080 + C00944	rxn02212
R_rxn02213	0	.	.	TRUE	3-Dehydroquinate hydr	[c] : C00944 <==> C00001 + C02637	rxn02213
R_rxn00874	0	.	.	TRUE	Acetyl-CoAacetyl-CoA C	[c] : C00024 + C00136 <==> C00010 + C05269	rxn00874
R_rxn00175	0	.	.	TRUE	AcetateCoA ligase (AMF	[c] : C00002 + C00010 + C00033 + C00080 <==> C00013 + C00020 + C0002	rxn00175
R_thymdt	0	Transport Databas	.	FALSE	thymdtransport	C00214[e] --> C00214[c]	rxn10916
R_rxn01923	0	.	.	FALSE	2-Methylpropanoyl-CoA	[c] : C00007 + 2 C00630 --> 2 C00001 + 2 C03460	rxn01923
R_SRC_C00063#_c	3.23316	SourceFlux	.	FALSE	. source flux	C00063#[b] --> C00063#[c]	
R_rxn00179	1000	.	.	TRUE	ATPL-glutamate 5-phos	[c] : C00002 + C00025 + C00080 <==> C00008 + C03287	rxn00179
R_rxn00178	0	.	.	TRUE	Acetyl-CoAacetyl-CoA C	[c] : 2 C00024 <==> C00010 + C00332	rxn00178
R_rxn01360	0	.	.	FALSE	(S)-Dihydroorotateoxyg	[c] : C00007 + C00337 --> C00027 + C00295	rxn01360
R_rxn05341	0	.	.	TRUE	(3R)-3-Hydroxyoctanoy	[c] : C00006 + C04620 <==> C00005 + C00080 + C05750	rxn05341
R_rxn01925	0	.	.	TRUE	2-methylpropanoyl-CoA	[c] : C00579 + C00630 <==> C00010 + C04424	rxn01925
R_rxn05545	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11582[e] --> C00008[c] + C00009[c] + C0008(	rxn05545
R_rxn05544	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11583[e] --> C00008[c] + C00009[c] + C0008(	rxn05544
R_rxn05547	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11580[e] --> C00008[c] + C00009[c] + C0008(	rxn05547
R_rxn05546	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11581[e] --> C00008[c] + C00009[c] + C0008(	rxn05546
R_rxn05541	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11586[e] --> C00008[c] + C00009[c] + C0008(	rxn05541
R_rxn05540	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11587[e] --> C00008[c] + C00009[c] + C0008(	rxn05540
R_rxn05543	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11584[e] --> C00008[c] + C00009[c] + C0008(	rxn05543
R_rxn05542	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11585[e] --> C00008[c] + C00009[c] + C0008(	rxn05542
R_rxn11268	0	.	.	FALSE	phosphate ABC transpo	C00013[c] + C00080[c] --> C00013[e] + C00080[e]	rxn11268
R_ESC_C14819_e	0	EscapeFlux	.	FALSE	. escape flux	C14819[e] --> C14819[b]	
R_cu2t	0	Transport Databas	.	FALSE	cu2transport	C00070[e] --> C00070[c]	rxn05212
R_ornt	0	Transport Databas	.	FALSE	orntransport	C00077[e] --> C00077[c]	rxn10824
R_rxn05734	0	.	.	TRUE	aldehyde dehydrogenas	[c] : C00001 + C00003 + C00048 <==> C00004 + 2 C00080 + C00209	rxn05734
R_SRC_C00010#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00010#[b] --> C00010#[c]	
R_so4t	1000	Transport Databas	.	FALSE	so4transport	C00059[e] --> C00059[c]	rxn05238
R_rxn01868	-1000	.	.	TRUE	p-Cumic alcoholNADP+	[c] : C00001 + C00006 + C00576 <==> C00005 + 2 C00080 + C00719	rxn01868
R_rxn01872	-1000	.	.	TRUE	succinyl-CoAenzyme N(	[c] : C00091 + C00579 <==> C00010 + C16254	rxn01872
R_nh4t	-1000	Transport Databas	.	TRUE	nh4transport	C01342[c] <==> C01342[e]	.
R_rxn05179	0	.	.	FALSE	L-Isoleucine-ABC transp	C00001[c] + C00002[c] + C00407[e] --> C00008[c] + C00009[c] + C00080[c	rxn05179
R_rxn09345	0	.	.	FALSE	Undecaprenyl diphosph	[c] : 8 C00129 + C00448 --> 8 C00013 + C04574	rxn09345
R_rxn05616	0	.	.	TRUE	magnesium transport in	C00305[c] <==> C00305[e]	rxn05616
R_rxn01867	1000	.	.	TRUE	p-cumic alcoholNAD+ o	[c] : C00001 + C00003 + C00576 <==> C00004 + 2 C00080 + C00719	rxn01867
R_rxn00190	0	.	.	FALSE	Deamido-NAD+L-glutar	[c] : C00001 + C00002 + C00064 + C00857 --> C00003 + C00013 + C00020	rxn00190
R_rxn09188	1000	.	.	TRUE	Proline dehydrogenase	[c] : C00016 + C00148 <==> C01352 + C03912	rxn09188
R_ESC_C00106_e	0	EscapeFlux	.	FALSE	. escape flux	C00106[e] --> C00106[b]	
R_rxn08803	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15313 <==> C00080 + C01233 + C02679	rxn08803
R_rxn00711	0	.	.	TRUE	UMPpyrophosphate ph	[c] : C00013 + C00105 <==> C00106 + C00119	rxn00711

R_rxn00710	0	.	.	FALSE	Orotidine-5'-phosphate	[c] : C00080 + C01103 --> C00011 + C00105	rxn00710
R_rxn00192	0	.	.	FALSE	Acetyl-CoAL-glutamate	[c] : C00024 + C00025 --> C00010 + C00080 + C00624	rxn00192
R_ESC_cpd15666#_	2.30212	EscapeFlux	.	FALSE	. escape flux	cpd15666#[c] --> cpd15666#[b]	
R_SRC_C00001#_c	866.228	SourceFlux	.	FALSE	. source flux	C00001#[b] --> C00001#[c]	
R_SRC_C00079#_c	4.49493	SourceFlux	.	FALSE	. source flux	C00079#[b] --> C00079#[c]	
R_SRC_Ala_DASH_L	0	SourceFlux	.	FALSE	. source flux	Ala-Leu[b] --> Ala-Leu[e]	
R_rxn12642	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11584 <==> C00041 + C00135	rxn12642
R_rxn12643	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11583 <==> C00041 + C00123	rxn12643
R_rxn12640	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11586 <==> C00025 + C00041	rxn12640
R_rxn12641	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11585 <==> C00037 + C00041	rxn12641
R_rxn12646	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11580 <==> C00037 + C00064	rxn12646
R_rxn12644	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11582 <==> C00041 + C00188	rxn12644
R_rxn12645	0	.	.	TRUE	aminopeptidase	[c] : C00001 + cpd11581 <==> C00037 + C00152	rxn12645
R_rxn08126	0	.	.	TRUE	Amylomaltase (maltotr	[c] : C00208 + C01835 <==> C00267 + C02052	rxn08126
R_rxn01274	0	.	.	FALSE	S-(2-Hydroxyacyl)gluta	[c] : C00001 + C03451 --> C00051 + C00080 + C00256	rxn01274
R_rxn02288	0	.	.	TRUE	Uroporphyrinogen-III c	[c] : 4 C00080 + C01051 <==> 4 C00011 + C03263	rxn02288
R_rxn02287	0	.	.	TRUE	S-Adenosyl-L-methioni	[c] : 2 C00019 + C01051 <==> 2 C00021 + 2 C00080 + C02463	rxn02287
R_rxn02286	0	.	.	FALSE	UDP-N-acetylmuramate	[c] : C00002 + C00041 + C01050 --> C00008 + C00009 + C00080 + C01212	rxn02286
R_rxn02285	0	.	.	FALSE	UDP-N-acetylmuramate	[c] : C00005 + C00080 + C04631 --> C00006 + C01050	rxn02285
R_rxn03540	0	.	.	TRUE	adenosylcobyric acid sy	[c] : 4 C00001 + 4 C00002 + 4 C00064 + C06506 <==> 4 C00008 + 4 C0000	rxn03540
R_rxn02666	0	.	.	FALSE	L-2-amino-3-oxobutanc	[c] : C00080 + C03508 --> C00011 + C01888	rxn02666
R_rxn02937	0	.	.	TRUE	2-(Formamido)-N1-(5-I	[c] : C00002 + C04640 <==> C00008 + C00009 + C00080 + C03373	rxn02937
R_nadt	0	Transport Databas	.	FALSE	nadtransport	C00003[e] --> C00003[c]	.
R_ESC_C01330_e	0	EscapeFlux	.	FALSE	. escape flux	C01330[e] --> C01330[b]	
R_rxn00214	0	.	.	TRUE	UDPglucose 4-epimeras	[c] : C00029 <==> C00052	rxn00214
R_rxn05289	0	.	.	TRUE	TRDR	[c] : C00005 + C00080 + C00343 <==> C00006 + C00342	rxn05289
R_rxn00213	0	.	.	TRUE	UTPalpha-D-glucose-1-	[c] : C00075 + C00103 <==> C00013 + C00029	rxn00213
R_adnt	0	Transport Databas	.	FALSE	adntransport	C00212[e] --> C00212[c]	rxn11000
R_rxn00211	0	.	.	TRUE	UDPglucoseNAD+ oxidd	[c] : C00001 + 2 C00003 + C00029 <==> 2 C00004 + 3 C00080 + C00167	rxn00211
R_rxn05040	0	.	.	FALSE	3,4-Dihydroxy-2-butan	[c] : C00199 --> C00058 + C00080 + C15556	rxn05040
R_rxn00409	0	.	.	TRUE	ATPnucleoside-diphosp	[c] : C00002 + C00112 <==> C00008 + C00063	rxn00409
R_rxn05168	0	.	.	FALSE	L-Valine-ABC transport	C00001[c] + C00002[c] + C00183[e] --> C00008[c] + C00009[c] + C00080[c	rxn05168
R_SRC_C00106_e	0	SourceFlux	.	FALSE	. source flux	C00106[b] --> C00106[e]	
R_rxn00566	0	.	.	TRUE	L-Cysteine L-homocyste	[c] : C00001 + C00097 <==> C01342 + C00022 + C00297	rxn00566
R_rxn05163	0	.	.	FALSE	Putrescine-ABC transpo	C00001[c] + C00002[c] + C00134[e] --> C00008[c] + C00009[c] + C00080[c	rxn05163
R_rxn03397	0	.	.	FALSE	UDP-L-rhamnoseflavon	[c] : C00019 + C05813 --> C00021 + C00080 + C05814	rxn03397
R_rxn05161	0	.	.	FALSE	L-Leucine-ABC transpo	C00001[c] + C00002[c] + C00123[e] --> C00008[c] + C00009[c] + C00080[c	rxn05161
R_SRC_gly_DASH_as	0	SourceFlux	.	FALSE	. source flux	gly-asn-L[b] --> gly-asn-L[e]	
R_rxn00407	0	.	.	FALSE	CTP aminohydrolase	[c] : C00001 + C00063 + C00080 --> C01342 + C00075	rxn00407
R_rxn05165	0	.	.	FALSE	L-Proline-ABC transpor	C00001[c] + C00002[c] + C00148[e] --> C00008[c] + C00009[c] + C00080[c	rxn05165
R_rxn01109	1000	.	.	TRUE	beta-D-GlucoseNADP+	[c] : C00006 + C00221 <==> C00005 + C00080 + C00198	rxn01109
R_rxn01108	-1000	.	.	TRUE	beta-D-GlucoseNAD+ 1-	[c] : C00003 + C00221 <==> C00004 + C00080 + C00198	rxn01108
R_rxn02402	0	.	.	TRUE	Nicotinate-nucleotidepy	[c] : C00011 + C00013 + C01185 <==> 2 C00080 + C00119 + C03722	rxn02402
R_ESC_C00080#_c	995.765	EscapeFlux	.	FALSE	. escape flux	C00080#[c] --> C00080#[b]	
R_ncamt	0	Transport Databas	.	FALSE	ncamtransport	C00153[e] --> C00153[c]	rxn10867
R_rxn00816	0	.	.	TRUE	Lactose galactohydrolas	[c] : C00001 + C00243 <==> C00267 + C00124	rxn00816
R_rxn09449	0	.	.	FALSE	fatty-acid--CoA ligase (c	[c] : C00002 + C00010 + C00080 + C01530 --> C00013 + C00020 + C00412	rxn09449

R_rxn01101	0	.	.	TRUE	3-Phospho-D-glycerate	[c] : C00003 + C00197 <==> C00004 + C00080 + C03232	rxn01101
R_rxn01100	-500	.	.	TRUE	ATP3-phospho-D-glyce	[c] : C00002 + C00080 + C00197 <==> C00008 + C00236	rxn01100
R_rxn01103	0	.	.	FALSE	3-Phospho-D-glyceroyl	[c] : C00001 + C00236 --> C00009 + 2 C00080 + C00197	rxn01103
R_rxn01102	-1000	.	.	TRUE	ATP(R)-glycerate 3-phd	[c] : C00002 + C00258 <==> C00008 + C00197	rxn01102
R_rxn02144	0	.	.	FALSE	4-Carboxymethylbut-3-	[c] : C00001 + C03586 --> C00080 + C00846	rxn02144
R_ribflvt	0	Transport Databas	.	FALSE	ribflvtransport	C00255[e] --> C00255[c]	rxn05224
R_rxn01106	500	.	.	TRUE	2-Phospho-D-glycerate	[c] : C00631 <==> C00197	rxn01106
R_SRC_C00208_e	0	SourceFlux	.	FALSE	. source flux	C00208[b] --> C00208[e]	
R_SRC_C00131#_c	0.29243	SourceFlux	.	FALSE	. source flux	C00131#[b] --> C00131#[c]	
R_ESC_C00013#_c	14.9961	EscapeFlux	.	FALSE	. escape flux	C00013#[c] --> C00013#[b]	
R_rxn03164	0	.	.	FALSE	UDP-N-acetylmuramoy	[c] : C00002 + C00993 + C04877 --> C00008 + C00009 + C00080 + C04882	rxn03164
R_SRC_C00086_e	0	SourceFlux	.	FALSE	. source flux	C00086[b] --> C00086[e]	
R_rxn00293	0	.	.	TRUE	UTPN-acetyl-alpha-D-g	[c] : C00075 + C04501 <==> C00013 + C00043	rxn00293
R_rxn08797	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15331 <==> C00080 + C00623 + C06424	rxn08797
R_SRC_C00041#_c	12.4485	SourceFlux	.	FALSE	. source flux	C00041#[b] --> C00041#[c]	
R_ESC_C00038_e	0	EscapeFlux	.	FALSE	. escape flux	C00038[e] --> C00038[b]	
R_ESC_C00073_e	0	EscapeFlux	.	FALSE	. escape flux	C00073[e] --> C00073[b]	
R_pydxt	0	Transport Databas	.	FALSE	pydxtransport	C00250[e] --> C00250[c]	rxn12666
R_rxn02345	1000	.	.	TRUE	(S)-3-Hydroxybutanoyl	[c] : C01144 <==> C03561	rxn02345
R_SRC_C00003#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00003#[b] --> C00003#[c]	
R_SRC_C00152#_c	5.84212	SourceFlux	.	FALSE	. source flux	C00152#[b] --> C00152#[c]	
R_phe_Lt	0	Transport Databas	.	FALSE	phe-Ltransport	C00079[e] --> C00079[c]	rxn11018
R_rxn10052	0	.	.	TRUE	adenylate kinase (Inorg	[c] : C00020 + C00080 + C00536 <==> C00008 + C00013	rxn10052
R_rxn00321	0	.	.	TRUE	L-Lysine 2,3-aminomut	[c] : C00047 <==> C01142	rxn00321
R_ESC_C00243_e	0	EscapeFlux	.	FALSE	. escape flux	C00243[e] --> C00243[b]	
R_rxn03910	0	.	.	TRUE	2-Phospho-4-(cytidine	[c] : C11436 <==> C00055 + C11453	rxn03910
R_rxn08796	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15325 <==> C00080 + C00623 + C02679	rxn08796
R_rxn00328	0	.	.	TRUE	4-Hydroxy-2-oxoglutar	[c] : C05946 <==> C00022 + C00048	rxn00328
R_SRC_C00716#_c	5.22034	SourceFlux	.	FALSE	. source flux	C00716#[b] --> C00716#[c]	
R_phemet	0	Transport Databas	.	FALSE	phemetransport	C00032[e] --> C00032[c]	rxn10919
R_clt	1000	Transport Databas	.	FALSE	cltransport	C00698[e] --> C00698[c]	rxn10473
R_rxn05293	0	.	.	FALSE	MECDPDH	[c] : C00004 + C00080 + C11453 --> C00001 + C00003 + C11811	rxn05293
R_rxn01362	0	.	.	TRUE	Orotidine-5'-phosphate	[c] : C00013 + C01103 <==> C00119 + C00295	rxn01362
R_rxn00285	0	.	.	TRUE	SuccinateCoA ligase (AI	[c] : C00002 + C00010 + C00042 <==> C00008 + C00009 + C00091	rxn00285
R_pit	1000	Transport Databas	.	FALSE	pitransport	C00009[e] --> C00009[c]	.
R_ESC_C00378_e	0	EscapeFlux	.	FALSE	. escape flux	C00378[e] --> C00378[b]	
R_rxn00283	-1000	.	.	TRUE	L-Alanine racemase	[c] : C00041 <==> C00133	rxn00283
R_rxn01834	0	.	.	TRUE	(R)-S-Lactoylglutathion	[c] : C03451 <==> C00051 + C00546	rxn01834
R_SRC_C00407_e	0	SourceFlux	.	FALSE	. source flux	C00407[b] --> C00407[e]	
R_rxn00288	0	.	.	TRUE	Succinate(acceptor) oxi	[c] : C00016 + C00042 <==> C00122 + C01352	rxn00288
R_SRC_cpd11581_e	0	SourceFlux	.	FALSE	. source flux	cpd11581[b] --> cpd11581[e]	
R_rxn10213	0	.	.	FALSE	stearoyl-1-acylglycerol-	[c] : C00412 + cpd15329 --> C00010 + cpd15526	rxn10213
R_rxn10212	0	.	.	FALSE	myristoyl-1-acylglycerd	[c] : C02593 + cpd15331 --> C00010 + cpd15522	rxn10212
R_rxn10211	0	.	.	FALSE	palmitoyl-1-acylglycerd	[c] : C00154 + cpd15327 --> C00010 + cpd15524	rxn10211
R_rxn05195	0	.	.	FALSE	Fe3+-ABC transport	C00001[c] + C00002[c] + C14819[e] --> C00008[c] + C00009[c] + C00080[c	rxn05195
R_rxn05440	0	.	.	FALSE	7-methyl-trans-oct-2-er	[c] : C00004 + C00080 + cpd11527 --> C00003 + cpd11528	rxn05440
R_rxn05441	0	.	.	FALSE	9-methyl-trans-dec-2-e	[c] : C00004 + C00080 + cpd11531 --> C00003 + cpd11532	rxn05441

R_rxn08823	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15357 <==> C00080 + C00623 + cpd15269	rxn08823
R_rxn08127	0	.	.	TRUE	Amylomaltase (maltote	[c] : C00208 + C02052 <==> C00267 + C06218	rxn08127
R_rxn08128	0	.	.	TRUE	Amylomaltase (maltope	[c] : C00208 + C06218 <==> C00267 + C01936	rxn08128
R_rxn08129	0	.	.	TRUE	Amylomaltase (maltohe	[c] : C00208 + C01936 <==> C00267 + C06216	rxn08129
R_rxn10219	0	.	.	FALSE	isohexadecanoyl-1-acyl	[c] : cpd11441 + cpd15676 --> C00010 + cpd15682	rxn10219
R_rxn02789	0	.	.	TRUE	2-Isopropylmalate hydr	[c] : C02504 <==> C00001 + C02631	rxn02789
R_rxn05448	0	.	.	FALSE	10-methyl-trans-undec	[c] : C00004 + C00080 + cpd11560 --> C00003 + cpd11561	rxn05448
R_rxn00882	0	.	.	FALSE	myo-Inositol 4-phospha	[c] : C00001 + C03546 --> C00009 + C00080 + C00137	rxn00882
R_rxn00881	0	.	.	TRUE	myo-Inositol 1-phospha	[c] : C00001 + C01177 <==> C00009 + C00080 + C00137	rxn00881
R_SRC_C00183#_c	10.2464	SourceFlux	.	FALSE	. source flux	C00183#[b] --> C00183#[c]	
R_rxn08312	0	.	.	TRUE	CDP-diacylglycerol synt	[c] : C00063 + cpd15527 <==> C00013 + cpd15420	rxn08312
R_rxn08311	0	.	.	TRUE	CDP-diacylglycerol synt	[c] : C00063 + cpd15526 <==> C00013 + cpd15421	rxn08311
R_rxn08310	0	.	.	TRUE	CDP-diacylglycerol synt	[c] : C00063 + cpd15525 <==> C00013 + cpd15418	rxn08310
R_rxn03437	0	.	.	FALSE	(R)-2,3-Dihydroxy-3-m	[c] : C04104 --> C00001 + C03465	rxn03437
R_rxn03436	0	.	.	TRUE	(S)-2-Aceto-2-hydroxyb	[c] : C00659 <==> C14463	rxn03436
R_rxn09657	0	.	.	FALSE	Thiamine transport in v	C00080[e] + C00378[e] --> C00080[c] + C00378[c]	rxn09657
R_rxn04464	0	.	.	TRUE	5,10-methylenetetrahy	[c] : C00143 + C00365 + C01352 <==> C00016 + C00101 + C00364	rxn04464
R_SRC_C00059_e	0	SourceFlux	.	FALSE	. source flux	C00059[b] --> C00059[e]	
R_malttrt	0	Transport Databas	.	FALSE	malttrtransport	C01835[e] --> C01835[c]	.
R_SRC_C15998_e	0	SourceFlux	.	FALSE	. source flux	C15998[b] --> C15998[e]	
R_rxn03536	1000	.	.	TRUE	Adenosyl cobinamide k	[c] : C00002 + C06508 <==> C00008 + C00080 + C06509	rxn03536
R_rxn03537	0	.	.	TRUE	Adenosyl cobinamide p	[c] : C00044 + C00080 + C06509 <==> C00013 + C06510	rxn03537
R_rxn03534	0	.	.	TRUE	Precorrin 5 = Precorrin	[c] : C00001 + C00019 + C06416 <==> C00021 + C00033 + 2 C00080 + C06	rxn03534
R_rxn03535	0	.	.	TRUE	ATPcob(I)yrinic acid-a,(	[c] : C00002 + C06505 <==> C00536 + C06506	rxn03535
R_rxn05418	0	.	.	TRUE	8-methyl-3-oxo-nonano	[c] : C00005 + C00080 + cpd11554 <==> C00006 + cpd11555	rxn05418
R_rxn01406	0	.	.	TRUE	S-Adenosylmethioninar	[c] : C00134 + C01137 <==> C00080 + C00170 + C00315	rxn01406
R_SRC_C00120_e	0	SourceFlux	.	FALSE	. source flux	C00120[b] --> C00120[e]	
R_rxn00139	-1000	.	.	TRUE	AMPpyrophosphate pho	[c] : C00013 + C00020 <==> C00119 + C00147	rxn00139
R_rxn00138	0	.	.	FALSE	Deamino-NAD+ammon	[c] : C00002 + C01342 + C00857 --> C00003 + C00013 + C00020	rxn00138
R_rxn00137	0	.	.	TRUE	Adenosine 3',5'-bisphos	[c] : C00001 + C00054 <==> C00009 + C00020 + C00080	rxn00137
R_SRC_cpd17043_c	0	SourceFlux	.	FALSE	. source flux	cpd17043[b] --> cpd17043[c]	
R_rxn00134	-1000	.	.	TRUE	ATPadenosine 5'-phosp	[c] : C00002 + C00212 <==> C00008 + C00020	rxn00134
R_SRC_cpd17041_c	0	SourceFlux	.	FALSE	. source flux	cpd17041[b] --> cpd17041[c]	
R_rxn01211	0	.	.	TRUE	5,10-Methenyltetrahyd	[c] : C00001 + C00445 <==> C00080 + C00234	rxn01211
R_rxn01210	0	.	.	FALSE	10-Formyltetrahydrofo	[c] : C00002 + C00025 + C00234 --> C00008 + C00009 + C00080 + C05928	rxn01210
R_rxn01213	0	.	.	FALSE	Dimethylallyl-diphosph	[c] : C00129 + C00235 --> C00013 + C00341	rxn01213
R_rxn01964	-1000	.	.	TRUE	L-Serine hydro-lyase (a	[c] : C00716 + C03506 <==> C00001 + C00078 + C00118	rxn01964
R_SRC_C00001_e	1000	SourceFlux	.	FALSE	. source flux	C00001[b] --> C00001[e]	
R_rxn08838	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15336 <==> C00080 + C01233 + C02679	rxn08838
R_rxn01219	0	.	.	TRUE	ATPCMP phosphotrans	[c] : C00002 + C00239 <==> C00008 + C00705	rxn01219
R_sucrt	0	Transport Databas	.	FALSE	sucrtransport	C00089[e] --> C00089[c]	.
R_rxn00992	0	.	.	TRUE	(R)-3-Hydroxybutanoat	[c] : C00003 + C01089 <==> C00004 + C00080 + C00164	rxn00992
R_rxn05223	0	.	.	FALSE	Biotin ABC transporter	C00001[c] + C00002[c] + C00120[e] --> C00008[c] + C00009[c] + C00080[c	rxn05223
R_rxn08707	0	.	.	TRUE	Heme O synthase	[c] : C00001 + C00032 + C00448 <==> C00013 + C15672	
R_rxn05225	-1000	.	.	TRUE	glucose/mannoseH+ pe	C00267[e] + C00080[c] + C00936[c] <==> C00267[c] + C00080[e] + C0093(	rxn05225
R_rxn10210	0	.	.	FALSE	isohexadecanoyl-glycer	[c] : C00623 + cpd11441 --> C00010 + cpd15676	rxn10210
R_rxn05343	0	.	.	FALSE	Octanoyl-[acyl-carrier p	[c] : C00080 + C05752 + C01209 --> C00011 + C05753 + C00229	rxn05343

R_rxn05342	0	.	.	TRUE	(3R)-3-Hydroxytetrade	[c] : C00006 + C04688 <==> C00005 + C00080 + C05759	rxn05342
R_rxn05613	0	.	.	FALSE	L-methionine S-oxide tr	C00001[c] + C00002[c] + C02989[e] --> C00008[c] + C00009[c] + C00080[c	rxn05613
R_rxn00952	0	.	.	TRUE	O-Acetyl-L-homoserine	[c] : C00297 + C01077 <==> C00033 + C00080 + C05330	rxn00952
R_rxn05347	0	.	.	FALSE	Acyl-[acyl-carrier-prote	[c] : C00080 + C01209 + C03939 --> C00011 + C05744 + C00229	rxn05347
R_rxn05346	0	.	.	FALSE	butyryl-[acyl-carrier pr	[c] : C00080 + C05745 + C01209 --> C00011 + C05746 + C00229	rxn05346
R_rxn05345	0	.	.	FALSE	dodecanoyl-[acyl-carrie	[c] : C00080 + C05223 + C01209 --> C00011 + C05759 + C00229	rxn05345
R_rxn12845	0	.	.	TRUE	Gly-Leu aminopeptidas	[c] : C00001 + cpd15604 <==> C00037 + C00123	rxn12845
R_SRC_C00019#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00019#[b] --> C00019#[c]	
R_rxn00777	0	.	.	TRUE	D-Ribose-5-phosphate I	[c] : C03736 <==> C00199	rxn00777
R_rxn05349	0	.	.	TRUE	acetyl-CoA[acyl-carrier-	[c] : C00024 + C00229 <==> C00010 + C03939	rxn05349
R_rxn05348	0	.	.	FALSE	Decanoyl-[acyl-carrier p	[c] : C00080 + C05755 + C01209 --> C00011 + C05756 + C00229	rxn05348
R_rxn00299	0	.	.	FALSE	GTP 7,8-8,9-dihydrolas	[c] : C00001 + C00044 --> C00058 + C00080 + C04895	rxn00299
R_rxn03541	1000	.	.	TRUE	adenosylcobinamide an	[c] : C03194 + C06507 <==> C00001 + C06508	rxn03541
R_rxn03236	0	.	.	TRUE	4a-hydroxytetrahydrob	[c] : C15522 <==> C00001 + C00268	rxn03236
R_acact	0	Transport Databas	.	FALSE	acactransport	C00164[c] --> C00164[e]	.
R_rxn09978	0	.	.	TRUE	beta-glucosidase (meth	[c] : C00001 + cpd15584 <==> C00267 + C00132	rxn09978
R_SRC_C00134_e	0	SourceFlux	.	FALSE	. source flux	C00134[b] --> C00134[e]	
R_SRC_C00175_e	0	SourceFlux	.	FALSE	. source flux	C00175[b] --> C00175[e]	
R_arg_Lt	0	Transport Databas	.	FALSE	arg-Ltransport	C00062[e] --> C00062[c]	rxn10840
R_rxn01492	250	.	.	TRUE	ATPD-fructose-1-phosp	[c] : C00002 + C01094 <==> C00008 + C00354	rxn01492
R_SRC_C00245_e	0	SourceFlux	.	FALSE	. source flux	C00245[b] --> C00245[e]	
R_SRC_C00075#_c	3.49181	SourceFlux	.	FALSE	. source flux	C00075#[b] --> C00075#[c]	
R_ESC_Ala_DASH_Le	0	EscapeFlux	.	FALSE	. escape flux	Ala-Leu[e] --> Ala-Leu[b]	
R_rxn01985	0	.	.	TRUE	Deoxyinosineorthophos	[c] : C00009 + C00080 + C05512 <==> C00262 + C00672	rxn01985
R_rxn10217	0	.	.	FALSE	isopentadecanoyl-1-acy	[c] : cpd11437 + cpd15674 --> C00010 + cpd15680	rxn10217
R_rxn01987	0	.	.	TRUE	Deoxyribokinase	[c] : C00008 + C00673 <==> C00002 + C01801	rxn01987
R_ESC_L_DASH_alan	0	EscapeFlux	.	FALSE	. escape flux	L-alanylglycine[e] --> L-alanylglycine[b]	
R_rxn12512	0	.	.	FALSE	(R)-4'-Phosphopantoth	[c] : C00002 + C00097 + C03492 --> C00013 + C00020 + C04352	rxn12512
R_SRC_C14818#_c	0.19441	SourceFlux	.	FALSE	. source flux	C14818#[b] --> C14818#[c]	
R_rxn08551	0	.	.	FALSE	glycerol-3-phosphate a	[c] : C00623 + cpd15268 --> C00229 + cpd15329	rxn08551
R_rxn08550	0	.	.	FALSE	glycerol-3-phosphate a	[c] : C00623 + C04364 --> C00229 + cpd15326	rxn08550
R_rxn08552	0	.	.	FALSE	glycerol-3-phosphate a	[c] : C00623 + C01203 --> C00229 + cpd15328	rxn08552
R_rxn05170	0	.	.	FALSE	Maltose-ABC transport	C00001[c] + C00002[c] + C00208[e] --> C00008[c] + C00009[c] + C00080[c	rxn05170
R_rxn02775	0	.	.	TRUE	S-Adenosyl-L-methioni	[c] : C00019 + C00080 + C02463 <==> C00021 + C05772	rxn02775
R_acetonet	0	Transport Databas	.	FALSE	acetonetransport	C00207[c] --> C00207[e]	.
R_rxn09979	0	.	.	TRUE	beta-glucosidase	[c] : C00001 + cpd15585 <==> C00267 + C00132	rxn09979
R_rxn00148	1000	.	.	TRUE	ATPpyruvate O2-phosp	[c] : C00002 + C00022 <==> C00008 + C00074	rxn00148
R_rxn10207	0	.	.	FALSE	isotetradecanoyl-glycer	[c] : C00623 + cpd11435 --> C00010 + cpd15673	rxn10207
R_strch2t	0	Transport Databas	.	FALSE	strch2transport	C00369[e] --> C00369[c]	.
R_SRC_cpd15665#_	2.30212	SourceFlux	.	FALSE	. source flux	cpd15665#[b] --> cpd15665#[c]	
R_ESC_cpd11416_c	0	EscapeFlux	.	FALSE	. escape flux	cpd11416[c] --> cpd11416[b]	
R_rxn00141	0	.	.	TRUE	S-Adenosyl-L-homocyst	[c] : C00001 + C00021 <==> C05330 + C00212	rxn00141
R_mobdt	0	Transport Databas	.	FALSE	mobdtransport	C06232[e] --> C06232[c]	.
R_rxn06335	0	.	.	TRUE	(S)-2-methylbutanoyl-C	[c] : C00579 + C01033 <==> C00010 + C15979	rxn06335
R_rxn00145	-1000	.	.	TRUE	(S)-Lactateferricytochr	[c] : 2 C01070 + C00186 <==> C00022 + 2 C00080 + 2 C01071	rxn00145
R_trp_Lt	0	Transport Databas	.	FALSE	trp-Ltransport	C00078[e] --> C00078[c]	rxn05222
R_rxn08807	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15317 <==> C00080 + C01233 + cpd15237	rxn08807

R_rxn05197	-1000	.	.	TRUE	Uracil ion-coupled tran	C00080[e] + C00106[e] <==> C00080[c] + C00106[c]	rxn05197
R_rxn05538	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11588[e] --> C00008[c] + C00009[c] + C0008(	rxn05538
R_rxn05539	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + C01419[e] --> C00008[c] + C00009[c] + C00080[c	rxn05539
R_rxn08806	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15316 <==> C00080 + C00249 + C01233	rxn08806
R_rxn05534	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11592[e] --> C00008[c] + C00009[c] + C0008(	rxn05534
R_rxn05535	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11591[e] --> C00008[c] + C00009[c] + C0008(	rxn05535
R_rxn06586	0	.	.	TRUE	3-methylbutanoyl-CoAd	[c] : C00579 + C02939 <==> C00010 + C15975	rxn06586
R_rxn08839	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15337 <==> C00080 + C01233 + C06424	rxn08839
R_rxn05533	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11593[e] --> C00008[c] + C00009[c] + C0008(	rxn05533
R_SRC_C00025#_c	6.37322	SourceFlux	.	FALSE	. source flux	C00025#[b] --> C00025#[c]	
R_glyt	0	Transport Databas	.	FALSE	glytransport	C00037[e] --> C00037[c]	rxn05218
R_rxn05425	0	.	.	FALSE	10-methyl-undecanoyl-	[c] : C00080 + C01209 + cpd11561 --> C00011 + C00229 + cpd11562	rxn05425
R_SRC_C00188#_c	6.14005	SourceFlux	.	FALSE	. source flux	C00188#[b] --> C00188#[c]	
R_rxn00395	-1000	.	.	TRUE	L-Arginine iminohydrol	[c] : C00001 + C00062 <==> C01342 + C00327	rxn00395
R_rxn05422	0	.	.	TRUE	10-methyl-3-oxo-undec	[c] : C00005 + C00080 + cpd11558 <==> C00006 + cpd11559	rxn05422
R_rxn09692	0	.	.	TRUE	choline transport via pr	C00080[e] + C00114[e] <==> C00080[c] + C00114[c]	rxn09692
R_rxn09272	1000	.	.	TRUE	succinate dehydrogenas	[c] : C00042 + C17569 <==> C00122 + C00390	rxn09272
R_ESC_C00208_e	0	EscapeFlux	.	FALSE	. escape flux	C00208[e] --> C00208[b]	
R_rxn08802	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15328 <==> C00080 + C00623 + cpd15269	rxn08802
R_rxn05737	0	.	.	FALSE	FMN-dependent monoo	[c] : C00007 + C00245 + C01847 --> C00001 + C00061 + C00094 + C06735	rxn05737
R_SRC_C00037#_c	14.832	SourceFlux	.	FALSE	. source flux	C00037#[b] --> C00037#[c]	
R_rxn05231	0	.	.	TRUE	Ribonucleotide reducta	[c] : C00008 + C00342 <==> C00001 + C00206 + C00343	rxn05231
R_rxn05172	0	.	.	FALSE	Taurine-ABC transport	C00001[c] + C00002[c] + C00245[e] --> C00008[c] + C00009[c] + C00080[c	rxn05172
R_rxn00441	1000	.	.	FALSE	2-OxoglutarateThiamin	[c] : C00026 + C00068 + C00080 --> C00011 + C05381	rxn00441
R_rxn09210	0	.	.	FALSE	Phosphatidylserine syn	[c] : C00716 + cpd15421 --> C00055 + C00080 + cpd15557	rxn09210
R_rxn00726	0	.	.	FALSE	Chorismate pyruvate-ly	[c] : C01342 + C00251 --> C00001 + C00022 + C00080 + C00108	rxn00726
R_rxn00727	0	.	.	FALSE	Chorismate pyruvate-ly	[c] : C00064 + C00251 --> C00022 + C00025 + C00080 + C00108	rxn00727
R_rxn08800	0	.	.	TRUE	Lysophospholipase L1 (	[c] : C00001 + cpd15326 <==> C00080 + C00623 + cpd15237	rxn08800
R_SRC_cpd17042_c	0	SourceFlux	.	FALSE	. source flux	cpd17042[b] --> cpd17042[c]	
R_rxn00449	0	.	.	TRUE	rxn00449	[c] : C00072 + C00080 <==> C03289	rxn00449
R_rxn08309	0	.	.	TRUE	CDP-diacylglycerol synt	[c] : C00063 + cpd15524 <==> C00013 + cpd15419	rxn08309
R_ESC_met_DASH_l	0	EscapeFlux	.	FALSE	. escape flux	met-L-ala-L[e] --> met-L-ala-L[b]	
R_rxn02185	0	.	.	TRUE	2-Acetolactate pyruvate	[c] : C00068 + C06010 <==> C00022 + C05125	rxn02185
R_rxn02186	1000	.	.	TRUE	2,3-Dihydroxy-3-methy	[c] : C00005 + C00080 + C06010 <==> C00006 + C04039	rxn02186
R_rxn02187	-1000	.	.	TRUE	2-Acetolactate methyln	[c] : C06010 <==> C04181	rxn02187
R_SRC_C01835_e	0	SourceFlux	.	FALSE	. source flux	C01835[b] --> C01835[e]	
R_rxn10214	0	.	.	FALSE	isoheptadecanoyl-1-acy	[c] : cpd11432 + cpd15671 --> C00010 + cpd15677	rxn10214
R_rxn01664	0	.	.	FALSE	2-Aminoadipate 6-semi	[c] : C04076 --> C00001 + C00080 + C00450	rxn01664
R_rxn08469	0	.	.	FALSE	FMNH2-dependent mor	[c] : C00007 + C01847 + cpd11579 --> C00001 + C00061 + C00084 + C0009	rxn08469
R_rxn03435	0	.	.	TRUE	(R)-2,3-Dihydroxy-3-m	[c] : C00006 + C04104 <==> C00005 + C00080 + C14463	rxn03435
R_rxn08040	0	.	.	TRUE	UDP-N-acetylglucosami	[c] : C00043 + C17556 <==> C00105 + C01289	rxn08040
R_ESC_C00080_e	0	EscapeFlux	.	FALSE	. escape flux	C00080[e] --> C00080[b]	
R_rxn00675	0	.	.	FALSE	Propinol adenylateCoA	[c] : C00010 + C05983 --> C00020 + C00100	rxn00675
R_rxn05340	0	.	.	TRUE	(3R)-3-Hydroxydodeca	[c] : C00006 + C05757 <==> C00005 + C00080 + C05756	rxn05340
R_rxn03538	0	.	.	TRUE	Adenosylcobalamin 5'-p	[c] : C05775 + C06510 <==> C00144 + C00194	rxn03538
R_rxn10228	0	.	.	FALSE	isotetradecanoyl-CDPdi	[c] : C00716 + cpd15685 --> C00055 + C00080 + cpd15691	rxn10228
R_rxn01019	0	.	.	TRUE	CarbamoyI-phosphateL	[c] : C00077 + C00169 <==> C00009 + 2 C00080 + C00327	rxn01019

R_rxn10174	0	.	.	FALSE	maltohexaose transport	C00001[c] + C00002[c] + C01936[e] --> C00008[c] + C00009[c] + C00080[c	rxn10174
R_rxn07295	0	.	.	FALSE	glycine oxidase	[c] : C00037 --> 3 C00080 + C15809	rxn07295
R_rxn01018	0	.	.	FALSE	Carbamoyl-phosphateL	[c] : C00049 + C00169 --> C00009 + 2 C00080 + C00438	rxn01018
R_rxn01917	-1000	.	.	TRUE	ATPN-acetyl-L-glutama	[c] : C00002 + C00080 + C00624 <==> C00008 + C04133	rxn01917
R_glu_Lt	0	Transport Databas	.	FALSE	glu-Ltransport	C00025[e] --> C00025[c]	rxn10917
R_rxn00085	1000	.	.	TRUE	L-GlutamateNADP+ oxi	[c] : C00006 + 2 C00025 <==> C00005 + C00026 + C00064 + C00080	rxn00085
R_rxn08307	0	.	.	TRUE	CDP-diacylglycerol synt	[c] : C00063 + cpd15522 <==> C00013 + cpd15423	rxn08307
R_ESC_gly_DASH_as	0	EscapeFlux	.	FALSE	. escape flux	gly-asp-L[e] --> gly-asp-L[b]	
R_rxn00789	0	.	.	TRUE	1-(5-Phospho-D-ribosy	[c] : C00013 + C02739 <==> C00002 + C00119	rxn00789
R_rxn11702	0	.	.	FALSE	2-succinyl-5-enolpyruv	[c] : C00026 + C00080 + C00885 --> C00011 + C16519	rxn11702
R_rxn00364	0	.	.	TRUE	ATPCMP phosphotrans	[c] : C00002 + C00055 <==> C00008 + C00112	rxn00364
R_ESC_C00011_e	500	EscapeFlux	.	FALSE	. escape flux	C00011[e] --> C00011[b]	
R_rxn03891	0	.	.	TRUE	trans-hexaprenyltranst	[c] : C00129 + C01230 <==> C00013 + C04216	rxn03891
R_rxn05192	0	.	.	FALSE	Crotono-betaine ABC tr	C00001[c] + C00002[c] + C11458[e] --> C00008[c] + C00009[c] + C00080[c	rxn05192
R_rxn00361	0	.	.	TRUE	ATPadenylylsulfate 3'-p	[c] : C00002 + C00224 <==> C00008 + C00053	rxn00361
R_rxn01000	0	.	.	FALSE	Prephenate hydro-lyase	[c] : C00080 + C00254 --> C00001 + C00011 + C00166	rxn01000
R_rxn00509	0	.	.	TRUE	Succinate-semialdehyd	[c] : C00001 + C00006 + C00232 <==> C00005 + C00042 + 2 C00080	rxn00509
R_rxn05392	0	.	.	FALSE	7-methyl-octanoyl-ACP	[c] : C00080 + C01209 + cpd11528 --> C00011 + C00229 + cpd11529	rxn05392
R_rxn09209	0	.	.	FALSE	Phosphatidylserine syn	[c] : C00716 + cpd15418 --> C00055 + C00080 + cpd15556	rxn09209
R_val_Lt	0	Transport Databas	.	FALSE	val-Ltransport	C00183[e] --> C00183[c]	rxn05245
R_rxn05396	0	.	.	FALSE	9-methyl-decanoyl-ACP	[c] : C00080 + C01209 + cpd11532 --> C00011 + C00229 + cpd11533	rxn05396
R_rxn05397	0	.	.	TRUE	11-methyl-3-oxo-doded	[c] : C00005 + C00080 + cpd11533 <==> C00006 + cpd11534	rxn05397
R_rxn09202	0	.	.	TRUE	Phosphatidylserine dec	[c] : 2 C00080 + cpd15557 <==> C00011 + cpd15533	rxn09202
R_dribt	0	Transport Databas	.	FALSE	dribtransport	C01801[e] --> C01801[c]	.
R_rxn01509	0	.	.	TRUE	ATP(d)GMP phosphotra	[c] : C00002 + C00362 <==> C00008 + C00361	rxn01509
R_rxn09201	0	.	.	TRUE	Phosphatidylserine dec	[c] : 2 C00080 + cpd15556 <==> C00011 + cpd15532	rxn09201
R_rxn09206	0	.	.	FALSE	Phosphatidylserine syn	[c] : C00716 + cpd15423 --> C00055 + C00080 + cpd15553	rxn09206
R_rxn09207	0	.	.	FALSE	Phosphatidylserine syn	[c] : C00716 + cpd15422 --> C00055 + C00080 + cpd15554	rxn09207
R_rxn09205	0	.	.	FALSE	Phosphatidylserine syn	[c] : C00716 + cpd15417 --> C00055 + C00080 + cpd15552	rxn09205
R_rxn05400	0	.	.	FALSE	11-methyl-dodecanoyl-	[c] : C00080 + C01209 + cpd11536 --> C00011 + C00229 + cpd11537	rxn05400
R_rxn05153	0	.	.	FALSE	Sulfate-ABC transport	C00001[c] + C00002[c] + C00059[e] --> C00008[c] + C00009[c] + C00059[c	rxn05153
R_rxn00410	-1000	.	.	TRUE	UTPammonia ligase(AD	[c] : C00002 + C01342 + C00075 <==> C00008 + C00009 + C00063 + 2 C00	rxn00410
R_rxn05537	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11589[e] --> C00008[c] + C00009[c] + C0008(	rxn05537
R_rxn05404	0	.	.	FALSE	13-methyl-tetra-decano	[c] : C00080 + C01209 + cpd11540 --> C00011 + C00229 + cpd11541	rxn05404
R_rxn05405	0	.	.	TRUE	15-methyl-3-oxo-hexa-(	[c] : C00005 + C00080 + cpd11541 <==> C00006 + cpd11542	rxn05405
R_rxn10259	0	.	.	TRUE	isoheptadecanoyl-CDPd	[c] : C00623 + cpd15683 <==> C00055 + cpd15716	rxn10259
R_rxn00927	0	.	.	TRUE	Adenosine ribohydrolas	[c] : C00001 + C00212 <==> C00121 + C00147	rxn00927
R_rxn05408	0	.	.	TRUE	2-methylpropionyl-CoA	[c] : C00630 + C00229 <==> C00010 + cpd11545	rxn05408
R_rxn00929	0	.	.	TRUE	L-ProlineNAD+ 5-oxido	[c] : C00003 + C00148 <==> C00004 + C00080 + C03912	rxn00929
R_rxn00438	0	.	.	TRUE	ATPthiamin-phosphate	[c] : C00002 + C01081 <==> C00008 + C00068	rxn00438
R_rxn00839	1000	.	.	TRUE	ATPnucleoside-diphosp	[c] : C00002 + C00206 <==> C00008 + C00131	rxn00839
R_SRC_cpd17043#_	24.8941	SourceFlux	.	FALSE	. source flux	cpd17043#[b] --> cpd17043#[c]	
R_cys_Lt	0	Transport Databas	.	FALSE	cys-Ltransport	C00097[e] --> C00097[c]	rxn10998
R_rxn02508	0	.	.	TRUE	N-(5-Phospho-beta-D-r	[c] : C04302 <==> C01302	rxn02508
R_rxn05149	0	.	.	FALSE	Manganese-ABC transp	C00001[c] + C00002[c] + C00034[e] --> C00008[c] + C00009[c] + C00034[c	rxn05149
R_rxn10314	0	.	.	TRUE	anteisopentadecanoyl-l	[c] : 24 C00043 + cpd15753 <==> 24 C00015 + cpd15771	rxn10314
R_rxn10315	0	.	.	TRUE	isohexadecanoyl-lipotei	[c] : 24 C00043 + cpd15754 <==> 24 C00015 + cpd15772	rxn10315

R_rxn10312	0	.	.	TRUE	isotetradecanoyl-lipote	[c] : 24 C00043 + cpd15751 <==> 24 C00015 + cpd15769	rxn10312
R_rxn10313	0	.	.	TRUE	isopentadecanoyl-lipot	[c] : 24 C00043 + cpd15752 <==> 24 C00015 + cpd15770	rxn10313
R_rxn10310	0	.	.	TRUE	isoheptadecanoyl-lipot	[c] : 24 C00043 + cpd15749 <==> 24 C00015 + cpd15767	rxn10310
R_rxn10311	0	.	.	TRUE	anteisoheptadecanoyl-l	[c] : 24 C00043 + cpd15750 <==> 24 C00015 + cpd15768	rxn10311
R_rxn00248	-1000	.	.	TRUE	(S)-malateNAD+ oxidor	[c] : C00003 + C00711 <==> C00004 + C00036 + C00080	rxn00248
R_SRC_C00122_e	500	SourceFlux	.	FALSE	. source flux	C00122[b] --> C00122[e]	
R_rxn02503	-500	.	.	TRUE	ATP2-amino-4-hydroxy	[c] : C00002 + C01300 <==> C00020 + C04807	rxn02503
R_rxn02056	0	.	.	TRUE	S-Adenosyl-L-methioni	[c] : 2 C00080 + C00748 <==> C05778 + C14818	rxn02056
R_rxn02507	0	.	.	FALSE	1-(2-Carboxyphenylam	[c] : C00080 + C01302 --> C00001 + C00011 + C03506	rxn02507
R_SRC_C00185_e	0	SourceFlux	.	FALSE	. source flux	C00185[b] --> C00185[e]	
R_rxn00478	0	.	.	FALSE	L-tryptophanoxygen 2,3	[c] : C00007 + C00078 --> C02700	rxn00478
R_rxn01446	0	.	.	TRUE	Deoxyguanosineorthop	[c] : C00009 + C00080 + C00330 <==> C00242 + C00672	rxn01446
R_ureat	0	Transport Databas	.	FALSE	ureatransport	C00086[c] --> C00086[e]	.
R_ESC_C00013_e	0	EscapeFlux	.	FALSE	. escape flux	C00013[e] --> C00013[b]	
R_ESC_C01835_e	0	EscapeFlux	.	FALSE	. escape flux	C01835[e] --> C01835[b]	
R_rxn00077	-1000	.	.	TRUE	ATPNAD+ 2'-phosphotr	[c] : C00002 + C00003 <==> C00006 + C00008	rxn00077
R_SRC_C00267_e	0	SourceFlux	.	FALSE	. source flux	C00267[b] --> C00267[e]	
R_rxn01485	0	.	.	TRUE	D-Glucosamine 1-phosp	[c] : C06156 <==> C00352	rxn01485
R_ESC_cpd11416#_	24.8941	EscapeFlux	.	FALSE	. escape flux	cpd11416#[c] --> cpd11416#[b]	
R_rxn00786	1000	.	.	TRUE	D-Fructose-1,6-bisphos	[c] : C00354 <==> C00111 + C00118	rxn00786
R_ESC_C00698_e	0	EscapeFlux	.	FALSE	. escape flux	C00698[e] --> C00698[b]	
R_rxn05430	0	.	.	TRUE	14-methyl-3-oxo-penta	[c] : C00005 + C00080 + cpd11566 <==> C00006 + cpd11567	rxn05430
R_rxn01255	0	.	.	FALSE	5-O-(1-Carboxyvinyl)-3	[c] : C01269 --> C00009 + C00080 + C00251	rxn01255
R_rxn01257	0	.	.	TRUE	chorismateL-glutamine	[c] : C00064 + C00251 <==> C00025 + C11355	rxn01257
R_rxn01256	0	.	.	TRUE	Chorismate pyruvatem	[c] : C00251 <==> C00254	rxn01256
R_rxn10291	0	.	.	TRUE	stearoyl-lipoteichoic ac	[c] : 24 C00513 + cpd15730 <==> 24 C00055 + cpd15748	rxn10291
R_rxn10218	0	.	.	FALSE	anteisopentadecanoyl-1	[c] : cpd11439 + cpd15675 --> C00010 + cpd15681	rxn10218
R_rxn01316	0	.	.	FALSE	N-Acetylneuraminate p	[c] : C00001 + C00074 + C00645 --> C00009 + C00080 + C00270	rxn01316
R_adet	0	Transport Databas	.	FALSE	adetransport	C00147[e] --> C00147[c]	rxn10918
R_rxn05614	0	.	.	FALSE	L-methionine R-oxide t	C00001[c] + C00002[c] + C15998[e] --> C00008[c] + C00009[c] + C00080[c	rxn05614
R_rxn05344	0	.	.	FALSE	Tetradecanoyl-[acyl-car	[c] : C00080 + C05761 + C01209 --> C00011 + C05762 + C00229	rxn05344
R_rxn05393	0	.	.	TRUE	9-methyl-3-oxo-decano	[c] : C00005 + C00080 + cpd11529 <==> C00006 + cpd11530	rxn05393
R_hxant	0	Transport Databas	.	FALSE	hxantransport	C00262[e] --> C00262[c]	rxn10143
R_rxn05651	-1000	.	.	TRUE	sulfate transport in via	C00059[e] + C00080[e] <==> C00059[c] + C00080[c]	rxn05651
R_strch1t	0	Transport Databas	.	FALSE	strch1transport	C00369[e] --> C00369[c]	
R_gthrdt	0	Transport Databas	.	FALSE	gthrdtransport	C00051[e] --> C00051[c]	rxn10829
R_rxn01343	-1000	.	.	TRUE	ATPSedoheptulose 7-ph	[c] : C00002 + C05382 <==> C00008 + C00447	rxn01343
R_rxn03514	0	.	.	TRUE	S-adenosyl-L-methionir	[c] : C00019 + C06407 <==> C00021 + C00080 + C06416	rxn03514
R_rxn08179	1000	.	.	TRUE	Biotin sulfoxide reducta	[c] : C00005 + C00080 + C20386 <==> C00001 + C00006 + C00120	rxn08179
R_rxn08178	-1000	.	.	TRUE	Biotin sulfoxide reducta	[c] : C00004 + C00080 + C20386 <==> C00001 + C00003 + C00120	rxn08178
R_ascb_Lt	0	Transport Databas	.	FALSE	ascb-Ltransport	C00072[e] --> C00072[c]	.
R_SRC_C00080_e	1000	SourceFlux	.	FALSE	. source flux	C00080[b] --> C00080[e]	
R_rxn10222	0	.	.	TRUE	isotetradecanoyl-phosp	[c] : C00063 + cpd15679 <==> C00013 + cpd15685	rxn10222
R_rxn10223	0	.	.	TRUE	isopentadecanoyl-phos	[c] : C00063 + cpd15680 <==> C00013 + cpd15686	rxn10223
R_rxn10220	0	.	.	TRUE	isoheptadecanoyl-phos	[c] : C00063 + cpd15677 <==> C00013 + cpd15683	rxn10220
R_rxn10221	0	.	.	TRUE	anteisoheptadecanoyl-p	[c] : C00063 + cpd15678 <==> C00013 + cpd15684	rxn10221
R_rxn08850	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15348 <==> C00080 + C01530 + C03274	rxn08850

R_rxn10227	0	.	.	FALSE	anteisoheptadecanoyl-(	[c] : C00716 + cpd15684 --> C00055 + C00080 + cpd15690	rxn10227
R_rxn10224	0	.	.	TRUE	anteisopentadecanoyl-p	[c] : C00063 + cpd15681 <==> C00013 + cpd15687	rxn10224
R_rxn10225	0	.	.	TRUE	isohexadecanoyl-phosp	[c] : C00063 + cpd15682 <==> C00013 + cpd15688	rxn10225
R_rxn01133	0	.	.	TRUE	Acetyl-CoAmaltose O-ac	[c] : C00024 + C00208 <==> C00010 + C02130	rxn01133
R_rxn03408	0	.	.	TRUE	UDP-N-acetylglucosami	[c] : C00043 + C05897 <==> C00015 + C05898	rxn03408
R_rxn12850	0	.	.	FALSE	Gly-Phe ABC transporte	C00001[c] + C00002[c] + cpd15605[e] --> C00008[c] + C00009[c] + cpd156	rxn12850
R_tyr_Lt	0	Transport Databas	.	FALSE	tyr-Ltransport	C00082[e] --> C00082[c]	rxn10974
R_rxn00806	0	.	.	TRUE	L-Leucine2-oxoglutarat	[c] : C00026 + C00123 <==> C00025 + C00233	rxn00806
R_rxn09109	0	.	.	TRUE	Phosphatidylglycerol sy	[c] : C00623 + cpd15423 <==> C00055 + cpd15543	rxn09109
R_rxn02804	0	.	.	TRUE	myristoyl-CoAacetylCoA	[c] : C00024 + C02593 <==> C00010 + C05259	rxn02804
R_rxn05229	0	.	.	FALSE	NCAIR synthetase and N	[c] : C00002 + C01353 + C03373 --> C00008 + C00009 + C00080 + C04751	rxn05229
R_rxn03406	0	.	.	FALSE	Undecaprenyl-diphospl	[c] : C00002 + C01342 + cpd03487 --> C00008 + C00009 + C00080 + cpd03	rxn03406
R_rxn01200	0	.	.	TRUE	Sedoheptulose-7-phosp	[c] : C00118 + C05382 <==> C03736 + C00231	rxn01200
R_SRC_C00062#_c	7.17635	SourceFlux	.	FALSE	. source flux	C00062#[b] --> C00062#[c]	
R_rxn05450	0	.	.	FALSE	14-methyl-trans-pentad	[c] : C00004 + C00080 + cpd11568 --> C00003 + cpd11569	rxn05450
R_SRC_C00009_e	0	SourceFlux	.	FALSE	. source flux	C00009[b] --> C00009[e]	
R_rxn08756	-1000	.	.	TRUE	1-hydroxy-2-methyl-2-(	[c] : C00004 + C00080 + C11811 <==> C00001 + C00003 + C00129	rxn08756
R_rxn00669	0	.	.	TRUE	PropanoateCoA ligase (	[c] : C00002 + C00010 + C00163 <==> C00008 + C00009 + C00100	rxn00669
R_rxn03409	0	.	.	FALSE	Undecaprenyl-diphospl	[c] : C00002 + C01342 + C05898 --> C00008 + C00009 + C00080 + cpd0349	rxn03409
R_rxn02988	0	.	.	TRUE	quinolinate synthase	[c] : 2 C00001 + C00009 + C00080 + C03722 <==> C00111 + C05840	rxn02988
R_rxn02929	0	.	.	TRUE	2,3,4,5-Tetrahydrodipic	[c] : C00006 + C03972 <==> C00005 + C00080 + C03340	rxn02929
R_SRC_C01413_e	0	SourceFlux	.	FALSE	. source flux	C01413[b] --> C01413[e]	
R_rxn06377	0	.	.	FALSE	glycinelipoylprotein oxi	[c] : C00037 + C00080 + C02051 --> C00011 + C01242	rxn06377
R_SRC_C00238_e	0	SourceFlux	.	FALSE	. source flux	C00238[b] --> C00238[e]	
R_rxn02853	0	.	.	TRUE	Imidazole acetaldehyde	[c] : C00001 + C00003 + C05130 <==> C00004 + 2 C00080 + C02835	rxn02853
R_rxn01204	0	.	.	TRUE	4-Aminobutanoate2-ox	[c] : C00026 + C00334 <==> C00025 + C00232	rxn01204
R_rxn00100	0	.	.	FALSE	ATPdephospho-CoA 3'-	[c] : C00002 + C00882 --> C00008 + C00010	rxn00100
R_rxn02200	500	.	.	TRUE	2-Amino-4-hydroxy-6-h	[c] : C00568 + C01300 <==> C00001 + C00921	rxn02200
R_rxn08847	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15345 <==> C00080 + C03274 + cpd15298	rxn08847
R_SRC_C01419_e	0	SourceFlux	.	FALSE	. source flux	C01419[b] --> C01419[e]	
R_rxn05573	-1000	.	.	TRUE	D-glucose transport in v	C00267[e] + C00080[e] <==> C00267[c] + C00080[c]	rxn05573
R_rxn00065	0	.	.	FALSE	ATP pyrophosphate-lya	[c] : C00002 --> C00013 + C00575	rxn00065
R_rxn04750	0	.	.	TRUE	(S)-3-hydroxyacyl-CoAl	[c] : C00003 + C14145 <==> C00004 + C00080 + C02232	rxn04750
R_rxn05219	0	.	.	FALSE	L-Methionine ABC trans	C00001[c] + C00002[c] + C00073[e] --> C00008[c] + C00009[c] + C00073[c	rxn05219
R_rxn05379	0	.	.	FALSE	12-methyl-tetra-decano	[c] : C00080 + C01209 + cpd11515 --> C00011 + C00229 + cpd11516	rxn05379
R_rxn01387	0	.	.	TRUE	IsocitrateNADP+ oxidor	[c] : C00006 + C00311 <==> C00005 + C00080 + C05379	rxn01387
R_rxn10216	0	.	.	FALSE	isotetradecanoyl-1-acyl	[c] : cpd11435 + cpd15673 --> C00010 + cpd15679	rxn10216
R_SRC_C00183_e	0	SourceFlux	.	FALSE	. source flux	C00183[b] --> C00183[e]	
R_rxn08808	0	.	.	FALSE	Lysophospholipase L1 (	[c] : C00001 + C00080 + C04438 --> C01233 + C01530	rxn08808
R_SRC_cpd17042#_	24.8941	SourceFlux	.	FALSE	. source flux	cpd17042#[b] --> cpd17042#[c]	
R_rxn05371	0	.	.	FALSE	8-methyl-decanoyl-ACP	[c] : C00080 + C01209 + cpd11507 --> C00011 + C00229 + cpd11508	rxn05371
R_rxn05376	0	.	.	TRUE	12-methyl-3-oxo-tetra-(	[c] : C00005 + C00080 + cpd11512 <==> C00006 + cpd11513	rxn05376
R_rxn08352	0	.	.	TRUE	1-hydroxy-2-methyl-2-(	[c] : C00004 + C00080 + C11811 <==> C00001 + C00003 + C00235	rxn08352
R_rxn04996	-1000	.	.	TRUE	dimethyallyl diphospha	[c] : C00001 + C00006 + C00235 <==> C00005 + C00080 + C11811	rxn04996
R_SRC_C14819#_c	0.19441	SourceFlux	.	FALSE	. source flux	C14819#[b] --> C14819#[c]	
R_rxn05150	0	.	.	FALSE	Zinc-ABC transport	C00001[c] + C00002[c] + C00038[e] --> C00008[c] + C00009[c] + C00038[c	rxn05150
R_maltt	0	Transport Databas	.	FALSE	malttransport	C00208[e] --> C00208[c]	.

R_rxn05536	0	.	.	FALSE	Dipeptide transport via	C00001[c] + C00002[c] + cpd11590[e] --> C00008[c] + C00009[c] + C0008(	rxn05536
R_rxn02380	-1000	.	.	TRUE	beta-D-Glucose 6-phosp	[c] : C01172 <==> C05345	rxn02380
R_chsterolt	0	Transport Databas	.	FALSE	chsteroltransport	C00187[e] --> C00187[c]	.
R_rxn01871	0	.	.	TRUE	acetyl-CoAenzyme N6-(	[c] : C00024 + C00579 <==> C00010 + C16255	rxn01871
R_rxn01870	-250	.	.	TRUE	D-Fructose 1-phosphat	[c] : C01094 <==> C00111 + C00577	rxn01870
R_rxn05461	0	.	.	TRUE	3-Hydroxyoctodecanoy	[c] : C00005 + C00080 + cpd11570 <==> C00006 + cpd11571	rxn05461
R_SRC_C00407#_c	7.03386	SourceFlux	.	FALSE	. source flux	C00407#[b] --> C00407#[c]	
R_b_D_glucoset	0	Transport Databas	.	FALSE	b-D-glucosetransport	C00221[e] --> C00221[c]	.
R_rxn01629	0	.	.	TRUE	(S)-4-Amino-5-oxopent	[c] : C00430 <==> C03741	rxn01629
R_rxn02933	0	.	.	TRUE	(2S,3S)-3-hydroxy-2-m	[c] : C00003 + C04405 <==> C00004 + C00080 + C03344	rxn02933
R_rxn08528	0	.	.	TRUE	fumarate reductase	[c] : C00122 + C19847 <==> C00042 + C05818	rxn08528
R_rxn02934	0	.	.	TRUE	(2S,3S)-3-Hydroxy-2-m	[c] : C04405 <==> C00001 + C03345	rxn02934
R_rxn01187	0	.	.	FALSE	D-Xylulose 5-phosphate	[c] : C00009 + C00080 + C00231 --> C00001 + C00118 + C00227	rxn01187
R_rxn00011	0	.	.	FALSE	pyruvatethiamin dipho	[c] : C00022 + C00068 + C00080 --> C00011 + C05125	rxn00011
R_rxn02938	0	.	.	FALSE	1-(5-Phospho-D-ribosy	[c] : C00080 + C04751 --> C00011 + C03373	rxn02938
R_rxn00808	0	.	.	TRUE	ATPD-galactose 1-phos	[c] : C00002 + C00124 <==> C00008 + C00446	rxn00808
R_rxn02473	0	.	.	FALSE	D-erythro-1-(Imidazol-	[c] : C04666 --> C00001 + C01267	rxn02473
R_rxn01452	0	.	.	TRUE	(S)-3-Hydroxybutanoyl	[c] : C00006 + C01144 <==> C00005 + C00080 + C00332	rxn01452
R_rxn10337	0	.	.	TRUE	isoheptadecanoyl-cardi	[c] : 2 cpd15722 <==> C00116 + cpd15794	rxn10337
R_rxn02474	0	.	.	TRUE	5-amino-6-(5-phosphor	[c] : C00006 + C04454 <==> C00005 + C00080 + C01268	rxn02474
R_rxn02475	0	.	.	FALSE	2,5-Diamino-6-hydroxy	[c] : C00001 + C00080 + C01304 --> C01342 + C01268	rxn02475
R_rxn02476	0	.	.	TRUE	Phosphoenolpyruvate3	[c] : C00074 + C03175 <==> C00009 + C00080 + C01269	rxn02476
R_celluloset	0	Transport Databas	.	FALSE	cellulosetransport	C00760[e] --> C00760[c]	.
R_rxn02373	-1000	.	.	TRUE	L-Glutamate-5-semialde	[c] : C00006 + C00009 + C01165 <==> C00005 + C03287	rxn02373
R_SRC_C00018#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00018#[b] --> C00018#[c]	
R_rxn01748	0	.	.	TRUE	Allantoin amidohydrola	[c] : C00001 + C01551 <==> C00080 + C00499	rxn01748
R_ESC_C00134_e	0	EscapeFlux	.	FALSE	. escape flux	C00134[e] --> C00134[b]	
R_rxn08817	0	.	.	TRUE	Lysophospholipase L2 (	[c] : C00001 + cpd15350 <==> C00080 + C00623 + C02679	rxn08817
R_rxn02374	0	.	.	FALSE	L-glutamate 5-semialde	[c] : C01165 --> C00001 + C00080 + C03912	rxn02374
R_SRC_C00936_e	0	SourceFlux	.	FALSE	. source flux	C00936[b] --> C00936[e]	
R_rxn03492	0	.	.	TRUE	precorrin-6YNADP+ ox	[c] : C00006 + C06319 <==> C00005 + C00080 + C06320	rxn03492
R_rxn05740	0	.	.	TRUE	cpd00155 phosphoryla	[c] : C00009 + C00080 + C00182 <==> C00103 + C00182	rxn05740
R_rxn00187	0	.	.	TRUE	L-Glutamateammonia li	[c] : C00002 + C01342 + C00025 <==> C00008 + C00009 + C00064 + C0008	rxn00187
R_rxn04050	0	.	.	TRUE	precorrin-6A reductase	[c] : C00005 + C00080 + C11542 <==> C00006 + C11543	rxn04050
R_rxn04052	0	.	.	TRUE	precorrin-8X methylmu	[c] : C11545 <==> C05773	rxn04052
R_rxn02279	0	.	.	FALSE	L-gulono-1,4-lactoneox	[c] : C00007 + C01040 --> C00027 + C03289	rxn02279
R_ESC_C00259_e	0	EscapeFlux	.	FALSE	. escape flux	C00259[e] --> C00259[b]	
R_rxn04113	0	.	.	FALSE	isopentenyl-diphosphat	[c] : C00005 + C00080 + C11811 --> C00001 + C00006 + C00129	rxn04113
R_rxn03990	1000	.	.	TRUE	nitric oxide, NAD(P)H2(	[c] : C00004 + 2 C00007 + 2 C00533 <==> C00003 + C00080 + 2 C00244	rxn03990
R_rxn03991	-1000	.	.	TRUE	nitric oxide, NADPH2ox	[c] : C00005 + 2 C00007 + 2 C00533 <==> C00006 + C00080 + 2 C00244	rxn03991
R_rxn00209	0	.	.	TRUE	Pyridoxine 5-phosphate	[c] : C00007 + C00627 <==> C00018 + C00027	rxn00209
R_rxn00208	0	.	.	TRUE	Pyridoxamine-5'-phosp	[c] : C00001 + C00007 + C00647 <==> C01342 + C00018 + C00027	rxn00208
R_SRC_C00016#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00016#[b] --> C00016#[c]	
R_rxn00499	-1000	.	.	TRUE	(S)-LactateNAD+ oxidor	[c] : C00003 + C00186 <==> C00004 + C00022 + C00080	rxn00499
R_rxn00182	0	.	.	TRUE	L-GlutamateNAD+ oxid(	[c] : C00001 + C00003 + C00025 <==> C00004 + C01342 + C00026 + C0008	rxn00182
R_SRC_C00148_e	0	SourceFlux	.	FALSE	. source flux	C00148[b] --> C00148[e]	
R_rxn00206	0	.	.	TRUE	Superoxidesuperoxide (	[c] : 2 C00704 <==> C00007 + C00027	rxn00206

R_rxn05654	1000	.	.	TRUE	succinate transporter ir	C00042[e] + C00080[e] <==> C00042[c] + C00080[c]	rxn05654
R_ESC_Gly_DASH_T	0	EscapeFlux	.	FALSE	. escape flux	Gly-Tyr[e] --> Gly-Tyr[b]	
R_rxn00183	0	.	.	TRUE	L-Glutamate 5-semialde	[c] : C00001 + C00003 + C01165 <==> C00004 + C00025 + 2 C00080	rxn00183
R_rxn05054	-1000	.	.	TRUE	adenosylcobyric acid(R	[c] : C00002 + C03194 + C06507 <==> C00008 + C00009 + C00080 + C065(	rxn05054
R_coat	0	Transport Databas	.	FALSE	coatransport	C00010[e] --> C00010[c]	rxn10832
R_rxn09240	-1000	.	.	TRUE	Sulfate adenyltransfera	[c] : C00001 + C00002 + C00044 + C00059 <==> C00009 + C00013 + C0003	rxn09240
R_ESC_C00315_e	0	EscapeFlux	.	FALSE	. escape flux	C00315[e] --> C00315[b]	
R_rxn10293	0	.	.	TRUE	anteisoheptadecanoyl-l	[c] : 24 C00513 + cpd15732 <==> 24 C00055 + cpd15750	rxn10293
R_rxn10292	0	.	.	TRUE	isoheptadecanoyl-lipote	[c] : 24 C00513 + cpd15731 <==> 24 C00055 + cpd15749	rxn10292
R_rxn00474	1000	.	.	TRUE	L-Serine hydro-lyase (a	[c] : C00716 + C00463 <==> C00001 + C00078	rxn00474
R_rxn10290	0	.	.	TRUE	myristoyl-lipoteichoic a	[c] : 24 C00513 + cpd15729 <==> 24 C00055 + cpd15747	rxn10290
R_rxn10297	0	.	.	TRUE	isohexadecanoyl-lipote	[c] : 24 C00513 + cpd15736 <==> 24 C00055 + cpd15754	rxn10297
R_rxn10296	0	.	.	TRUE	anteisopentadecanoyl-l	[c] : 24 C00513 + cpd15735 <==> 24 C00055 + cpd15753	rxn10296
R_rxn10295	0	.	.	TRUE	isopentadecanoyl-lipote	[c] : 24 C00513 + cpd15734 <==> 24 C00055 + cpd15752	rxn10295
R_rxn10294	0	.	.	TRUE	isotetradecanoyl-lipote	[c] : 24 C00513 + cpd15733 <==> 24 C00055 + cpd15751	rxn10294
R_rxn00770	1000	.	.	TRUE	ATPD-ribose-5-phospha	[c] : C00002 + C03736 <==> C00020 + C00119	rxn00770
R_ni2t	0	Transport Databas	.	FALSE	ni2transport	C00291[e] --> C00291[c]	.
R_rxn00772	1000	.	.	TRUE	ATPD-ribose 5-phospho	[c] : C00002 + C00121 <==> C00008 + C03736	rxn00772
R_rxn01138	1000	.	.	TRUE	Adenosineorthophosph	[c] : C00009 + C00080 + C00212 <==> C00147 + C00620	rxn01138
R_rxn00802	-1000	.	.	TRUE	N-(L-Argininosuccinate	[c] : C03406 <==> C00062 + C00122	rxn00802
R_rxn02159	0	.	.	TRUE	L-HistidinolNAD+ oxidc	[c] : C00003 + C00860 <==> C00004 + C00080 + C01929	rxn02159
R_rxn07438	0	.	.	TRUE	peptide-methioninethic	[c] : C00001 + C00343 + C03023 <==> C00342 + C15653	rxn07438
R_rxn01134	0	.	.	TRUE	Maltose alpha-D-glucos	[c] : C00208 <==> C01083	rxn01134
R_frut	0	Transport Databas	.	FALSE	frutransport	C10906[e] --> C10906[c]	rxn12996
R_rxn02155	0	.	.	TRUE	ATPnicotinamide-nucle	[c] : C00002 + C01185 <==> C00013 + C00857	rxn02155
R_rxn01137	0	.	.	FALSE	Adenosine aminohydro	[c] : C00001 + C00080 + C00212 --> C01342 + C00294	rxn01137
R_SRC_C00042_e	1000	SourceFlux	.	FALSE	. source flux	C00042[b] --> C00042[e]	
R_SRC_C00229#_c	0.19441	SourceFlux	.	FALSE	. source flux	C00229#[b] --> C00229#[c]	
R_rxn03012	0	.	.	FALSE	rxn03012	[c] : C03871 --> C00001 + C00080 + C03972	rxn03012
R_rxn10042	-1000	.	.	TRUE	ATP synthase (four pro	C00008[c] + C00009[c] + 4 C00080[e] <==> C00001[c] + C00002[c] + 3 C0(	rxn10042
R_rxn10043	-1000	.	.	TRUE	cytochrome-c oxidase (	0.5 C00007[c] + 6 C00080[c] + 2 C01071[c] <==> C00001[c] + 4 C00080[e]	rxn10043
R_rxn03384	0	.	.	TRUE	Uroporphyrinogen I car	[c] : 4 C00080 + C05766 <==> 4 C00011 + C05768	rxn03384
R_rxn05736	0	.	.	FALSE	fatty-acid--CoA ligase (t	[c] : C00002 + C00010 + C00080 + C06424 --> C00013 + C00020 + C02593	rxn05736
R_rxn02201	-500	.	.	TRUE	2-Amino-4-hydroxy-6-h	[c] : C00568 + C04807 <==> C00013 + C00921	rxn02201
R_act	0	Transport Databas	.	TRUE	actransport	C00033[c] <==> C00033[e]	.
R_rxn02011	0	.	.	FALSE	UDP-N-acetylmuramoy	[c] : C00002 + C00680 + C00692 --> C00008 + C00009 + C00080 + C04877	rxn02011
R_rxn00762	-250	.	.	TRUE	GlycerolNAD+ oxidored	[c] : C00003 + C00116 <==> C00004 + C00080 + C00184	rxn00762
R_ESC_C00267_e	250	EscapeFlux	.	FALSE	. escape flux	C00267[e] --> C00267[b]	

Appendix - A - Tfu_v2 - yaml Model With Constraints

ID	Flux	Pathways	ECs	Reversibl	Name	Equation
R_R07268	0	Porphyrin and chlorophyll metabolism	2.5.1.17	TRUE	ATP:cobinamide Cobeta-adenosyltransfe	[c] : C00002 + C05774 <==> C00536 + C06508
R_R01421	0	Benzoate degradation via CoA ligation	3.6.1.7	TRUE	Benzoyl phosphate phosphohydrolase	[c] : C06206 + C00001 <==> C00180 + C00009
R_R05001	0	Phenylalanine metabolism	1.14.13.-	TRUE	.	[c] : 2hyoxplac <==> C06207
R_CTPS2	0	Pyrimidine metabolism	6.3.4.2	FALSE	UTP:ammonia ligase(ADP-forming)	[c] : C00002 + C00064 + C00001 + C00075 --> C00008 + C00063 + C00025 + 2 C00080 + C0
R_R07263	0	Ubiquinone and menaquinone biosynt	4.1.3.36	TRUE	.	[c] : C03160 <==> C15547 + C00001
R_ESC_C00	380.6247	EscapeFlux	.	FALSE	. escape flux	C00183[c] --> C00183[b]
R_CTPS1	9.962462	Pyrimidine metabolism	6.3.4.2	FALSE	UTP:ammonia ligase(ADP-forming)	[c] : C00002 + C01342 + C00075 --> C00008 + C00063 + 2 C00080 + C00009
R_ALDD2x	0	Glycolysis / Gluconeogenesis; Pyruvate	1.2.1.5; 1.2	FALSE	Acetaldehyde:NAD+ oxidoreductase	[c] : C00084 + C00001 + C00003 --> C00033 + 2 C00080 + C00004
R_ALDD2y	0	Pyruvate metabolism	1.2.1.5; 1.2	FALSE	Acetaldehyde:NADP+ oxidoreductase	[c] : C00084 + C00001 + C00006 --> C00033 + 2 C00080 + C00005
R_R01049	56.16209	Purine metabolism; Pentose phosphate	2.7.6.1	TRUE	ATP:D-ribose-5-phosphate diphosphotra	[c] : C00002 + C03736 <==> C00020 + C00119
R_DHPSm	0	Folate biosynthesis	2.5.1.15	FALSE	2-Amino-4-hydroxy-6-hydroxymethyl-7	[c] : 2ahhmp + C00568 --> C00921 + C00001
R_R06884	0	Bisphenol A degradation	1.14.13.-	TRUE	.	[c] : C13624 + C00004 + C00080 + C00007 <==> C13631 + C00003 + C00001
R_R04966	0	Fatty acid biosynthesis	2.3.1.86; 1.	TRUE	Tetradecanoyl-[acyl-carrier protein]:ma	[c] : C05761 + C00003 <==> C05760 + C00004 + C00080
R_R07302	0	Porphyrin and chlorophyll metabolism	6.3.1.10	TRUE	adenosylcobyric acid:(R)-1-aminopropa	[c] : C00002 + C06507 + C03194 <==> C00008 + C00009 + C06508
R_IZPN	0	Histidine metabolism	3.5.2.7	FALSE	4-imidazolone-5-propanoate amidohydr	[c] : C03680 + C00001 --> C00439 + C00080
R_R04961	0	Fatty acid biosynthesis	2.3.1.86; 1.	TRUE	Decanoyl-[acyl-carrier protein]:malonyl	[c] : dcaACP + C00003 <==> C05754 + C00004 + C00080
R_R06883	0	Bisphenol A degradation	1.14.13.-	TRUE	.	[c] : C13624 + C00004 + C00080 + C00007 <==> C13629 + C00003 + C00001
R_R04963	0	Fatty acid biosynthesis	2.3.1.41; 2.	TRUE	Decanoyl-[acyl-carrier protein]:malonyl	[c] : dcaACP + C01209 <==> C05756 + C00011 + apoACP_ACP
R_R04968	0	Fatty acid biosynthesis	2.3.1.41; 2.	TRUE	Tetradecanoyl-[acyl-carrier protein]:ma	[c] : C05761 + C01209 <==> C05762 + C00011 + apoACP_ACP
R_R06888	0	Bisphenol A degradation	1.14.13.-	TRUE	.	[c] : C13631 + C00004 + C00080 + C00007 <==> C13634 + C00003 + C00001
R_IPMD	0	Valine, leucine and isoleucine biosynth	1.1.1.85	FALSE	3-Isopropylmalate:NAD+ oxidoreductase	[c] : C04411 + C00003 --> C04236 + C00080 + C00004
R_THRTRS	0	Glycine, serine and threonine metaboli	6.1.1.3	FALSE	L-Threonine:tRNA(Thr) ligase (AMP-for	[c] : C00002 + C00188 + C01651 --> C00020 + C00013 + C02992
R_mg2t	0.549348	Transport Database	.	FALSE	mg2transport	C00305[e] --> C00305[c]
R_BETALD	0	Glycine, serine and threonine metaboli	1.2.1.8	FALSE	p-cumic alcohol:NAD+ oxidoreductase	[c] : C00576 + C00001 + C00003 --> C00719 + 2 C00080 + C00004
R_R02661	0	Valine, leucine and isoleucine degradat	1.3.99.12;	TRUE	2-methylpropanoyl-CoA:(acceptor) 2,3-d	[c] : C00630 + C00028 <==> C03460 + C00030
R_PYDXNO	0	Vitamin B6 metabolism	1.1.3.12; 1.	TRUE	Pyridoxine:oxygen oxidoreductase (dear	[c] : C00007 + C00314 <==> C00027 + C00250
R_PANTS	0	Pantothenate and CoA biosynthesis; be	6.3.2.1	FALSE	(R)-Pantoate:beta-alanine ligase (AMP-f	[c] : C00099 + C00002 + C00522 --> C00020 + C00080 + C00864 + C00013
R_FBA3	0	Carbon fixation in photosynthetic orga	4.1.2.13	TRUE	Sedoheptulose 1,7-bisphosphate D-glyce	[c] : C00447 <==> C00111 + C00279
R_ALATRS	0	Alanine and aspartate metabolism	6.1.1.7	FALSE	L-Alanine:tRNA(Ala) ligase (AMP-formin	[c] : C00041 + C00002 + C01635 --> C00886 + C00020 + C00013
R_NADDPe	0	Nicotinate and nicotinamide metabolis	3.6.1.22; 3.	FALSE	NAD+ phosphohydrolase	[e] : C00001 + C00003 --> C00020 + 2 C00080 + C00455
R_H2CO3D	40.38509	Nitrogen metabolism	4.2.1.1	TRUE	Carbonic acid hydro-lyase	[c] : C00011 + C00001 <==> C01353
R_R01940	0	Lysine degradation	1.2.4.2	TRUE	2-Oxoadipate:lipoamde 2-oxidoreductas	[c] : C00322 + C15972 <==> C06157 + C00011
R_R04990	0	Ubiquinone and menaquinone biosynt	2.1.1.-	TRUE	UDP-L-rhamnose:flavonol-3-O-D-glucos	[c] : C05813 + C00019 <==> C05814 + C00021
R_GLYCL	0	Nitrogen metabolism	1.4.4.2; 2.1	FALSE	glycine synthase; glycine cleavage syste	[c] : C00037 + C00003 + C00101 --> C00011 + C00143 + C00004 + C01342
R_GLYCK	0	Glycerolipid metabolism; Glyoxylate an	2.7.1.31	FALSE	ATP:(R)-glycerate 3-phosphotransferase	[c] : C00002 + C00258 --> C00197 + C00008 + C00080
R_R05810	0	Porphyrin and chlorophyll metabolism	2.1.1.133	TRUE	cobalt-precorrin-4 methyltransferase	[c] : C11540 + C00019 <==> C16242 + C00021
R_R02111	888.1152	Starch and sucrose metabolism	2.4.1.1	TRUE	1,4-alpha-D-Glucan:orthophosphate alpl	[c] : strch2_strch1 + C00009 <==> C00718 + C00103
R_TMN	0	Thiamine metabolism	3.5.99.2	FALSE	Thiamin hydrolase	[c] : C00001 + C00378 --> C01279 + C04294 + C00080
R_ABTArm	0	Butanoate metabolism; Glutamate met	2.6.1.19	TRUE	4-Aminobutanoate:2-oxoglutarate amino	[c] : C00334 + C00026 <==> C00025 + C00232
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00631[c] --> C00631[b]
R_SPMS	0	Methionine metabolism; Urea cycle and	2.5.1.16	FALSE	S-adenosylmethioninamine:putrescine 3	[c] : C01137 + C00134 --> C00170 + C00080 + C00315
R_cellobios	0.2	Transport Database	.	FALSE	cellobiosetransport	C00185[e] --> C00185[c]
R_urit	0	Transport Database	.	FALSE	uritransport	C00299[e] --> C00299[c]
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00116[c] --> C00116[b]
R_BACCLm	0	Biotin metabolism	6.3.4.10; 6.	FALSE	biotin:CoA ligase (AMP-forming); biotin:	[c] : C00002 + C00120 + C00080 --> C05921 + C00013
R_DNTPPA	0	Folate biosynthesis	3.6.1.-	FALSE	.	[c] : C04895 + C00001 --> C05925 + C00080 + C00013
R_SELADT	0	Selenoamino acid metabolism	2.7.7.4	FALSE	ATP:sulfate adenylyltransferase	[c] : C00002 + C00080 + sel --> adsel + C00013
R_R04964	0	Fatty acid biosynthesis	1.1.1.100; 1	TRUE	(3R)-3-Hydroxydodecanoyl-[acyl-carrie	[c] : C05757 + C00006 <==> C05756 + C00005 + C00080
R_SRC_C00	1000	SourceFlux	.	FALSE	. source flux	C00123[b] --> C00123[e]
R_VALTAm	-409.578	Valine, leucine and isoleucine degradat	2.6.1.6; 2.6	TRUE	L-Valine:2-oxoglutarate aminotransferas	[c] : C00026 + C00183 <==> C00141 + C00025
R_R03909	0	Cyanoamino acid metabolism	3.5.1.4	TRUE	Monocarboxylic acid amide amidohydro	[c] : C03620 + C00001 <==> C00060 + C01342

R_MMMm	0	Valine, leucine and isoleucine degradat	5.4.99.2	TRUE	(R)-Methylmalonyl-CoA CoA-carbonylm	[c] : C01213 <==> C00091
R_R03616	0	Glycerolipid metabolism	3.2.1.23	TRUE	Galactosylglycerol galactohydrolase	[c] : C05401 + C00001 <==> C01582 + C00116
R_cd2t	0	Transport Database	.	FALSE	cd2transport	C01413[e] --> C01413[c]
R_NNATn	1.098696	Nicotinate and nicotinamide metabolis	2.7.7.1; 2.7	FALSE	ATP:nicotinamide-nucleotide adenylyltr	[c] : C00002 + C00080 + C01185 --> C00857 + C00013
R_R01273	-1000	Nicotinate and nicotinamide metabolis	3.2.2.1	TRUE	N-ribosylnicotinamide ribohydrolase	[c] : C03150 + C00001 <==> C00153 + C00121
R_SERTRS	0	Glycine, serine and threonine metaboli	6.1.1.11	FALSE	L-Serine:tRNA(Ser) ligase (AMP-forming	[c] : C00002 + C00716 + C01650 --> C00020 + C00013 + C02553
R_R03683	0	Porphyrin and chlorophyll metabolism	1.14.99.3	TRUE	Hemoglobin:oxygen oxidoreductase (alp	[c] : C01708 + C01352 + 3 C00007 <==> C06258 + biliverd + C00237 + C14819 + C00016 +
R_ESC_C10	0	EscapeFlux	.	FALSE	. escape flux	C10906[c] --> C10906[b]
R_UAPGR	0	Aminosugars metabolism	1.1.1.158	FALSE	UDP-N-acetylmuramate:NADP+ oxidore	[c] : C00080 + C00005 + C04631 --> C00006 + C01050
R_R01830	220.586	Pentose phosphate pathway	2.2.1.1	TRUE	beta-D-Fructose 6-phosphate:D-glyceral	[c] : f6p-B + C00118 <==> C00279 + C00231
R_CS	0	Glyoxylate and dicarboxylate metaboli	2.3.3.1; 2.3	FALSE	Citrate oxaloacetate-lyase ((pro-3S)-CH2	[c] : C00024 + C00001 + C00036 --> C00158 + C00010 + C00080
R_EDA	0	Pentose and glucuronate interconversi	4.1.2.-; 4.1.	FALSE	2-dehydro-3-deoxy-D-gluconate-6-phos	[c] : C04442 --> C00118 + C00022
R_R04546	0	Bile acid biosynthesis	2.3.1.16	TRUE	Propanoyl-CoA:acetyl-CoA C-acyltransfe	[c] : C00100 + dcholcoa <==> C00010 + dhcholestancoa
R_R04547	0	Bile acid biosynthesis	1.3.99.-	TRUE	.	[c] : dhcholestancoa + C00016 <==> dhcholoylcoa + C01352
R_R07767	-1000	Lipoic acid metabolism	2.8.1.8	TRUE	protein N6-(octanoyl)lysine:sulfur sulfu	[c] : C16236 + 2 C00087 + 2 C00019 <==> C16237 + 2 C00073 + 2 C05198
R_R07766	-999.451	Lipoic acid metabolism	2.3.1.181	TRUE	octanoyl-[acp]:protein N6-octanoyltrans	[c] : C05752 + C03688 <==> C16236 + apoACP_ACP
R_R07765	0	Fatty acid biosynthesis	1.3.1.-	TRUE	.	[c] : C16221 + C00004 + C00080 <==> C04088 + C00003
R_R07769	1000	Lipoic acid metabolism	2.3.1.181	TRUE	lipoyl-[acp]:protein N6-lipoyltransferase	[c] : C16239 + C03688 <==> C16237 + apoACP_ACP
R_R07768	1000	Lipoic acid metabolism	2.8.1.8	TRUE	octanoyl-[acp]:sulfur sulfurtransferase	[c] : C05752 + 2 C00087 + 2 C00019 <==> C16239 + 2 C00073 + 2 C05198
R_PUNP1m	-1000	Purine metabolism	2.4.2.1	TRUE	Adenosine:phosphate alpha-D-ribosyltra	[c] : C00212 + C00009 <==> C00147 + C00620
R_CPC3MT	0	Porphyrin and chlorophyll metabolism	2.1.1.131	FALSE	.	[c] : C00019 + C11539 --> C00021 + C11540
R_mn2t	0.549348	Transport Database	.	FALSE	mn2transport	C00034[e] --> C00034[c]
R_R01209	409.5784	Pantothenate and CoA biosynthesis	4.2.1.9	TRUE	2,3-Dihydroxy-3-methylbutanoate hydr	[c] : C04039 <==> C00141 + C00001
R_DGK1	0	Purine metabolism	2.7.4.12; 2.	TRUE	ATP:dGMP phosphotransferase	[c] : C00002 + C00362 <==> C00008 + C00361
R_R01752	0	Glycerolipid metabolism	1.2.1.3	TRUE	D-Glyceraldehyde:NAD+ oxidoreductase	[c] : C00577 + C00003 + C00001 <==> C00258 + C00004 + C00080
R_SHK3Dr	26.02546	Phenylalanine, tyrosine and tryptopha	1.1.1.282;	TRUE	Shikimate:NADP+ 3-oxidoreductase	[c] : C02637 + C00080 + C00005 <==> C00006 + C00493
R_ADSELK	0	Selenoamino acid metabolism	2.7.1.25	FALSE	ATP:adenylylsulfate 3'-phosphotransfer	[c] : adsel + C00002 --> 3padsel + C00008 + C00080
R_TRDRm	3.305323	Pyrimidine metabolism	1.8.1.9	FALSE	NADPH:oxidized-thioredoxin oxidoredu	[c] : C00080 + C00005 + C00343 --> C00006 + C00342
R_ESC_C01	911.7296	EscapeFlux	.	FALSE	. escape flux	C01342[e] --> C01342[b]
R_ESC_C00	180.4544	EscapeFlux	.	FALSE	. escape flux	C00080[e] --> C00080[b]
R_DURIPP	0	Pyrimidine metabolism	2.4.2.23; 2.	TRUE	deoxyuridine:orthophosphate 2-deoxy-I	[c] : C00526 + C00009 <==> C00672 + C00106
R_SDPDS	0	Lysine biosynthesis	3.5.1.18	FALSE	N-Succinyl-LL-2,6-diaminoheptanedioat	[c] : C00001 + C04421 --> C00666 + C00042
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00266[e] --> C00266[b]
R_avite1t	0	Transport Database	.	FALSE	avite1transport	avite1[e] --> avite1[c]
R_R04969	0	Fatty acid biosynthesis	2.3.1.86; 1.	TRUE	Hexadecanoyl-[acyl-carrier protein]:mal	[c] : palmACP + C00003 <==> C05763 + C00004 + C00080
R_ATPM	0	Purine metabolism	3.6.3.9; 3.6	FALSE	ATP phosphohydrolase (protein-secretin	[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_R02520	0	Tyrosine metabolism	1.13.12.-	TRUE	.	[c] : C00544 + C00007 <==> C05585 + C00011 + C00001
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00719[c] --> C00719[b]
R_PAPSR	0	Sulfur metabolism	1.8.4.8	FALSE	adenosine 3',5'-bisphosphate,sulfite:oxid	[c] : C00053 + C00342 --> 2 C00080 + C00054 + C00094 + C00343
R_FBP	0	Carbon fixation in photosynthetic orga	3.1.3.11	FALSE	D-Fructose-1,6-bisphosphate 1-phospho	[c] : C00354 + C00001 --> C05345 + C00009
R_CLPNS_E	0	Glycerophospholipid metabolism	2.7.8.-	TRUE	.	[c] : 0.04 pg_EC <==> 0.02 C05980 + C00116
R_R04640	0	Histidine metabolism	5.3.1.16	TRUE	N-(5'-Phospho-D-ribosylformimino)-5-a	[c] : C04896 <==> C04916
R_R00994	0	Valine, leucine and isoleucine biosynth	1.1.1.85	TRUE	(2R,3S)-3-methylmalate:NAD+ oxidored	[c] : C00109 + C00011 + C00004 + C00080 <==> C06032 + C00003
R_lys_Lt	23.46317	Transport Database	.	FALSE	lys-Ltransport	C00047[e] --> C00047[c]
R_GUAPRT	0	Purine metabolism	2.4.2.22; 2.	FALSE	GMP:diphosphate 5-phospho-alpha-D-ri	[c] : C00242 + C00119 --> C00144 + C00013
R_R02740	888.1152	Glycolysis / Gluconeogenesis; Starch a	5.3.1.9	TRUE	alpha-D-Glucose 6-phosphate ketol-isom	[c] : C00668 <==> f6p-B
R_R03088	1000	Androgen and estrogen metabolism	1.14.13.-	TRUE	.	[c] : C00951 + C00080 + C00007 + C00004 <==> C05301 + C00003 + C00001
R_R03089	0	Androgen and estrogen metabolism	1.14.13.-	TRUE	.	[c] : C00951 + C00080 + C00007 + C00005 <==> C05141 + C00006 + C00001
R_R07697	0	Naphthalene and anthracene degradat	1.14.-.-	TRUE	.	[c] : C16200 + C00007 <==> C00146 + C00001
R_R04953	0	Fatty acid biosynthesis	1.1.1.100;	TRUE	(3R)-3-Hydroxyhexanoyl-[acyl-carrier-p	[c] : C05747 + C00006 <==> C05746 + C00005 + C00080
R_AACOAT	-124.522	Butanoate metabolism	6.2.1.16	TRUE	Acetoacetate:CoA ligase (AMP-forming)	[c] : C00164 + C00002 + C00010 <==> C00332 + C00020 + C00013
R_DHAK	0	Glycerolipid metabolism	2.7.1.29	FALSE	ATP:glycerone phosphotransferase	[c] : C00002 + C01227 --> C00008 + C00111 + C00080
R_R00026	-70.1447	Starch and sucrose metabolism	3.2.1.21	TRUE	beta-D-Glucoside glucohydrolase	[c] : C00185 + C00001 <==> 2 C00221
R_PUTA3	0	Arginine and proline metabolism	1.5.1.12	FALSE	L-Glutamate 5-semialdehyde:NAD+ oxid	[c] : C01165 + C00001 + C00003 --> C00025 + 2 C00080 + C00004
R_ALAR	0	Alanine and aspartate metabolism; D-A	5.1.1.1	TRUE	L-Alanine racemase	[c] : C00041 <==> C00133
R_R01051	0	Pentose phosphate pathway	2.7.1.15	TRUE	ATP:D-ribose 5-phosphotransferase	[c] : C00002 + C00121 <==> C00008 + C03736

R_strch2t	0	Transport Database	.	FALSE	strch2transport	C00369[e] --> C00369[c]
R_R04394	0	Glycolysis / Gluconeogenesis	2.7.1.69	TRUE	Protein-N(pai)-phosphohistidine:sugar I	[c] : C04261 + C01451 <==> C00615 + C06188
R_R04391	0	Pantothenate and CoA biosynthesis	2.7.1.33	TRUE	ATP:pantothenate 4'-phosphotransferas	[c] : C00002 + C04079 <==> C00008 + C04352
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00082[c] --> C00082[b]
R_R08165	0	Ubiquinone and menaquinone biosynt	2.2.1.9	TRUE	2-succinyl-5-enolpyruvyl-6-hydroxy-3-c	[c] : C00885 + C00026 <==> C16519 + C00011
R_PRAMPC	0	Histidine metabolism	3.5.4.19	FALSE	1-(5-phospho-D-ribosyl)-AMP 1,6-hydrc	[c] : C00001 + C02741 --> C04896
R_NAPRT	0	Nicotinate and nicotinamide metabolis	2.4.2.11	FALSE	Nicotinate D-ribonucleotide:diphosphat	[c] : C00080 + C11486 + C00119 --> C01185 + C00013
R_5HOXIN	0	Tryptophan metabolism	1.2.1.3	FALSE	5-Hydroxyindoleacetaldehyde:NAD+ oxi	[c] : 5hoxindact + C00001 + C00003 --> 5hoxindoa + 2 C00080 + C00004
R_R02571	0	Lysine degradation	2.3.1.61	TRUE	Glutaryl-CoA:dihydrolipoamide S-succin	[c] : C00527 + C15973 <==> C00010 + C06157
R_ADCS	0	Folate biosynthesis	2.6.1.85	FALSE	chorismate:L-glutamine aminotransfera	[c] : C00251 + C00064 --> C11355 + C00025
R_R02570	503.5043	Citrate cycle (TCA cycle)	2.3.1.61	TRUE	succinyl-CoA:enzyme N6-(dihydrolipoyl	[c] : C00091 + C15973 <==> C00010 + C16254
R_btnt	0	Transport Database	.	FALSE	btntransport	C00120[e] --> C00120[c]
R_R04432	0	Propanoate metabolism	1.3.99.3	TRUE	Propanoyl-CoA:(acceptor) 2,3-oxidoredu	[c] : etfox + C00100 <==> etfrd + prpncoa
R_DHDPRy	27.7166	Lysine biosynthesis	1.3.1.26	FALSE	2,3,4,5-Tetrahydrodipicolinate:NADP+ o	[c] : C03340 + C00080 + C00005 --> C00006 + C03972
R_R00316	-1000	Pyruvate metabolism	6.2.1.1	TRUE	Acetate:CoA ligase (AMP-forming)	[c] : C00002 + C00033 <==> C00013 + C05993
R_NTPP10	0	Purine metabolism	3.6.1.19	FALSE	2'-Deoxyinosine-5'-triphosphate pyroph	[c] : C01345 + C00001 --> C06196 + C00080 + C00013
R_NTPP11	0	Purine metabolism	3.6.1.19	FALSE	XTP pyrophosphohydrolase	[c] : C00001 + C00700 --> C00080 + C00013 + C00655
R_R04805	0	Bile acid biosynthesis	1.1.1.1	TRUE	.	[c] : xol7ah3 + C00003 <==> xol7ah2al + C00004 + C00080
R_R03012	0	Histidine metabolism	1.1.1.23	TRUE	L-Histidinol:NAD+ oxidoreductase	[c] : C00860 + C00003 <==> C01929 + C00004 + C00080
R_FBA2	0	Fructose and mannose metabolism	4.1.2.13	TRUE	D-Fructose 1-phosphate D-glyceraldehy	[c] : C01094 <==> C00111 + C00577
R_R04801	0	Carotenoid biosynthesis	.	TRUE	.	[c] : C05431 <==> C05434
R_R00691	0	Phenylalanine, tyrosine and tryptopha	4.2.1.51; 4.	TRUE	L-Arogenate hydro-lyase (decarboxylati	[c] : C00826 <==> C00079 + C00001 + C00011
R_UDPG4E	0	Nucleotide sugars metabolism; Galacto	5.1.3.2	TRUE	UDPglucose 4-epimerase	[c] : C00029 <==> C00052
R_R06782	0	Phenylalanine metabolism	1.14.12.19	TRUE	3-phenylpropanoate,NADH:oxygen oxid	[c] : C05629 + C00007 + C00004 + C00080 <==> C11588 + C00003
R_FMETTR	0	Methionine metabolism; One carbon p	2.1.2.9	FALSE	10-Formyltetrahydrofolate:L-methionyl	[c] : C00234 + C02430 --> C03294 + C00080 + C00101
R_SHKK	26.02546	Phenylalanine, tyrosine and tryptopha	2.7.1.71	FALSE	ATP:shikimate 3-phosphotransferase	[c] : C00002 + C00493 --> C00008 + C00080 + C03175
R_GLUTRS	0	Glutamate metabolism; Porphyrin and	6.1.1.24; 6.	FALSE	L-Glutamate:tRNA(Glu) ligase (AMP-forr	[c] : C00002 + C00025 + C01641 --> C00020 + C02987 + C00013
R_GLUTRR	0	Porphyrin and chlorophyll metabolism	1.2.1.70	FALSE	L-glutamate-semialdehyde: NADP+ oxid	[c] : C02987 + C00080 + C00005 --> C03741 + C00006 + C01641
R_R05233	0	3-Chloroacrylic acid degradation	1.1.1.1	TRUE	.	[c] : C06611 <==> C06613 + 2 C00080
R_G5SD	0	Urea cycle and metabolism of amino gr	1.2.1.41	FALSE	L-Glutamate-5-semialdehyde:NADP+ 5-(	[c] : C03287 + C00080 + C00005 --> C01165 + C00006 + C00009
R_xyltt	0	Transport Database	.	FALSE	xylttransport	C00379[e] --> C00379[c]
R_R05237	0	3-Chloroacrylic acid degradation	1.2.1.3	TRUE	.	[c] : C06613 + C00001 <==> C06614 + 2 C00080
R_R05629	0	Peptidoglycan biosynthesis	2.7.8.13	TRUE	UDPMurAc(oyl-L-Ala-D-gamma-Glu-L-Ly	[c] : C04702 + C17556 <==> C00105 + C04851
R_ANS	0	Phenylalanine, tyrosine and tryptopha	4.1.3.27	FALSE	Chorismate pyruvate-lyase (amino-acce	[c] : C00251 + C00064 --> C00108 + C00025 + C00080 + C00022
R_R05234	0	3-Chloroacrylic acid degradation	1.1.1.1	TRUE	.	[c] : C06612 <==> C16348 + 2 C00080
R_HSTPT	0	Histidine metabolism	2.6.1.9	FALSE	5-Amino-2-oxopentanoate:2-oxoglutara	[c] : C00025 + C01267 --> C00026 + C01100
R_R07934	0	Biosynthesis of unsaturated fatty acids	1.3.3.6	TRUE	.	[c] : C16168 + C00016 <==> C16374 + C01352
R_R05627	-6.50523	Peptidoglycan biosynthesis	3.6.1.27	TRUE	Undecaprenyl-diphosphate phosphohyd	[c] : C04574 + C00001 <==> C17556 + C00009
R_MMSAD1	759.9417	Inositol phosphate metabolism	1.2.1.18; 1.	FALSE	3-Oxopropanoate:NAD+ oxidoreductase	[c] : C00010 + C00222 + C00003 --> C00024 + C00011 + C00004
R_ile_Lt	0	Transport Database	.	FALSE	ile-Ltransport	C00407[e] --> C00407[c]
R_R05623	0	Methane metabolism	1.14.13.-	TRUE	.	[c] : C00565 + C00004 + C00080 + C00007 <==> C01104 + C00003 + C00001
R_R00428	0	Folate biosynthesis	3.5.4.16	TRUE	GTP 7,8-8,9-dihydrolase	[c] : C00044 + C00001 <==> C05922
R_GLU5Km	0	Urea cycle and metabolism of amino gr	2.7.2.11	FALSE	ATP:L-glutamate 5-phosphotransferase	[c] : C00002 + C00025 --> C00008 + C03287
R_ADSL2r	30.52756	Purine metabolism	4.3.2.2	TRUE	1-(5'-Phosphoribosyl)-5-amino-4-(N-suc	[c] : C04823 <==> C04677 + C00122
R_MI3PP	0	Inositol phosphate metabolism	3.1.3.25	FALSE	1D-myo-Inositol 3-phosphate phosphoh	[c] : C00001 + C04006 --> C00137 + C00009
R_R01374	0	Phenylalanine metabolism	1.4.99.1	TRUE	D-phenylalanine:acceptor oxidoreductas	[c] : C02265 + C00001 + C00028 <==> C00166 + C01342 + C00030
R_ESC_C00	1000	EscapeFlux	.	FALSE	. escape flux	C00001[e] --> C00001[b]
R_acetonet	0	Transport Database	.	FALSE	acetonetransport	C00207[c] --> C00207[e]
R_SPRMS	0	beta-Alanine metabolism	2.5.1.22; 2.	FALSE	S-adenosylmethioninamine:spermidine	[c] : C01137 + C00315 --> C00170 + C00080 + C00750
R_coat	0.549348	Transport Database	.	FALSE	coatransport	C00010[e] --> C00010[c]
R_SRC_C00	17.31399	SourceFlux	.	FALSE	. source flux	C00097[b] --> C00097[e]
R_R01542	0	Pentose and glucuronate interconversi	1.1.1.127;	TRUE	2-Dehydro-3-deoxy-D-gluconate:NAD+ 5	[c] : C00204 + C00003 <==> C04349 + C00004 + C00080
R_R04939	0	Selenoamino acid metabolism	2.1.1.-	TRUE	.	[c] : C05693 + C05691 <==> C05694 + seahcys
R_AMMQT	0	Ubiquinone and menaquinone biosynt	2.1.1.-	FALSE	.	[c] : C05818 + C00019 --> C00021 + C00080 + mqn6
R_ICHORT	0	Biosynthesis of siderophore group non	3.3.2.1	FALSE	Isochorismate pyruvate-hydrolase	[c] : C00001 + C00885 --> C04171 + C00022
R_GNNUC	0	Purine metabolism	3.2.2.8; 3.2	FALSE	Guanosine ribohydrolase	[c] : C00387 + C00001 --> C00242 + C00121

R_SRC_C00	0.549348	SourceFlux	.	FALSE	. source flux	C00034[b] --> C00034[e]
R_R00471	0	Arginine and proline metabolism	4.1.1.3; 4.1	TRUE	D-4-Hydroxy-2-oxoglutarate glyoxylate-	[c] : C05946 <==> C00022 + C00048
R_HSK	13.10453	Glycine, serine and threonine metaboli	2.7.1.39	FALSE	ATP:L-homoserine O-phosphotransferas	[c] : C00002 + C00263 --> C00008 + C00080 + C01102
R_AMID	0	Urea cycle and metabolism of amino gr	3.5.1.4	FALSE	4-Guanidinobutanamide amidohydrolas	[c] : C03078 + C00001 --> 4gudbutn + C01342
R_TRPO2	0	Tryptophan metabolism	1.13.11.11	FALSE	L-tryptophan:oxygen 2,3-oxidoreductas	[c] : C00007 + C00078 --> C02700
R_DHNAOT	0	Ubiquinone and menaquinone biosynt	2.5.1.-	FALSE	.	[c] : C03657 + C04146 --> C05818 + C00011 + C00080 + C00013
R_HPROxm	0	Arginine and proline metabolism	1.5.1.2	FALSE	trans-4-Hydroxy-L-proline:NAD+ 5-oxid	[c] : C01157 + C00003 --> C04281 + 2 C00080 + C00004
R_GALUi	888.1152	Starch and sucrose metabolism; Nucle	2.7.7.9	FALSE	UTP:alpha-D-glucose-1-phosphate uridy	[c] : C00103 + C00080 + C00075 --> C00013 + C00029
R_galt	0	Transport Database	.	FALSE	galtransport	C00124[e] --> C00124[c]
R_pro_Lt	0	Transport Database	.	FALSE	pro-Ltransport	C00148[e] --> C00148[c]
R_R00878	-1000	Fructose and mannose metabolism	5.3.1.5	TRUE	alpha-D-Glucose ketol-isomerase	[c] : C00267 <==> C10906
R_guat	0	Transport Database	.	FALSE	guatransport	C00242[e] --> C00242[c]
R_PRDX	0	Methane metabolism	1.11.1.6; 1.	FALSE	Hydorogen-peroxide:hydrogen-peroxide	[c] : C00027 + C00132 --> C00067 + 2 C00001
R_SRC_C00	0.549348	SourceFlux	.	FALSE	. source flux	C00238[b] --> C00238[e]
R_R06636	0	Biosynthesis of type II polyketide back	.	TRUE	.	[c] : C00100 + 7 C00083 <==> C12349 + 7 C00011 + 7 C00010
R_R06637	0	Biosynthesis of type II polyketide back	.	TRUE	.	[c] : C00136 + 7 C00083 <==> C12350 + 7 C00011 + 7 C00010
R_UMPK	20.65581	Pyrimidine metabolism	2.7.4.4; 2.7	TRUE	ATP:nucleoside-phosphate phosphotran	[c] : C00002 + C00105 <==> C00008 + C00015
R_R06635	0	Biosynthesis of type II polyketide back	.	TRUE	.	[c] : C00024 + 7 C00083 <==> C12348 + 7 C00011 + 7 C00010
R_GF6PTA	0	Aminosugars metabolism; Glutamate m	2.6.1.16	FALSE	L-Glutamine:D-fructose-6-phosphate am	[c] : C05345 + C00064 --> C00352 + C00025
R_glc_Dt	0	Transport Database	.	FALSE	glc-Dtransport	C00267[e] --> C00267[c]
R_SRC_C00	1.098696	SourceFlux	.	FALSE	. source flux	C00255[b] --> C00255[e]
R_ser_Lt	0	Transport Database	.	FALSE	ser-Ltransport	C00716[e] --> C00716[c]
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00047[c] --> C00047[b]
R_PROTRS	0	Arginine and proline metabolism	6.1.1.15	FALSE	L-Proline:tRNA(Pro) ligase (AMP-formin	[c] : C00002 + C00148 + C01649 --> C00020 + C00013 + C02702
R_THFGLU	0	Folate biosynthesis	6.3.2.17	TRUE	Tetrahydrofolate:L-glutamate gamma-lig	[c] : C00002 + C00025 + C00101 <==> C00008 + C00080 + C00009 + C03541
R_KYN	0	Tryptophan metabolism	3.7.1.3	FALSE	L-Kynurenine hydrolase	[c] : Lkynr + C00001 --> C00041 + C00108 + C00080
R_R01899	-1000	Citrate cycle (TCA cycle)	1.1.1.42	TRUE	Isocitrate:NADP+ oxidoreductase (decar	[c] : C00311 + C00006 <==> C05379 + C00005 + C00080
R_R02110	888.1152	Starch and sucrose metabolism	2.4.1.18	TRUE	1,4-alpha-D-Glucan:1,4-alpha-D-glucan 6	[c] : C00718 <==> strch2_strch1
R_R01710	0	Vitamin B6 metabolism	1.4.3.5	TRUE	Pyridoxamine:oxygen oxidoreductase (d	[c] : C00534 + C00001 + C00007 <==> C00250 + C01342 + C00027
R_METB1	0	Methionine metabolism	2.5.1.49	FALSE	O-Acetyl-L-homoserine succinate-lyase (	[c] : C01077 + C00097 --> C00033 + cyst-L + C00080
R_tyr_Lt	0	Transport Database	.	FALSE	tyr-Ltransport	C00082[e] --> C00082[c]
R_ARGTRS	0	Arginine and proline metabolism	6.1.1.19	FALSE	L-Arginine:tRNA(Arg) ligase (AMP-form	[c] : C00062 + C00002 + C01636 --> C00020 + C02163 + C00013
R_TPI	331.5805	Glycolysis / Gluconeogenesis; Carbon f	5.3.1.1	TRUE	D-glyceraldehyde-3-phosphate aldose-k	[c] : C00111 <==> C00118
R_pyrt	0	Transport Database	.	TRUE	pyrtransport	C00022[c] <==> C00022[e]
R_2OXOAD	0	Tryptophan metabolism	2.3.1.61; 1.	FALSE	2-oxoadipate dehydrogenase complex	[c] : C00322 + C00010 + C00003 --> C00011 + C00527 + C00004
R_fe2t	0.549348	Transport Database	.	FALSE	fe2transport	C14818[e] --> C14818[c]
R_xant	0	Transport Database	.	FALSE	xantransport	C00385[e] --> C00385[c]
R_MTHFCr	61.05511	One carbon pool by folate; Glyoxylate a	3.5.4.9	TRUE	5,10-Methenyltetrahydrofolate 5-hydrol	[c] : C00001 + C00445 <==> C00234 + C00080
R_R07807	0	Glycosaminoglycan degradation	3.2.1.23	TRUE	.	[c] : G13032 + C00001 <==> G06780 + C00124
R_NDPK6	0	Pyrimidine metabolism	2.7.4.6	TRUE	ATP:dUDP phosphotransferase	[c] : C00002 + C01346 <==> C00008 + C00460
R_NDPK5	-999.174	Purine metabolism	2.7.4.6	TRUE	ATP:dGDP phosphotransferase	[c] : C00002 + C00361 <==> C00008 + C00286
R_NDPK4	0.826331	Pyrimidine metabolism	2.7.4.6	TRUE	ATP:dTDP phosphotransferase	[c] : C00002 + C00363 <==> C00008 + C00459
R_zn2t	0.549348	Transport Database	.	FALSE	zn2transport	C00038[e] --> C00038[c]
R_NDPK1	-327.72	Purine metabolism	2.7.4.6	TRUE	ATP:GDP phosphotransferase	[c] : C00002 + C00035 <==> C00008 + C00044
R_ALDD20	0	Tryptophan metabolism	1.2.1.3	FALSE	Indole-3-acetaldehyde:NAD+ oxidoredu	[c] : C00001 + C00637 + C00003 --> 2 C00080 + C00954 + C00004
R_PGPPT	0	Glycerophospholipid metabolism	2.7.8.5	FALSE	CDP-diacylglycerol:sn-glycerol-3-phospl	[c] : cdpdag_hs + C00623 --> C00055 + C00080 + pgp_hs
R_PSSA_HE	0	Glycerophospholipid metabolism; Glyc	2.7.8.8	TRUE	CDP-diacylglycerol:L-serine 3-phosphati	[c] : cdpdag_HP + C00716 <==> C00055 + C00080 + ps_HP
R_GPDDA2	0	Glycerophospholipid metabolism	3.1.4.46; 3.	FALSE	sn-Glycero-3-phosphoethanolamine glyc	[c] : C01233 + C00001 --> C00189 + C00623 + C00080
R_SRC_C00	0.549348	SourceFlux	.	FALSE	. source flux	C00010[b] --> C00010[e]
R_LEUTAm	0	Valine, leucine and isoleucine degradat	2.6.1.6; 2.6	TRUE	L-Leucine:2-oxoglutarate aminotransfer	[c] : C00026 + C00123 <==> C00233 + C00025
R_PYAM5P	0	Vitamin B6 metabolism	1.4.3.5	TRUE	Pyridoxamine-5'-phosphate:oxygen oxid	[c] : C00001 + C00007 + C00647 <==> C00027 + C01342 + C00018
R_R03270	-496.496	Glycolysis / Gluconeogenesis; Pyruvate	1.2.4.1	TRUE	.	[c] : C05125 + C15972 <==> C16255 + C00068
R_ala_Lt	0	Transport Database	.	FALSE	ala-Ltransport	C00041[e] --> C00041[c]
R_SCP2x	0	Bile acid biosynthesis	2.3.1.16	FALSE	Propanoyl-CoA:acetyl-CoA C-acyltransfe	[c] : C00010 + dhocholoylcoa --> dgcholcoa + C00100
R_R04592	0	Bile acid biosynthesis	1.3.99.-	TRUE	.	[c] : cholcoar + C00016 <==> cholcoads + C01352
R_R01159	0	Histidine metabolism	2.1.1.-	TRUE	S-adenosyl-L-methionine:L-histidine N-r	[c] : C00135 + C00019 <==> C01152 + C00021

R_ENO	1000	Glycolysis / Gluconeogenesis	4.2.1.11	TRUE	2-Phospho-D-glucerate hydro-lyase	[c] : C00631 <==> C00001 + C00074
R_R08245	0	Drug metabolism - other enzymes	2.4.2.8	TRUE	6-thioguanosine monophosphate:diphos	[c] : C07648 + C00119 <==> C16619 + C00013
R_R08244	0	Drug metabolism - other enzymes	6.3.5.2	TRUE	6-thioxanthine 5'-monophosphate:L-glu	[c] : C16618 + C00002 + C00064 + C00001 <==> C16619 + C00020 + C00013 + C00025
R_R01253	984.8459	Arginine and proline metabolism	1.5.99.8	TRUE	L-proline:(acceptor) oxidoreductase	[c] : C00148 + C00028 <==> C03912 + C00030
R_GLUR	0	Glutamate metabolism; D-Glutamine a	5.1.1.3	TRUE	L-Glutamate racemase	[c] : C00217 <==> C00025
R_DCTPD2	0	Pyrimidine metabolism	3.5.4.13	FALSE	CTP aminohydrolase	[c] : C00063 + C00080 + C00001 --> C01342 + C00075
R_R08240	0	Drug metabolism - other enzymes	1.1.1.205	TRUE	6-thioinosine 5'-monophosphate:NAD+ (	[c] : C04646 + C00003 + C00001 <==> C16618 + C00004 + C00080
R_DADAe	0	Purine metabolism	3.5.4.4	FALSE	Deoxyadenosine aminohydrolase	[e] : C00559 + C00080 + C00001 --> C05512 + C01342
R_R04111	0	Starch and sucrose metabolism	2.7.1.69	TRUE	Protein-N(pai)-phosphohistidine:sugar I	[c] : C04261 + C00208 <==> C00615 + C05737
R_ESC_C16	0.549348	EscapeFlux	.	FALSE	. escape flux	C16236[c] --> C16236[b]
R_THFATm	0	One carbon pool by folate	2.1.2.10	FALSE	S-Aminomethyldihydrolipoylprotein:(6S	[c] : C00001 + C00445 --> C03479 + C00080
R_GND	0	Glutathione metabolism; Pentose phos	1.1.1.44	FALSE	6-phospho-D-gluconate:NADP+ 2-oxidor	[c] : C00345 + C00006 --> C00011 + C00005 + C00199
R_R02279	0	Ascorbate and aldarate metabolism	4.2.1.41	TRUE	5-Dehydro-4-deoxy-D-glucarate hydro-l	[c] : 5dh4dglc <==> C00433 + C00001 + C00011
R_R04506	0	Bile acid biosynthesis	1.2.1.3	TRUE	3alpha,7alpha-Dihydroxy-5beta-cholest	[c] : xol7ah2al + C00003 + C00001 <==> dhcholestanate + C00004 + C00080
R_pit	74.20598	Transport Database	.	FALSE	pitransport	C00009[e] --> C00009[c]
R_R07895	0	alpha-Linolenic acid metabolism	2.3.1.16	TRUE	.	[c] : C16335 + C00024 <==> C00010 + C16334
R_BAMPPA	0	beta-Alanine metabolism	1.2.1.3	FALSE	beta-Aminopropion aldehyde:NAD+ oxid	[c] : bamppald + C00001 + C00003 --> C00099 + 2 C00080 + C00004
R_R07896	0	alpha-Linolenic acid metabolism	1.3.3.6	TRUE	.	[c] : C16335 + C00016 <==> C16336 + C01352
R_R07891	0	alpha-Linolenic acid metabolism	2.3.1.16	TRUE	.	[c] : C16331 + C00024 <==> C00010 + C16330
R_ACSm	20.22547	Reductive carboxylate cycle (CO2 fixat	6.2.1.1	FALSE	Acetate:CoA ligase (AMP-forming)	[c] : C00033 + C00002 + C00010 --> C00024 + C00020 + C00013
R_R07892	0	alpha-Linolenic acid metabolism	1.3.3.6	TRUE	.	[c] : C16331 + C00016 <==> C16332 + C01352
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00711[e] --> C00711[b]
R_amett	0	Transport Database	.	FALSE	amettransport	C00019[e] --> C00019[c]
R_IMACTD	0	Histidine metabolism	1.2.1.3	FALSE	Imidazole acetaldehyde:NAD+ oxidoredu	[c] : C00001 + im4act + C00003 --> 2 C00080 + im4ac + C00004
R_R04379	0	Tyrosine metabolism	5.3.3.10	TRUE	5-Carboxymethyl-2-hydroxymuconate d	[c] : C04186 <==> C04052
R_R04378	0	Purine metabolism	2.4.2.7	TRUE	1-(5'-Phosphoribosyl)-5-amino-4-imida	[c] : C04677 + C00013 <==> C04051 + C00119
R_4abzt	0	Transport Database	.	FALSE	4abztransport	C00568[e] --> C00568[c]
R_R03051	-590.422	Pantothenate and CoA biosynthesis	1.1.1.86	TRUE	2,3-Dihydroxy-3-methylbutanoate:NADI	[c] : C00900 + C00005 + C00080 <==> C04039 + C00006
R_R03050	1000	Butanoate metabolism	2.2.1.6	TRUE	2-Acetolactate pyruvate-lyase (carboxyl	[c] : C00900 + C00068 <==> C05125 + C00022
R_inostt	0	Transport Database	.	FALSE	inosttransport	C00137[e] --> C00137[c]
R_OCBT	20.27863	Urea cycle and metabolism of amino gr	2.1.3.3	TRUE	Carbamoyl-phosphate:L-ornithine carba	[c] : C00169 + C00077 <==> C00327 + C00080 + C00009
R_ALPHNH	0	Urea cycle and metabolism of amino gr	3.5.1.54	FALSE	Urea-1-carboxylate amidohydrolase	[c] : C01010 + 3 C00080 + C00001 --> 2 C00011 + 2 C01342
R_GLYCTO	0	Glyoxylate and dicarboxylate metaboli	1.1.3.15	FALSE	(S)-2-Hydroxy-acid:oxygen 2-oxidoredu	[c] : C00160 + C00007 --> C00048 + C00027
R_ADOCBL	0	Porphyrin and chlorophyll metabolism	2.7.8.26	FALSE	.	[c] : C06510 + C05775 --> C00194 + C00144 + C00080
R_SRC_C00	0.549348	SourceFlux	.	FALSE	. source flux	C00038[b] --> C00038[e]
R_SRC_C04	0.549348	SourceFlux	.	FALSE	. source flux	C04619[b] --> C04619[c]
R_CINNDO	0	Phenylalanine metabolism	1.14.12.19	FALSE	trans-cinnamate,NADH:oxygen oxidored	[c] : C00423 + C00080 + C00004 + C00007 --> C12622 + C00003
R_R02971	0	Pantothenate and CoA biosynthesis	2.7.1.33; 2.	TRUE	ATP:pantothenate 4'-phosphotransferas	[c] : C00002 + C00831 <==> C00008 + C01134
R_ACBIPGT	0	Porphyrin and chlorophyll metabolism	2.7.7.62	FALSE	.	[c] : C06509 + C00044 + C00080 --> C06510 + C00013
R_R06558	0	Porphyrin and chlorophyll metabolism	2.7.1.156	TRUE	.	[c] : C06508 + C00044 <==> C06509 + C00035
R_GMPS	15.5355	Purine metabolism	6.3.5.2; 6.3	FALSE	Xanthosine-5'-phosphate:ammonia ligas	[c] : C00002 + C01342 + C00655 --> C00020 + C00144 + 2 C00080 + C00013
R_R07955	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07481 + C00004 + C00080 + C00007 <==> C07480 + C00003 + C00067 + C00001
R_st	0	Transport Database	.	FALSE	stransport	C00087[e] --> C00087[c]
R_TYRTAp	-9.44384	Tyrosine metabolism; Phenylalanine, t	2.6.1.9; 2.6	TRUE	L-Tyrosine:2-oxoglutarate aminotransfe	[c] : C00026 + C00082 <==> C01179 + C00025
R_R07970	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C16358 + C00005 + C00080 + C00007 <==> C00385 + C00006 + C00067 + C00001
R_R07971	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07481 + C00004 + C00080 + C00007 <==> C07130 + C00003 + C00067 + C00001
R_R07976	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07130 + C00005 + C00080 + C00007 <==> C16358 + C00006 + C00067 + C00001
R_R07809	0	Glycosaminoglycan degradation	3.2.1.52	TRUE	.	[c] : G13033 + C00001 <==> G08421 + C01132
R_GCCbim	0.248494	One carbon pool by folate; Glycine, ser	2.1.2.10	FALSE	S-aminomethyldihydrolipoylprotein:(6S	[c] : C01242 + C00101 --> C02972 + C00143 + C01342
R_R07975	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07130 + C00004 + C00080 + C00007 <==> C16358 + C00003 + C00067 + C00001
R_R08231	0	Drug metabolism - other enzymes	2.4.2.10	TRUE	5-fluorouridine monophosphate:diphos	[c] : C07649 + C00119 <==> C16634 + C00013
R_na1t	0	Transport Database	.	FALSE	na1transport	C01330[e] --> C01330[c]
R_ICL	0	Glyoxylate and dicarboxylate metaboli	4.1.3.1	FALSE	Isocitrate glyoxylate-lyase	[c] : C00311 --> C00048 + C00042
R_R08237	0	Drug metabolism - other enzymes	2.4.2.8	TRUE	6-thioinosine 5'-monophosphate:diphos	[c] : C02380 + C00119 <==> C04646 + C00013
R_R08238	0	Drug metabolism - other enzymes	2.4.2.8	TRUE	6-methylthiopurine 5'-monophosphate r	[c] : C16614 + C00119 <==> C16615 + C00013
R_AHCi	0	Methionine metabolism	3.3.1.1	FALSE	S-Adenosyl-L-homocysteine hydrolase	[c] : C00021 + C00001 --> C00212 + C05330

R_R02687	0	Glycerolipid metabolism	3.1.1.3	TRUE	1,2-Diacyl-sn-glycerol acylhydrolase	[c] : 12dgr_SC_12dgr_EC + C00001 <==> mag_hs + C00162
R_SUCBZS	0	Ubiquinone and menaquinone biosynt	4.2.1.113	FALSE	.	[c] : C05817 --> C00001 + C02730
R_TMPKr	0	Thiamine metabolism	2.7.4.16	TRUE	ATP:thiamin-phosphate phosphotransfe	[c] : C00002 + C01081 <==> C00008 + C00068
R_FCLTm	0	Porphyrin and chlorophyll metabolism	4.99.1.1	FALSE	Protoporphyrin ferro-lyase	[c] : C14818 + C02191 --> 2 C00080 + C00032
R_R00829	0	Benzoate degradation via hydroxylatio	2.3.1.16; 2.	TRUE	Succinyl-CoA:acetyl-CoA C-acyltransfera	[c] : C00091 + C00024 <==> C00010 + C02232
R_urat	0	Transport Database	.	FALSE	uratransport	C00106[e] --> C00106[c]
R_R00430	-357.422	Purine metabolism	2.7.1.40	TRUE	GTP:pyruvate 2-O-phosphotransferase	[c] : C00044 + C00022 <==> C00035 + C00074
R_ESC_C00	113.2408	EscapeFlux	.	FALSE	. escape flux	C00049[c] --> C00049[b]
R_R05150	0	Porphyrin and chlorophyll metabolism	1.3.1.54	TRUE	precorrin-6Y:NADP+ oxidoreductase	[c] : C06319 + C00006 <==> C06320 + C00005 + C00080
R_FDH	0	Methane metabolism; Glyoxylate and d	1.2.1.2	FALSE	Formate:NAD+ oxidoreductase	[c] : C00058 + C00003 --> C00011 + C00004
R_R00006	-409.578	Pantothenate and CoA biosynthesis	2.2.1.6	TRUE	2-Acetolactate pyruvate-lyase (carboxyl	[c] : C00900 + C00011 <==> 2 C00022
R_ESC_C00	969.1428	EscapeFlux	.	FALSE	. escape flux	C00123[c] --> C00123[b]
R_NADK	0.549348	Nicotinate and nicotinamide metabolis	2.7.1.23	FALSE	ATP:NAD+ 2'-phosphotransferase	[c] : C00002 + C00003 --> C00008 + C00080 + C00006
R_SUCD1i	0	Butanoate metabolism; Reductive carb	1.3.99.1	FALSE	Succinate:(acceptor) oxidoreductase	[c] : C00016 + C00042 --> C01352 + C00122
R_ACOAD8	0	Valine, leucine and isoleucine degradat	1.3.99.10;	FALSE	3-Methylbutanoyl-CoA:(acceptor) 2,3-ox	[c] : C00016 + C02939 --> C03069 + C01352
R_R04673	19.87598	Valine, leucine and isoleucine biosynth	2.2.1.6	TRUE	(S)-2-Aceto-2-hydroxybutanoate pyruva	[c] : C00109 + C05125 <==> C00659 + C00068
R_ASPO6	1.098696	Nicotinate and nicotinamide metabolis	1.4.3.16	FALSE	.	[c] : C00049 + C00007 --> C00027 + C05840
R_R03599	35.17646	Selenoamino acid metabolism	4.4.1.16	TRUE	Selenocysteine reductase	[c] : C05688 + C00030 <==> C01528 + C00041 + C00028
R_SELMET	0	Selenoamino acid metabolism	2.5.1.6	FALSE	ATP:L-methione S-adenosyltransferase	[c] : C00002 + C00001 + C05335 --> C00009 + C00013 + C05691
R_gsnt	0	Transport Database	.	FALSE	gsntransport	C00387[e] --> C00387[c]
R_UGMDDS	0	Peptidoglycan biosynthesis; Lysine bio	6.3.2.10	FALSE	UDP-N-acetylmuramoyl-L-alanyl-D-gluta	[c] : C00993 + C00002 + C04877 --> C00008 + C00080 + C00009 + C04882
R_FT	0	Terpenoid biosynthesis	2.5.1.-	FALSE	Farnesyl diphosphate:Isopentenyl dipho	[c] : C00448 + C00129 --> C00013 + ttc-ggdp
R_tcyntt	0	Transport Database	.	FALSE	tcynttransport	C01755[e] --> C01755[c]
R_PUNP4	0	Purine metabolism	2.4.2.1; 2.4	TRUE	Deoxyguanosine:orthophosphate ribosy	[c] : C00330 + C00009 <==> C00672 + C00242
R_R01900	432.0533	Reductive carboxylate cycle (CO2 fixati	4.2.1.3	TRUE	isocitrate hydro-lyase (cis-aconitate-for	[c] : C00311 <==> C00417 + C00001
R_ARGSS	0	Alanine and aspartate metabolism; Urc	6.3.4.5	FALSE	L-Citrulline:L-aspartate ligase (AMP-for	[c] : C00049 + C00002 + C00327 --> C00020 + C03406 + C00080 + C00013
R_R07959	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C13747 + C00004 + C00080 + C00007 <==> C16358 + C00003 + C00067 + C00001
R_MMEm	0	Valine, leucine and isoleucine degradat	5.1.99.1	TRUE	Methylmalonyl-CoA epimerase	[c] : C01213 <==> C00683
R_R05579	0	Benzoate degradation via CoA ligation	1.3.99.7	TRUE	Glutaryl-CoA:(acceptor) 2,3-oxidoreduct	[c] : C00527 + C00028 <==> C02411 + C00030
R_SEAHCY	0	Selenoamino acid metabolism	3.3.1.1	FALSE	Se-Adenosylselenohomocysteine hydrol	[c] : C00001 + seahcys --> C00212 + selhcys
R_gln_Lt	0	Transport Database	.	FALSE	gln-Ltransport	C00064[e] --> C00064[c]
R_cytdt	0	Transport Database	.	FALSE	cytdtransport	cytd[e] --> cytd[c]
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00073[c] --> C00073[b]
R_SRC_C00	6.515515	SourceFlux	.	FALSE	. source flux	C00135[b] --> C00135[e]
R_PPBNGS	0	Porphyrin and chlorophyll metabolism	4.2.1.24	FALSE	5-Aminolevulinate hydro-lyase(adding 5	[c] : 2 C00430 --> C00080 + 2 C00001 + C00931
R_TMABAL	0	Lysine degradation	1.2.1.47; 1.	FALSE	4-Trimethylammoniobutanal:NAD+ 1-ox	[c] : 4tmeabut + C00001 + C00003 --> 4tmeabutn + 2 C00080 + C00004
R_CYTK1	0	Pyrimidine metabolism	2.7.4.14	TRUE	ATP:CMP phosphotransferase	[c] : C00002 + C00055 <==> C00008 + C00112
R_R01325	-432.053	Reductive carboxylate cycle (CO2 fixati	4.2.1.4; 4.2	TRUE	citrate hydro-lyase (cis-aconitate-formir	[c] : C00158 <==> C00417 + C00001
R_SRC_C00	0.549348	SourceFlux	.	FALSE	. source flux	C00305[b] --> C00305[e]
R_phe_Lt	0	Transport Database	.	FALSE	phe-Ltransport	C00079[e] --> C00079[c]
R_IPPSm	0	Valine, leucine and isoleucine biosynth	2.3.3.13	FALSE	acetyl-CoA:3-methyl-2-oxobutanoate C-a	[c] : C00141 + C00024 + C00001 --> C02504 + C00010 + C00080
R_ESC_met	0	EscapeFlux	.	FALSE	. escape flux	metmal[c] --> metmal[b]
R_NP1	0	Nicotinate and nicotinamide metabolis	2.4.2.1	FALSE	Nicotinate D-ribonucleoside:orthophosp	[c] : C00080 + C11486 + C00620 --> nicrns + C00009
R_PGM	-1000	Glycolysis / Gluconeogenesis	5.4.2.1	TRUE	2-Phospho-D-glycerate 2,3-phosphomut	[c] : C00631 <==> C00197
R_MPML	0	Porphyrin and chlorophyll metabolism	6.6.1.1	TRUE	Magnesium-protoporphyrin IX chelatase	[c] : C00002 + C00001 + C00305 + C02191 <==> C00008 + 3 C00080 + C03516 + C00009
R_PGK	-1000	Glycolysis / Gluconeogenesis; Carbon f	2.7.2.3	TRUE	ATP:3-phospho-D-glycerate 1-phosphot	[c] : C00197 + C00002 <==> C00236 + C00008
R_R06983	0	Methane metabolism	1.1.1.284	TRUE	S-(hydroxymethyl)glutathione dehydrog	[c] : C14180 + C00003 <==> Sfglutth + C00004 + C00080
R_R05884	0	Biosynthesis of steroids	1.17.1.2	TRUE	isopentenyl-diphosphate:NAD(P)+ oxidc	[c] : C11811 + C00005 + C00080 <==> C00129 + C00006 + C00001
R_ARGDr	-20.2786	Arginine and proline metabolism	3.5.3.6	TRUE	L-Arginine iminohydrolase	[c] : C00062 + C00001 <==> C00327 + C01342
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00256[c] --> C00256[b]
R_TRPS3	0	Phenylalanine, tyrosine and tryptopha	4.1.2.8; 4.2	FALSE	(1S,2R)-1-C-(indol-3-yl)glycerol 3-phosp	[c] : C03506 --> C00118 + C00463
R_TRPS2	0	Phenylalanine, tyrosine and tryptopha	4.2.1.20	FALSE	L-Serine hydro-lyase (adding indoleglyc	[c] : C00463 + C00716 --> C00001 + C00078
R_TRPS1	3.880026	Phenylalanine, tyrosine and tryptopha	4.2.1.20	FALSE	L-Serine hydro-lyase (adding indoleglyc	[c] : C03506 + C00716 --> C00118 + C00001 + C00078
R_zymstt	0	Transport Database	.	FALSE	zymsttransport	C05437[e] --> C05437[c]
R_R06004	0	Glycosphingolipid biosynthesis - gangl	3.2.1.52	TRUE	.	[c] : G00109 + C00001 <==> G00108 + C01132
R_R02056	0	Glycerophospholipid metabolism; Glyc	2.1.1.17	TRUE	S-Adenosyl-L-methionine:phosphatidyle	[c] : C00019 + pe_EC_pe_SC_pe_HP_pe_hs_pe_SA <==> C00021 + C01241

R_biomass	70.34473	BiomassObjective	.	FALSE	BiomassRxn	[c] : 34.7964804614 C00001 + 40.1701382876 C00002 + 0.00780937124549 C00003 + 0.0
R_R02355	1000	Androgen and estrogen metabolism	1.14.13.-	TRUE	.	[c] : C00468 + C00080 + C00007 + C00005 <==> C05298 + C00006 + C00001
R_R02354	-1000	Androgen and estrogen metabolism	1.14.13.-	TRUE	.	[c] : C00468 + C00080 + C00007 + C00004 <==> C05298 + C00003 + C00001
R_folt	0	Transport Database	.	FALSE	foltransport	C00504[e] --> C00504[c]
R_R02356	0	Androgen and estrogen metabolism	1.14.13.-	TRUE	.	[c] : C00468 + C00080 + C00007 + C00005 <==> C05300 + C00006 + C00001
R_APRAUR	0	Riboflavin metabolism	1.1.1.193	FALSE	5-amino-6-(5-phosphoribitylamino)urac	[c] : C01268 + C00080 + C00005 --> C04454 + C00006
R_GLUDym	1000	Glutamate metabolism; Nitrogen metal	1.4.1.3; 1.4	TRUE	L-Glutamate:NADP+ oxidoreductase (de	[c] : C00025 + C00001 + C00006 <==> C00026 + C00080 + C00005 + C01342
R_R03896	0	Valine, leucine and isoleucine biosynth	4.2.1.35	TRUE	(R)-2-Methylmalate hydro-lyase	[c] : C02612 <==> C02226 + C00001
R_R03898	0	Valine, leucine and isoleucine biosynth	.	TRUE	.	[c] : C02226 + C00001 <==> C06032
R_R07759	0	Biosynthesis of unsaturated fatty acids	1.1.1.-	TRUE	.	[c] : C16216 + C00005 + C00080 <==> C16217 + C00006
R_GMPS2	0	Glutamate metabolism; Purine metabo	6.3.5.2	FALSE	Xanthosine-5'-phosphate:L-glutamine ar	[c] : C00002 + C00064 + C00001 + C00655 --> C00020 + C00025 + C00144 + 2 C00080 + C0
R_AGPR	-20.2786	Urea cycle and metabolism of amino gr	1.2.1.38	TRUE	N-Acetyl-L-glutamate-5-semialdehyde:N	[c] : C01250 + C00006 + C00009 <==> C04133 + C00080 + C00005
R_nact	0	Transport Database	.	FALSE	nactransport	C11486[e] --> C11486[c]
R_R01747	0	Glyoxylate and dicarboxylate metaboli	1.1.1.60	TRUE	(R)-Glycerate:NADP+ oxidoreductase	[c] : C00258 + C00006 <==> 2h3oppan + C00005 + C00080
R_GLACO	0	Ascorbate and aldarate metabolism	1.2.1.3	FALSE	D-Glucuronolactone:NAD+ oxidoreducta	[c] : glac + 2 C00001 + C00003 --> C00818 + 3 C00080 + C00004
R_R07858	0	Carotenoid biosynthesis	.	TRUE	.	[c] : C16340 <==> C15943
R_GLYKm	0	Glycerolipid metabolism	2.7.1.30	FALSE	ATP:glycerol 3-phosphotransferase	[c] : C00002 + C00116 --> C00008 + C00623 + C00080
R_R04859	964.8235	Cysteine metabolism	2.5.1.49; 2.	TRUE	O3-Acetyl-L-serine acetate-lyase (adding	[c] : C00979 + C05529 + C00342 + C00080 <==> C00097 + C00094 + C00343 + C00033
R_GUACYC	0	Purine metabolism	4.6.1.1; 4.6	FALSE	GTP pyrophosphate-lyase (cyclizing)	[c] : C00044 --> C00942 + C00013
R_R06890	0	Bisphenol A degradation	1.14.13.-	TRUE	.	[c] : C13637 + C00005 + C00080 + C00007 <==> C13638 + C00006 + C00001
R_R07857	0	Carotenoid biosynthesis	.	TRUE	.	[c] : caro <==> C16340
R_R07856	0	Carotenoid biosynthesis	.	TRUE	.	[c] : C05434 <==> C16291
R_R06917	0	1- and 2-Methylnaphthalene degradati	1.1.1.1	TRUE	alcohol:NAD+ oxidoreductase	[c] : C14089 + C00003 <==> C14090 + C00004 + C00080
R_R06916	0	1- and 2-Methylnaphthalene degradati	1.14.13.-	TRUE	.	[c] : C14082 + C00007 + C00004 + C00080 <==> C14089 + C00003 + C00001
R_R06858	0	Ubiquinone and menaquinone biosynt	2.5.1.-	TRUE	.	[c] : C03657 + C05427 <==> C13309 + C00011 + C00013
R_R06859	0	Ubiquinone and menaquinone biosynt	2.1.1.-	TRUE	.	[c] : C13309 + C00019 <==> phyQ + C00021
R_R06851	0	gamma-Hexachlorocyclohexane degrad	1.14.13.-	TRUE	.	[c] : C02389 + C00005 + C00080 + C00007 <==> C02814 + C00006 + C00001
R_R04726	0	Fatty acid biosynthesis	2.3.1.41; 2.	TRUE	dodecanoyl-[acyl-carrier-protein]:malor	[c] : C05223 + C01209 <==> C05759 + C00011 + apoACP_ACP
R_R07763	0	Biosynthesis of unsaturated fatty acids	1.1.1.100	TRUE	.	[c] : C16219 + C00005 + C00080 <==> C16220 + C00006
R_R04724	0	Fatty acid biosynthesis	2.3.1.86; 1.	TRUE	Dodecanoyl-[acyl-carrier protein]:malor	[c] : C05223 + C00003 <==> C05758 + C00004 + C00080
R_34DHOX	0	Tyrosine metabolism	1.1.1.1	TRUE	3,4-Dihydroxyphenylethyleneglycol:NAI	[c] : 34dhmald + C00080 + C00004 <==> 34dhoxpeg + C00003
R_R07762	0	Fatty acid biosynthesis	2.3.1.179;	TRUE	.	[c] : palmACP + C01209 <==> C16219 + apoACP_ACP + C00011
R_ASPTRS	0	Alanine and aspartate metabolism	6.1.1.23; 6.	FALSE	L-Aspartate:tRNA(Asp) ligase (AMP-forr	[c] : C00049 + C00002 + C01638 --> C00020 + C02984 + C00013
R_thft	0	Transport Database	.	FALSE	thftransport	C00101[e] --> C00101[c]
R_PPNCL2	0	Pantothenate and CoA biosynthesis	6.3.2.5	FALSE	(R)-4'-Phosphopantothenate:L-cysteine	[c] : C03492 + C00063 + C00097 --> C04352 + C00055 + C00080 + C00013
R_PPNCL3	0	Pantothenate and CoA biosynthesis	6.3.2.5	FALSE	(R)-4'-Phosphopantothenate:L-cysteine	[c] : C03492 + C00002 + C00097 --> C04352 + C00020 + C00080 + C00013
R_R03527	0	Starch and sucrose metabolism	3.2.1.21	TRUE	D-Glucoside glucohydrolase	[c] : C01798 + C00001 <==> C01335 + C00267
R_strch1t	0	Transport Database	.	FALSE	strch1transport	C00369[e] --> C00369[c]
R_SUCBZL	0	Ubiquinone and menaquinone biosynt	6.2.1.26	FALSE	O-Succinylbenzoate:CoA ligase (AMP-for	[c] : C00002 + C00010 + C02730 --> C00020 + C00013 + C03160
R_OOR	0	Reductive carboxylate cycle (CO2 fixati	1.2.7.3	FALSE	2-oxoglutarate:ferredoxin oxidoreductas	[c] : C00026 + C00010 + C00139 + C00080 --> C00011 + C00138 + C00091
R_ECOAH9	0	Valine, leucine and isoleucine degradat	4.2.1.17	TRUE	(2S,3S)-3-Hydroxy-2-methylbutanoyl-Cc	[c] : C03345 + C00001 <==> C04405
R_mant	0	Transport Database	.	FALSE	mantransport	C00936[e] --> C00936[c]
R_NDPK2n	907.9447	Pyrimidine metabolism	2.7.4.6	TRUE	ATP:UDP phosphotransferase	[c] : C00002 + C00015 <==> C00008 + C00075
R_pnto_Rt	0	Transport Database	.	FALSE	pnto-Rtransport	C00864[e] --> C00864[c]
R_SRC_C14	0.549348	SourceFlux	.	FALSE	. source flux	C14818[b] --> C14818[e]
R_thymt	0	Transport Database	.	FALSE	thymtransport	C00178[e] --> C00178[c]
R_R04543	0	Fatty acid biosynthesis	1.1.1.100;	TRUE	(3R)-3-Hydroxypalmitoyl-[acyl-carrier-p	[c] : C04633 + C00006 <==> C05762 + C00005 + C00080
R_R05332	0	Aminosugars metabolism	2.3.1.157	TRUE	Acetyl-CoA:D-glucosamine-1-phosphate	[c] : C00024 + C06156 <==> C00010 + C04501
R_CBPSn	40.93444	Pyrimidine metabolism; Glutamate me	6.3.5.5	FALSE	hydrogen-carbonate:L-glutamine amido	[c] : 2 C00002 + C00064 + C00001 + C01353 --> 2 C00008 + C00169 + C00025 + 2 C00080 +
R_ADCPS2	0	Porphyrin and chlorophyll metabolism	6.3.1.10	FALSE	adenosylcobyric acid:(R)-1-aminopropa	[c] : C06507 + C04122 + C00002 --> C06509 + C00008 + C00080 + C00009
R_R01056	138.3985	Pentose phosphate pathway; Carbon fi	5.3.1.6	TRUE	D-ribose-5-phosphate aldose-ketose-iso	[c] : C03736 <==> C00199
R_HPROym	0	Arginine and proline metabolism	1.5.1.2	FALSE	trans-4-Hydroxy-L-proline:NADP+ 5-oxi	[c] : C01157 + C00006 --> C04281 + 2 C00080 + C00005
R_fmnt	0	Transport Database	.	FALSE	fmntransport	C00061[e] --> C00061[c]
R_NADS2	1.098696	Nicotinate and nicotinamide metabolis	6.3.5.1	FALSE	Deamido-NAD+:L-glutamine amido-ligas	[c] : C00002 + C00857 + C00064 + C00001 --> C00020 + C00025 + C00080 + C00003 + C00
R_csnt	0	Transport Database	.	FALSE	csntransport	C00380[e] --> C00380[c]
R_AGMT	0	Urea cycle and metabolism of amino gr	3.5.3.11	FALSE	Agmatine amidinohydrolase	[c] : C00179 + C00001 --> C00134 + C00086

R_R04558	0	Histidine metabolism	4.1.3.-; 2.4.	TRUE	.	[c] : C04916 + C00064 <==> C04666 + C04677 + C00025
R_PSERT	0	Glycine, serine and threonine metaboli	2.6.1.52	FALSE	3-Phosphoserine:2-oxoglutarate aminot	[c] : C03232 + C00025 --> C00026 + C01005
R_DB4PS	0	Riboflavin metabolism	.	FALSE	3,4-Dihydroxy-2-butanone 4-phosphate	[c] : C00199 --> C15556 + C00058 + C00080
R_R07618	-1000	Valine, leucine and isoleucine degradat	1.8.1.4	TRUE	enzyme N6-(dihydrolipoyl)lysine:NAD+	[c] : C15973 + C00003 <==> C15972 + C00004 + C00080
R_SERD_Lr	-115.441	Glycine, serine and threonine metaboli	4.3.1.19; 4.	TRUE	L-serine ammonia-lyase	[c] : C00716 <==> C01342 + C00022
R_MALS	0	Pyruvate metabolism; Glyoxylate and c	2.3.3.9	FALSE	L-Malate glyoxylate-lyase (CoA-acetylati	[c] : C00024 + C00048 + C00001 --> C00010 + C00080 + C00711
R_R00919	0	Propanoate metabolism	1.3.1.-	TRUE	.	[c] : C00100 + C00006 <==> prpncoa + C00005 + C00080
R_lac_Dt	0	Transport Database	.	TRUE	lac-Dtransport	C00256[c] <==> C00256[e]
R_R08176	0	Biosynthesis of unsaturated fatty acids	3.1.2.2	TRUE	Oleoyl-CoA hydrolase	[c] : C00510 + C00001 <==> C00010 + C00712
R_GNK	0	Pentose phosphate pathway	2.7.1.12	FALSE	ATP:D-Gluconate 6-phosphotransferase	[c] : C00002 + C00257 --> C00345 + C00008 + C00080
R_IMPC	-30.5276	Purine metabolism	3.5.4.10; 2.	TRUE	IMP 1,2-hydrolase (decyclizing)	[c] : C00001 + C00130 <==> C04734
R_R04429	0	Fatty acid biosynthesis	2.3.1.86; 1.	TRUE	Butyryl-[acyl-carrier protein]:malonyl-C	[c] : C05745 + C00003 <==> C04246 + C00004 + C00080
R_ht	180.4544	Transport Database	.	FALSE	htransport	C00080[c] --> C00080[e]
R_UPPRT	0	Pyrimidine metabolism	2.4.2.9	FALSE	UMP:diphosphate phospho-alpha-D-ribo	[c] : C00119 + C00106 --> C00013 + C00105
R_DUTPDP	0	Pyrimidine metabolism	3.6.1.23; 3.	FALSE	dUTP nucleotidohydrolase	[c] : C00460 + C00001 --> C00365 + C00080 + C00013
R_R06010	0	Glycosphingolipid biosynthesis - gangl	3.2.1.23	TRUE	.	[c] : G00110 + C00001 <==> G00109 + C00124
R_R07035	0	Arachidonic acid metabolism	1.11.1.9	TRUE	Glutathione: 15-HPETE oxidoreductase	[c] : 2 C00051 + 15HPET <==> C00127 + C04742 + C00001
R_R07034	0	Arachidonic acid metabolism	1.11.1.9	TRUE	Glutathione: 5-HPETE oxidoreductase	[c] : 2 C00051 + 5HPET <==> C00127 + C04805 + C00001
R_DDGLK	0	Pentose and glucuronate interconversi	2.7.1.45	FALSE	ATP:2-dehydro-3-deoxy-D-gluconate 6-p	[c] : C00204 + C00002 --> C04442 + C00008 + C00080
R_his_Lt	6.515515	Transport Database	.	FALSE	his-Ltransport	C00135[e] --> C00135[c]
R_R00761	552.9957	Carbon fixation in photosynthetic orga	4.1.2.22	TRUE	D-fructose-6-phosphate D-erythrose-4-p	[c] : C05345 + C00009 <==> C00227 + C00279 + C00001
R_UAMAS	0	Peptidoglycan biosynthesis; D-Glutami	6.3.2.8	FALSE	UDP-N-acetylmuramate:L-alanine ligase	[c] : C00041 + C00002 + C01050 --> C00008 + C00080 + C00009 + C01212
R_PUNP5	-1000	Purine metabolism	2.4.2.1; 2.4	TRUE	inosine:phosphate alpha-D-ribosyltranst	[c] : C00294 + C00009 <==> C00262 + C00620
R_R08091	0	Geraniol degradation	2.3.1.16	TRUE	7-methyl-3-oxo-6-octenoyl-CoA:acetyl-C	[c] : C16466 + C00010 <==> C16470 + C00024
R_R08092	0	Geraniol degradation	1.3.99.-	TRUE	.	[c] : C16470 + C00016 <==> C16468 + C01352
R_R08093	0	Geraniol degradation	4.2.1.17	TRUE	3-hydroxy-5-methylhex-4-enoyl-CoA hy	[c] : C16468 + C00001 <==> C16469
R_R02940	0	Propanoate metabolism	1.2.1.3	TRUE	2-Propyn-1-al:NAD+ oxidoreductase	[c] : C05985 + C00003 + C00001 <==> C00804 + C00004 + C00080
R_R08095	0	Geraniol degradation	2.3.1.16	TRUE	3-methylcrotonyl-CoA:acetyl-CoA C-acyl	[c] : C16471 + C00010 <==> C03069 + C00024
R_PUNP3	0	Purine metabolism	2.4.2.1; 2.4	TRUE	guanosine:orthophosphate ribosyltranst	[c] : C00387 + C00009 <==> C00242 + C00620
R_PUNP2	0	Purine metabolism	2.4.2.1	TRUE	Deoxyadenosine:orthophosphate ribosy	[c] : C00559 + C00009 <==> C00672 + C00147
R_SRC_C00	0.549348	SourceFlux	.	FALSE	. source flux	C00175[b] --> C00175[c]
R_PTE2x	0	Biosynthesis of unsaturated fatty acids	3.1.2.22; 3.	FALSE	Palmitoyl-CoA hydrolase	[c] : C00001 + C00154 --> C00010 + C00080 + C00249
R_cholt	0	Transport Database	.	FALSE	choltransport	C00114[e] --> C00114[c]
R_lac_Lt	0	Transport Database	.	TRUE	lac-Ltransport	C00186[c] <==> C00186[e]
R_R08306	0	Drug metabolism - cytochrome P450	1.1.1.1	TRUE	2-phenyl-1,3-propanediol monocarbama	[c] : C16586 + C00003 <==> C16587 + C00004 + C00080
R_R03090	-1000	Androgen and estrogen metabolism	1.14.13.-	TRUE	.	[c] : C00951 + C00080 + C00007 + C00005 <==> C05301 + C00006 + C00001
R_MI4PP	0	Inositol phosphate metabolism	3.1.3.25	FALSE	1D-myo-Inositol 4-phosphate phosphoh	[c] : C00001 + C03546 --> C00137 + C00009
R_C2M26D	0	Limonene and pinene degradation	4.2.1.17	TRUE	cis-2-Methyl-5-isopropylhexa-2,5-dieno	[c] : c2m26dcoa + C00001 <==> 3h26dm5coa
R_AMAA	0	Peptidoglycan biosynthesis	3.5.1.28	FALSE	N-Acetylmuramoyl-Ala amidohydrolase	[c] : C02999 + C00001 --> C02713 + C00041
R_CDPMEK	0	Biosynthesis of steroids	2.7.1.148	FALSE	ATP: 4-(Cytidine 5'-diphospho)-2-C-met	[c] : C11435 + C00002 --> C11436 + C00008 + C00080
R_SRC_C00	0.549348	SourceFlux	.	FALSE	. source flux	C00070[b] --> C00070[e]
R_UAMAGS	0	Peptidoglycan biosynthesis; D-Glutami	6.3.2.9	FALSE	UDP-N-acetylmuramoyl-L-alanine:D-glu	[c] : C00002 + C00217 + C01212 --> C00008 + C00080 + C00009 + C00692
R_NDPK10	0	Purine metabolism	2.7.4.6	TRUE	ATP:dIDP phosphotransferase	[c] : C00002 + C01344 <==> C00008 + C01345
R_R05068	-19.876	Valine, leucine and isoleucine biosynth	1.1.1.86	TRUE	(R)-2,3-Dihydroxy-3-methylpentanoate:	[c] : C04104 + C00006 <==> C14463 + C00005 + C00080
R_IMPD	15.5355	Purine metabolism	1.1.1.205	FALSE	IMP:NAD+ oxidoreductase	[c] : C00001 + C00130 + C00003 --> C00080 + C00004 + C00655
R_mal_Lt	0	Transport Database	.	TRUE	mal-Ltransport	C00711[c] <==> C00711[e]
R_R01819	0	Fructose and mannose metabolism	5.3.1.8	TRUE	D-mannose-6-phosphate aldose-ketose-	[c] : C00275 <==> f6p-B
R_SHCHD2	0	Porphyrin and chlorophyll metabolism	1.3.1.76	FALSE	S-Adenosyl-L-methionine:uroporphyrin-	[c] : dscl + C00003 --> C00080 + C00004 + C05778
R_SRC_C00	0.549348	SourceFlux	.	FALSE	. source flux	C00076[b] --> C00076[e]
R_retinolt	0	Transport Database	.	FALSE	retinoltransport	C00473[e] --> C00473[c]
R_fumt	0	Transport Database	.	TRUE	fumtransport	C00122[c] <==> C00122[e]
R_MTHFR2	0	Methane metabolism; One carbon pool	1.5.1.20	FALSE	5-methyltetrahydrofolate:NAD+ oxidore	[c] : C00080 + C00143 + C00004 --> C00440 + C00003
R_ANPRT	3.880026	Phenylalanine, tyrosine and tryptopha	2.4.2.18	FALSE	N-(5-Phospho-D-ribosyl)anthranilate:py	[c] : C00108 + C00119 --> C00013 + C04302
R_FTHFD	0	One carbon pool by folate; Glyoxylate a	3.5.1.10	FALSE	10-Formyltetrahydrofolate amidohydro	[c] : C00234 + C00001 --> C00058 + C00080 + C00101
R_SUCR	0	Galactose metabolism	3.2.1.20	FALSE	alpha-D-Glucoside glucohydrolase	[c] : C00001 + C00089 --> C10906 + C00267
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00407[c] --> C00407[b]

R_DHNPAr	0	Folate biosynthesis	4.1.2.25	FALSE	2-Amino-4-hydroxy-6-(D-erythro-1,2,3-	[c] : C04874 --> 2ahhmp + C00266 + C00080
R_R05590	0	Benzoate degradation via CoA ligation	3.5.1.4	TRUE	Acylamide aminohydrolase	[c] : C09815 + C00001 <==> C00180 + C01342
R_R07324	0	Inositol phosphate metabolism	5.5.1.4	TRUE	1D-myo-inositol-3-phosphate lyase (isor	[c] : C00668 <==> C04006
R_thr_Lt	1000	Transport Database	.	FALSE	thr-Ltransport	C00188[e] --> C00188[c]
R_PRPNCO	0	Propanoate metabolism; beta-Alanine	4.2.1.17	FALSE	3-Hydroxypropionyl-CoA hydro-lyase	[c] : C00001 + prpncoa --> 3hpcoa
R_GPDDA1	0	Glycerophospholipid metabolism	3.1.4.46; 3.	FALSE	sn-Glycero-3-phosphocholine glyceroph	[c] : C00670 + C00001 --> C00114 + C00623 + C00080
R_asn_Lt	0	Transport Database	.	FALSE	asn-Ltransport	C00152[e] --> C00152[c]
R_R02488	0	Lysine degradation; Tryptophan metal	1.3.99.7	TRUE	Glutaryl-CoA:(acceptor) 2,3-oxidoreduct	[c] : C00527 + C00028 <==> b2coa + C00030 + C00011
R_DAPE	0	Lysine biosynthesis	5.1.1.7	TRUE	LL-2,6-Diaminoheptanedioate 2-epimera	[c] : C00666 <==> C00680
R_R05119	0	Butanoate metabolism	1.2.1.3	TRUE	3-Butyn-1-al:NAD+ oxidoreductase	[c] : C06145 + C00003 + C00001 <==> C06144 + C00004 + C00080
R_R05448	0	1,4-Dichlorobenzene degradation	1.14.13.-	TRUE	.	[c] : C07096 + C00007 + C00004 + C00080 <==> C07097 + C00003 + C00001
R_METAT	0.549348	Methionine metabolism	2.5.1.6	FALSE	ATP:L-methione S-adenosyltransferase	[c] : C00002 + C00001 + C00073 --> C00019 + C00009 + C00013
R_NTPP8	0	Pyrimidine metabolism	3.6.1.8; 3.6	FALSE	Uridine triphosphate pyrophosphohydro	[c] : C00001 + C00075 --> C00080 + C00013 + C00105
R_NTPP9	0	Purine metabolism	3.6.1.8; 3.6	FALSE	Inosine 5'-triphosphate pyrophosphohy	[c] : C00001 + C00081 --> C00080 + C00130 + C00013
R_R07899	0	alpha-Linolenic acid metabolism	2.3.1.16	TRUE	.	[c] : C16339 + C00024 <==> C00010 + C16338
R_R00867	-1000	Fructose and mannose metabolism	2.7.1.4; 2.7	TRUE	ATP:D-fructose 6-phosphotransferase	[c] : C00002 + C10906 <==> C00008 + f6p-B
R_PMETM_	0	Glycerophospholipid metabolism; Glyc	2.1.1.71	FALSE	S-Adenosyl-L-methionine:phosphatidyl-	[c] : C00019 + 0.01 C04308 --> C00021 + C00080 + 0.01 C00157
R_RNDR2	0.826331	Purine metabolism	1.17.4.1	FALSE	2'-Deoxyguanosine 5'-diphosphate:oxidi	[c] : C00035 + C00342 --> C00361 + C00001 + C00343
R_RNDR3	0.826331	Pyrimidine metabolism	1.17.4.1	FALSE	2'-Deoxycytidine diphosphate:oxidized-	[c] : C00112 + C00342 --> C00705 + C00001 + C00343
R_RNDR1	0.826331	Purine metabolism	1.17.4.1	FALSE	2'-Deoxyadenosine 5'-diphosphate:oxidi	[c] : C00008 + C00342 --> C00206 + C00001 + C00343
R_SHSL4r	-975.878	Methionine metabolism	2.5.1.48	TRUE	O-Succinyl-L-homoserine succinate-lyas	[c] : C00001 + C01118 <==> C00109 + C00080 + C01342 + C00042
R_R03601	35.17646	Selenoamino acid metabolism	2.5.1.47	TRUE	O3-Acetyl-L-serine acetate-lyase (adding	[c] : C00979 + C01528 <==> C05688 + C00033
R_PYK	0	Glycolysis / Gluconeogenesis; Pyruvate	2.7.1.40	FALSE	ATP:pyruvate 2-O-phosphotransferase	[c] : C00008 + C00080 + C00074 --> C00002 + C00022
R_THDPS	0	Lysine biosynthesis	2.3.1.117	FALSE	Succinyl-CoA:2,3,4,5-tetrahydropyridine	[c] : C00001 + C00091 + C03972 --> C00010 + C04462
R_CHORS	26.02546	Phenylalanine, tyrosine and tryptopha	4.2.3.5	FALSE	5-O-(1-Carboxyvinyl)-3-phosphoshikima	[c] : C01269 --> C00251 + C00009
R_R02508	0	Sulfur metabolism	2.5.1.48	TRUE	.	[c] : C00542 + C00042 <==> C01118 + C00097
R_ACGK	20.27863	Urea cycle and metabolism of amino gr	2.7.2.8	FALSE	ATP:N-acetyl-L-glutamate 5-phosphotra	[c] : C00624 + C00002 --> C04133 + C00008
R_NDPK7n	0.826331	Pyrimidine metabolism	2.7.4.6	TRUE	ATP:dCDP phosphotransferase	[c] : C00002 + C00705 <==> C00008 + C00458
R_PGAMT	0	Aminosugars metabolism	5.4.2.10	TRUE	D-Glucosamine 1-phosphate 1,6-phosph	[c] : C06156 <==> C00352
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00164[c] --> C00164[b]
R_thmt	0	Transport Database	.	FALSE	thmtransport	C00378[e] --> C00378[c]
R_CHORM	22.14543	Phenylalanine, tyrosine and tryptopha	5.4.99.5	FALSE	Chorismate pyruvatemutase	[c] : C00251 --> C00254
R_ATPPRT	0	Histidine metabolism	2.4.2.17	FALSE	1-(5-phospho-D-ribosyl)-ATP:diphospha	[c] : C00002 + C00119 --> C00013 + C02739
R_RBFSb	0	Riboflavin metabolism	2.5.1.9	FALSE	6,7-Dimethyl-8-(1-D-ribityl)lumazine:6,	[c] : 2 C04332 --> C04732 + C00255
R_RBFSa	0	Riboflavin metabolism	.	FALSE	6,7-Dimethyl-8-(1-D-ribityl)lumazine:6,	[c] : C04732 + C15556 --> C04332 + 2 C00001 + C00009
R_R07810	0	Glycosaminoglycan degradation	3.2.1.52	TRUE	.	[c] : G06780 + C00001 <==> G08421 + C01132
R_etoht	0	Transport Database	.	FALSE	etohtransport	C00469[c] --> C00469[e]
R_DASYNn	0	Glycerophospholipid metabolism	2.7.7.41	TRUE	CTP:phosphatidate cytidyltransferase	[c] : C00063 + C00080 + 0.01 C00416 <==> 0.01 cdpdag_SC + C00013
R_R00268	-1000	Citrate cycle (TCA cycle)	1.1.1.42	TRUE	Oxalosuccinate:NADP+ oxidoreductase (	[c] : C05379 <==> C00026 + C00011
R_4HTHRS	0	Vitamin B6 metabolism	4.2.3.1	FALSE	O-Phospho-4-hydroxy-L-threonine phos	[c] : C00001 + C06055 --> C06056 + C00009
R_HEX1	888.1152	Streptomycin biosynthesis	2.7.1.2; 2.7	FALSE	ATP:D-glucose 6-phosphotransferase	[c] : C00002 + C00267 --> C00008 + C00668 + C00080
R_PPC	0	Reductive carboxylate cycle (CO2 fixati	4.1.1.31	FALSE	Orthophosphate:oxaloacetate carboxyl-l	[c] : C00011 + C00001 + C00074 --> C00080 + C00036 + C00009
R_PPCDC	0	Pantothenate and CoA biosynthesis	4.1.1.36	FALSE	N-[(R)-4'-Phosphopantothenoyl]-L-cyste	[c] : C04352 + C00080 --> C00011 + C01134
R_frut	0	Transport Database	.	FALSE	frutransport	C10906[e] --> C10906[c]
R_AHSERL	0	Methionine metabolism	2.5.1.49	FALSE	O-acetyl-L-homoserine:hydrogen sulfide	[c] : C01077 + C00297 --> C00033 + C00080 + C05330
R_kt	0.549348	Transport Database	.	FALSE	ktransport	C00238[e] --> C00238[c]
R_R07665	0	Toluene and xylene degradation	1.14.13.-	TRUE	.	[c] : C01467 + C00007 + C00004 + C00080 <==> C03351 + C00003 + C00001
R_PPNDH	12.70159	Phenylalanine, tyrosine and tryptopha	4.2.1.51; 4.	FALSE	prephenate hydro-lyase (decarboxylatin	[c] : C00080 + C00254 --> C00011 + C00001 + C00166
R_HKYNH	0	Tryptophan metabolism	3.7.1.3	FALSE	3-Hydroxy-L-kynurenine hydrolase	[c] : C00001 + C03227 --> C00632 + C00041
R_PSCVT	26.02546	Phenylalanine, tyrosine and tryptopha	2.5.1.19	TRUE	Phosphoenolpyruvate:3-phosphoshikim	[c] : C00074 + C03175 <==> C01269 + C00009
R_ADSK	0	Sulfur metabolism; Purine metabolism	2.7.1.25	FALSE	ATP:adenylylsulfate 3'-phosphotransfer	[c] : C00224 + C00002 --> C00008 + C00080 + C00053
R_R03791	0	Toluene and xylene degradation	5.1.2.2	TRUE	mandelate racemase	[c] : C01984 <==> C01983
R_LFORKY	0	Tryptophan metabolism	3.7.1.3	FALSE	Formylkynurenine hydrolase	[c] : C02700 + C00001 --> C00041 + C00080 + nformanth
R_SRC_C00	1000	SourceFlux	.	FALSE	. source flux	C00188[b] --> C00188[e]
R_RNDR4n	0.826331	Pyrimidine metabolism	1.17.4.1	FALSE	2'-Deoxyuridine 5'-diphosphate:oxidize	[c] : C00342 + C00015 --> C01346 + C00001 + C00343
R_ADSS	14.99205	Alanine and aspartate metabolism; Pur	6.3.4.4	FALSE	IMP:L-aspartate ligase (GDP-forming)	[c] : C00049 + C00044 + C00130 --> C03794 + C00035 + 2 C00080 + C00009

R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00041[c] --> C00041[b]
R_VALTRS	0	Valine, leucine and isoleucine biosynth	6.1.1.9	FALSE	L-Valine:tRNAVal ligase (AMP-forming)	[c] : C00002 + C01653 + C00183 --> C00020 + C00013 + C02554
R_DTMPK	0.826331	Pyrimidine metabolism	2.7.4.12; 2.	TRUE	ATP:dTMP phosphotransferase	[c] : C00002 + C00364 <==> C00008 + C00363
R_R07460	0	Thiamine metabolism	2.8.1.7	TRUE	L-cysteine:[ThiI] sulfurtransferase	[c] : C15811 + C00097 <==> C15812 + C00041
R_DHAD2r	19.87598	Valine, leucine and isoleucine biosynth	4.2.1.9	FALSE	(R)-2,3-Dihydroxy-3-methylpentanoate	[c] : C04104 --> C03465 + C00001
R_succt	446.1651	Transport Database	.	TRUE	succtransport	C00042[c] <==> C00042[e]
R_R06398	0	Limonene and pinene degradation	1.14.13.-	TRUE	(+)-limonene,NADH:oxygen oxidoreduct	[c] : C06099 + C00004 + C00007 <==> C07271 + C00003 + C01328
R_ACOTA	-20.2786	Urea cycle and metabolism of amino gr	2.6.1.11	TRUE	N2-Acetyl-L-ornithine:2-oxoglutarate an	[c] : C00437 + C00026 <==> C01250 + C00025
R_P4508E	0	Bile acid biosynthesis	1.14.13.-; 1	FALSE	7alpha-hydroxycholest-4-en-3-one,NAD	[c] : C00080 + C00005 + C00007 + xol7aone --> C00001 + C00006 + xoldiolone
R_uratet	0	Transport Database	.	FALSE	uratetransport	C00366[e] --> C00366[c]
R_R06905	0	1- and 2-Methylnaphthalene degradati	1.3.99.-	TRUE	.	[c] : C14116 <==> C14117 + 2 C00080
R_DHQD	26.02546	Phenylalanine, tyrosine and tryptopha	4.2.1.10	TRUE	3-Dehydroquinate hydro-lyase	[c] : C00944 <==> C02637 + C00001
R_R04161	0	Benzoate degradation via hydroxylatio	5.1.2.2	TRUE	(S)-4-Hydroxymandelate racemase	[c] : C03198 <==> C05343
R_CPC6R	0	Porphyrin and chlorophyll metabolism	1.3.1.54	FALSE	.	[c] : C11542 + C00080 + C00005 --> C11543 + C00006
R_R07710	1000	Naphthalene and anthracene degradat	1.14.13.-	TRUE	.	[c] : C00805 + C00005 + C00007 + C00080 <==> C00628 + C00006 + C00001
R_MOHMT	0	Pantothenate and CoA biosynthesis	2.1.2.11	FALSE	5,10-Methylenetetrahydrofolate:3-meth	[c] : C00141 + C00001 + C00143 --> C00966 + C00101
R_ACLS	0	C5-Branched dibasic acid metabolism	2.2.1.6	FALSE	(S)-2-Acetolactate pyruvate-lyase (carbo	[c] : C00080 + 2 C00022 --> C06010 + C00011
R_DNMPPA	0	Folate biosynthesis	3.6.1.-	FALSE	.	[c] : C05925 + C00001 --> C04874 + C00009
R_DNADDI	0	Nicotinate and nicotinamide metabolis	3.6.1.22; 3.	FALSE	Deamino-NAD+ nucleotidohydrolase	[c] : C00857 + C00001 --> C00020 + 2 C00080 + C01185
R_GALK	0	Galactose metabolism	2.7.1.6	FALSE	ATP:D-galactose 1-phosphotransferase	[c] : C00002 + C00124 --> C00008 + C00446 + C00080
R_DDPAm	26.02546	Phenylalanine, tyrosine and tryptopha	2.5.1.54	FALSE	Phosphoenolpyruvate:D-erythrose-4-ph	[c] : C00279 + C00001 + C00074 --> C04691 + C00009
R_R06962	0	Carotenoid biosynthesis	.	TRUE	.	[c] : C08586 <==> C05433
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00469[c] --> C00469[b]
R_DHQS	26.02546	Phenylalanine, tyrosine and tryptopha	4.2.3.4	FALSE	2-Dehydro-3-deoxy-D-arabino-heptonat	[c] : C04691 --> C00944 + C00009
R_R04306	0	Tyrosine metabolism	1.14.13.-	TRUE	.	[c] : C04353 + C00005 + C00080 + C00007 <==> C00650 + C00006 + 2 C00001
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00311[c] --> C00311[b]
R_R00726	-589.701	Glycolysis / Gluconeogenesis; Pyruvate	4.1.1.32	TRUE	ITP:oxaloacetate carboxy-lyase (transph	[c] : C00081 + C00036 <==> C00104 + C00074 + C00011
R_GTPDPK	0	Purine metabolism	2.7.6.5	FALSE	ATP:GTP 3'-pyrophosphotransferase	[c] : C00002 + C00044 --> C00020 + C04494 + C00080
R_SRC_C01	1000	SourceFlux	.	FALSE	. source flux	C01342[b] --> C01342[e]
R_GALS3	0	Galactose metabolism	3.2.1.22; 3.	FALSE	melibiose galactohydrolase	[c] : C00001 + C05402 --> C00124 + C00267
R_PUNP7	1000	Purine metabolism	2.4.2.1	TRUE	Xanthosine:orthophosphate ribosyltrans	[c] : C00009 + C01762 <==> C00620 + C00385
R_R07973	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07130 + C00004 + C00080 + C00007 <==> C16357 + C00003 + C00067 + C00001
R_R06401	0	Limonene and pinene degradation	1.14.-.-	TRUE	alpha-Pinene dehydrogenase	[c] : C09880 + C00030 <==> C11938 + C00001 + C00028
R_R06400	0	Limonene and pinene degradation	1.14.13.-	TRUE	(1S,4R)-1-hydroxy-2-oxolimonene, NAD	[c] : C11937 + C00005 + C00007 <==> C11405 + C00006 + C01328
R_R03105	0	Cysteine metabolism	2.8.1.2	TRUE	3-Mercaptopyruvate:cyanide sulfurtrans	[c] : C00957 + C00094 <==> C05529 + C00022
R_PUNP6	0	Purine metabolism	2.4.2.1; 2.4	TRUE	Deoxyinosine:orthophosphate ribosyltra	[c] : C05512 + C00009 <==> C00672 + C00262
R_R02984	0	Nucleotide sugars metabolism	5.1.3.2	TRUE	dTDPglucose 4-epimerase	[c] : C00842 <==> C02097
R_R06404	0	Limonene and pinene degradation	1.14.-.-	TRUE	alpha-Pinene monooxygenase	[c] : C09880 + C00007 + C00080 <==> C11941 + C00001
R_R06406	0	Limonene and pinene degradation	1.14.13.-	TRUE	alpha-Pinene monooxygenase	[c] : C09880 + C00004 + C00080 + C00007 <==> apnnox + C00003 + C00001
R_h2ot	801.5873	Transport Database	.	TRUE	h2otransport	C00001[c] <==> C00001[e]
R_R08094	0	Geraniol degradation	1.1.1.35	TRUE	3-hydroxy-5-methylhex-4-enoyl-CoA:NA	[c] : C16469 + C00003 <==> C16471 + C00004 + C00080
R_R01856	0	Purine metabolism	3.1.5.1	TRUE	dGTP triphosphohydrolase	[c] : C00286 + C00001 <==> C00330 + C00536
R_TRPTRS	0	Tryptophan metabolism	6.1.1.2	FALSE	L-Tryptophan -tRNA(Trp) ligase (AMP-f	[c] : C00002 + C01652 + C00078 --> C00020 + C00013 + C03512
R_R00014	-476.62	Pyruvate metabolism; Butanoate meta	4.1.1.1; 2.2	TRUE	pyruvate:thiamin diphosphate acetaldeh	[c] : C00022 + C00068 <==> C05125 + C00011
R_R01138	999.1737	Purine metabolism	2.7.1.40	TRUE	dATP:pyruvate 2-O-phosphotransferase	[c] : C00131 + C00022 <==> C00206 + C00074
R_PRO1x	0	Arginine and proline metabolism	1.5.1.2	FALSE	L-Proline:NAD+ 5-oxidoreductase	[c] : C00003 + C00148 --> C03912 + 2 C00080 + C00004
R_R07969	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C16358 + C00004 + C00080 + C00007 <==> C00385 + C00003 + C00067 + C00001
R_R07968	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C16357 + C00005 + C00080 + C00007 <==> C00385 + C00006 + C00067 + C00001
R_PAPPT3	0	Peptidoglycan biosynthesis	2.7.8.13	FALSE	UDPMurAc(oyl-L-Ala-D-gamma-Glu-L-L	[c] : C17556 + C04882 --> C05897 + C00105
R_R07965	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C16353 + C00004 + C00080 + C00007 <==> C00385 + C00003 + C00067 + C00001
R_R07964	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07480 + C00005 + C00080 + C00007 <==> C16357 + C00006 + C00067 + C00001
R_R07967	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C16357 + C00004 + C00080 + C00007 <==> C00385 + C00003 + C00067 + C00001
R_R07966	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C16353 + C00005 + C00080 + C00007 <==> C00385 + C00006 + C00067 + C00001
R_R07961	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07480 + C00004 + C00080 + C00007 <==> C16353 + C00003 + C00067 + C00001
R_R07960	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C13747 + C00005 + C00080 + C00007 <==> C16358 + C00006 + C00067 + C00001
R_R07963	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07480 + C00004 + C00080 + C00007 <==> C16357 + C00003 + C00067 + C00001

R_HMBS	0	Porphyrin and chlorophyll metabolism	2.5.1.61	FALSE	Porphobilinogen ammonia-lyase (polym	[c] : C00001 + 4 C00931 --> C01024 + 4 C01342
R_R00790	0	Nitrogen metabolism	1.7.7.1	TRUE	Ammonia:ferredoxin oxidoreductase	[c] : C01342 + 2 C00001 + 6 C00139 <==> C00088 + 6 C00138 + 7 C00080
R_pydxnt	0	Transport Database	.	FALSE	pydxntransport	C00314[e] --> C00314[c]
R_R04764	0	Androgen and estrogen metabolism	2.1.1.-	TRUE	.	[c] : C05301 + C00019 <==> C05302 + C00021
R_R00926	0	Propanoate metabolism	6.2.1.17; 6.	TRUE	Propionyladenylate:CoA propionyltrans	[c] : C05983 + C00010 <==> C00020 + C00100
R_R03191	0	Aminosugars metabolism	1.1.1.158	TRUE	UDP-N-acetylmuramate:NADP+ oxidore	[c] : C01050 + C00003 <==> C04631 + C00004 + C00080
R_UPP3MT	0	Porphyrin and chlorophyll metabolism	2.1.1.107	FALSE	S-Adenosyl-L-methionine:uroporphyrin-	[c] : 2 C00019 + C01051 --> 2 C00021 + dscl + C00080
R_DHBD	0	Biosynthesis of siderophore group non	1.3.1.28	TRUE	2,3-dihydro-2,3-dihydroxybenzoate:NAI	[c] : C04171 + C00003 <==> C00196 + C00080 + C00004
R_THRS	13.10453	Glycine, serine and threonine metaboli	4.2.3.1	FALSE	O-phospho-L-homoserine phosphate-lya	[c] : C00001 + C01102 --> C00009 + C00188
R_R04949	0	Cyanoamino acid metabolism	3.2.1.21	TRUE	Cyanoglycoside glucohydrolase	[c] : C05713 + C00001 <==> C05712 + C00267
R_R05145	0	Biotin metabolism	6.3.4.10; 6.	TRUE	Biotinyl-5'-AMP:apo-[carboxylase] ligase	[c] : C05921 + C06249 <==> C00020 + C06250
R_NDPK8n	1000	Purine metabolism	2.7.4.6	TRUE	ATP:dADP phosphotransferase	[c] : C00002 + C00206 <==> C00008 + C00131
R_R05149	0	Porphyrin and chlorophyll metabolism	2.1.1.132	TRUE	S-Adenosyl-L-methionine:1-precorrin-6	[c] : 2 C00019 + C06319 <==> 2 C00021 + C06408 + C00011
R_P5CR	1000	Arginine and proline metabolism	1.5.1.2	FALSE	L-Proline:NADP+ 5-oxidoreductase	[c] : C03912 + 2 C00080 + C00005 --> C00006 + C00148
R_R04536	0	Fatty acid biosynthesis	1.1.1.100; 1	TRUE	(3R)-3-Hydroxyoctanoyl-[acyl-carrier-p	[c] : C04620 + C00006 <==> C05750 + C00005 + C00080
R_R04946	0	Selenoamino acid metabolism	2.5.1.48	TRUE	O-Succinyl-L-homoserine succinate-lyas	[c] : C05701 + C05688 <==> selcyst + C00042
R_orott	0	Transport Database	.	TRUE	orottransport	C00295[c] <==> C00295[e]
R_R04944	0	Selenoamino acid metabolism	2.5.1.48	TRUE	O-Phosphorylhomoserine succinate-lyas	[c] : C05702 + C05688 <==> selcyst + C00009
R_R04945	0	Selenoamino acid metabolism	2.5.1.48	TRUE	O-Acetylhomoserine succinate-lyase (ad	[c] : C05700 + C05688 <==> selcyst + C00033
R_R08174	0	Biosynthesis of unsaturated fatty acids	3.1.2.2	TRUE	Stearoyl-CoA hydrolase	[c] : C00412 + C00001 <==> C00010 + C01530
R_G3PD2	-1000	Glycerophospholipid metabolism	1.1.1.94	TRUE	sn-Glycerol-3-phosphate:NADP+ 2-oxido	[c] : C00623 + C00006 <==> C00111 + C00080 + C00005
R_G3PD1	999.1737	Glycerophospholipid metabolism	1.1.1.94; 1.	TRUE	sn-Glycerol-3-phosphate:NAD+ 2-oxidor	[c] : C00623 + C00003 <==> C00111 + C00080 + C00004
R_R04780	-414.983	Fructose and mannose metabolism; Gly	3.1.3.11	TRUE	beta-D-Fructose 1,6-bisphosphate 1-pho	[c] : C05378 + C00001 <==> f6p-B + C00009
R_DHFS	0	Folate biosynthesis	6.3.2.12; 6.	FALSE	7,8-dihydropteroate:L-glutamate ligase (	[c] : C00002 + C00921 + C00025 --> C00008 + C00415 + C00009
R_ADAe	0	Purine metabolism	3.5.4.4	FALSE	Adenosine aminohydrolase	[e] : C00212 + C00080 + C00001 --> C00294 + C01342
R_P5CD	0	Arginine and proline metabolism; Glut	1.5.1.12	FALSE	L-1-Pyrroline-5-carboxylate:NAD+ oxido	[c] : C03912 + 2 C00001 + C00003 --> C00025 + C00080 + C00004
R_R03424	0	Glycerophospholipid metabolism; Glyc	2.1.1.71	TRUE	S-Adenosyl-L-methionine:phosphatidyl-	[c] : C00019 + C01241 <==> C00021 + C04308
R_DAPDC	0	Lysine biosynthesis	4.1.1.20	FALSE	meso-2,6-Diaminoheptanedioate carbox	[c] : C00680 + C00080 --> C00011 + C00047
R_SRC_C17	6.505233	SourceFlux	.	FALSE	. source flux	C17556[b] --> C17556[c]
R_DXPS	0	Biosynthesis of steroids	2.2.1.7	FALSE	1-Deoxy-D-xylulose-5-phosphate pyruva	[c] : C00118 + C00080 + C00022 --> C00011 + C11437
R_R02912	0	Tryptophan metabolism	2.1.1.-	TRUE	serotonin O-methyltransferase	[c] : srtn + C00440 <==> C05659 + C00101
R_SRC_C00	74.20598	SourceFlux	.	FALSE	. source flux	C00009[b] --> C00009[e]
R_IGPDH	0	Histidine metabolism	4.2.1.19	FALSE	D-erythro-1-(Imidazol-4-yl)glycerol 3-p	[c] : C04666 --> C00001 + C01267
R_PMPK	0	Thiamine metabolism	2.7.4.7	FALSE	ATP:4-amino-2-methyl-5-phosphomethy	[c] : C04556 + C00002 --> C04752 + C00008
R_met_Lt	0	Transport Database	.	FALSE	met-Ltransport	C00073[e] --> C00073[c]
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00058[c] --> C00058[b]
R_nmnt	0	Transport Database	.	FALSE	nmntransport	C00455[e] --> C00455[c]
R_ILETRS	0	Valine, leucine and isoleucine biosynth	6.1.1.5	FALSE	L-Isoleucine:tRNA(Ile) ligase (AMP-form	[c] : C00002 + C00407 + C01644 --> C00020 + C03127 + C00013
R_asp_Lt	0	Transport Database	.	FALSE	asp-Ltransport	C00049[e] --> C00049[c]
R_R07916	0	Carotenoid biosynthesis	2.5.1.32	TRUE	.	[c] : C00353 <==> C05413
R_LEUTRS	0	Valine, leucine and isoleucine biosynth	6.1.1.4	FALSE	L-Leucine:tRNA(Leu) ligase (AMP-formi	[c] : C00002 + C00123 + C01645 --> C00020 + C02047 + C00013
R_G3PDm	0.826331	Glycerophospholipid metabolism	1.1.5.3	FALSE	sn-Glycerol-3-phosphate:(acceptor) 2-ox	[c] : C00016 + C00623 --> C00111 + C01352
R_ADNK1n	0	Purine metabolism	2.7.1.74; 2.	FALSE	ATP:adenosine 5'-phosphotransferase	[c] : C00212 + C00002 --> C00008 + C00020 + C00080
R_R01354	0	Propanoate metabolism	6.2.1.17; 6.	TRUE	ATP:propanoate adenyltransferase	[c] : C00002 + C00163 <==> C00013 + C05983
R_GK1	15.5355	Purine metabolism	2.7.4.8	TRUE	ATP:(d)GMP phosphotransferase	[c] : C00002 + C00144 <==> C00008 + C00035
R_APAT2rn	759.9417	Alanine and aspartate metabolism; Pro	2.6.1.19; 2.	TRUE	3-Aminopropanoate:2-oxoglutarate ami	[c] : C00026 + C00099 <==> C00025 + C00222
R_R02780	-888.115	Starch and sucrose metabolism	2.7.1.69	TRUE	.	[c] : C01083 + C04261 <==> C00689 + C00615
R_CLS_hs	0	Glycerophospholipid metabolism	2.7.8.-	FALSE	CDP-diacylglycerol:phosphatidylglycero	[c] : cdpdag_hs + pglyc_hs --> clpn_hs + C00055 + C00080
R_ECOAH1	0	Butanoate metabolism; Benzoate degra	4.2.1.17	TRUE	(S)-3-Hydroxybutanoyl-CoA hydro-lyase	[c] : 3hbcoa <==> b2coa + C00001
R_R00621	-503.504	Citrate cycle (TCA cycle)	1.2.4.2	TRUE	.	[c] : C00026 + C00068 <==> C05381 + C00011
R_R01986	0	Urea cycle and metabolism of amino gr	1.2.1.3	TRUE	4-Aminobutyraldehyde:NAD+ oxidoredu	[c] : C00555 + C00006 + C00001 <==> C00334 + C00005 + C00080
R_XYLK	0	Pentose and glucuronate interconversi	2.7.1.17	FALSE	ATP:D-xylulose 5-phosphotransferase	[c] : C00002 + C00310 --> C00008 + C00080 + C00231
R_THRD_L	995.7542	Valine, leucine and isoleucine biosynth	4.3.1.19	FALSE	L-threonine ammonia-lyase (2-oxobutan	[c] : C00188 --> C00109 + C01342
R_URIDK2r	-0.82633	Pyrimidine metabolism	2.7.4.4; 2.7.	TRUE	ATP:dUMP phosphotransferase	[c] : C00002 + C00365 <==> C00008 + C01346
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00334[c] --> C00334[b]
R_R03920	0	Starch and sucrose metabolism	2.7.1.4; 2.7.	TRUE	ATP:D-fructose 6-phosphotransferase	[c] : C00002 + C02336 <==> C00008 + f6p-B

R_co2t	0	Transport Database	.	TRUE	co2transport	C00011[c] <==> C00011[e]
R_FUMm	-904.15	Reductive carboxylate cycle (CO2 fixat	4.2.1.2	TRUE	(S)-malate hydro-lyase (fumarate-formi	[c] : C00122 + C00001 <==> C00711
R_AICART	30.52756	One carbon pool by folate; Purine meta	2.1.2.3	TRUE	10-Formyltetrahydrofolate:5'-phosphor	[c] : C00234 + C04677 <==> C04734 + C00101
R_R07972	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07481 + C00005 + C00080 + C00007 <==> C07130 + C00006 + C00067 + C00001
R_R05028	0	Peptidoglycan biosynthesis	6.3.1.2	TRUE	Undecaprenyl-diphospho-N-acetylmura	[c] : C00002 + C05889 + C01342 <==> C00008 + C00009 + C05890
R_R02737	888.1152	Starch and sucrose metabolism	2.4.1.15	TRUE	UDPglucose:D-glucose-6-phosphate 1-al	[c] : C00029 + C00668 <==> C00015 + C00689
R_R02736	0	Glutathione metabolism; Pentose phos	1.1.1.49	TRUE	beta-D-Glucose-6-phosphate:NADP+ 1-o	[c] : C01172 + C00006 <==> C01236 + C00005 + C00080
R_arab_Dt	0	Transport Database	.	FALSE	arab-Dtransport	C00216[e] --> C00216[c]
R_G6PI2	859.7105	Glycolysis / Gluconeogenesis	5.3.1.9	TRUE	beta-D-Glucose 6-phosphate ketol-isome	[c] : C01172 <==> f6p-B
R_R02739	1000	Glycolysis / Gluconeogenesis; Pentose	5.3.1.9; 5.1	TRUE	alpha-D-Glucose 6-phosphate ketol-isom	[c] : C00668 <==> C01172
R_R02738	888.1152	Glycolysis / Gluconeogenesis	2.7.1.69	TRUE	Protein-N(pai)-phosphohistidine:sugar I	[c] : C04261 + C00267 <==> C00615 + C00668
R_R02320	0	Pyruvate metabolism; Carbon fixation	2.7.1.40	TRUE	NTP:pyruvate O2-phosphotransferase	[c] : C00201 + C00022 <==> C00454 + C00074
R_R05027	0	Peptidoglycan biosynthesis	2.4.1.227	TRUE	.	[c] : C05888 + C00043 <==> C05889 + C00015
R_AGDC_r	0	Aminosugars metabolism	3.5.1.25	TRUE	N-Acetyl-D-glucosamine-6-phosphate an	[c] : C00357 + C00001 <==> C00033 + C00352
R_R06613	0.826331	Pyrimidine metabolism; One carbon po	2.1.1.148	TRUE	5,10-methylenetetrahydrofolate,FADH2	[c] : C00143 + C00365 + C01352 <==> C00101 + C00364 + C00016
R_R02250	0	Glycerolipid metabolism	3.1.1.3	TRUE	Triacylglycerol acylhydrolase	[c] : triglyc_SC_tag_hs + C00001 <==> 12dgr_SC_12dgr_EC + C00162
R_AIRCr	30.52756	Purine metabolism	4.1.1.21	TRUE	1-(5-Phospho-D-ribosyl)-5-amino-4-imi	[c] : C03373 + C00011 <==> C04751 + C00080
R_mobdt	0	Transport Database	.	FALSE	mobdtransport	C06232[e] --> C06232[c]
R_inst	0	Transport Database	.	FALSE	instransport	C00294[e] --> C00294[c]
R_R07974	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07130 + C00005 + C00080 + C00007 <==> C16357 + C00006 + C00067 + C00001
R_AMID3	0	Tryptophan metabolism	3.5.1.4	FALSE	Indole-3-acetamide amidohydrolase	[c] : C00001 + C02693 --> C00954 + C01342
R_GCCcm	0.248494	Glycine, serine and threonine metaboli	1.8.1.4	TRUE	dihydrolipoylprotein:NAD+ oxidoreduct	[c] : C02972 + C00003 <==> C00080 + C02051 + C00004
R_HMPK1	0	Thiamine metabolism	2.7.1.49	FALSE	ATP:4-amino-5-hydroxymethyl-2-methy	[c] : C01279 + C00002 --> C04556 + C00008 + C00080
R_AMID5	0	Styrene degradation	3.5.1.4	FALSE	.	[c] : C01659 + C00001 --> C00511 + C01342
R_R01678	0	Galactose metabolism	3.2.1.108; 1	TRUE	Lactose galactohydrolase	[c] : C00243 + C00001 <==> C00267 + C00124
R_R00357	-21.7545	Alanine and aspartate metabolism	1.4.3.16; 1.	TRUE	L-Aspartic acid:oxygen oxidoreductase (	[c] : C00049 + C00001 + C00007 <==> C00036 + C01342 + C00027
R_PPCOAC	0	Valine, leucine and isoleucine degradat	6.4.1.3	FALSE	Propanoyl-CoA:carbon-dioxide ligase (A	[c] : C00002 + C01353 + C00100 --> C00008 + C00080 + C00683 + C00009
R_thymdt	0	Transport Database	.	FALSE	thymdtransport	C00214[e] --> C00214[c]
R_ACACT1	124.5222	Synthesis and degradation of ketone b	2.3.1.16; 2.	FALSE	Acetyl-CoA:acetyl-CoA C-acetyltransfera	[c] : 2 C00024 --> C00332 + C00010
R_R05069	19.87598	Valine, leucine and isoleucine biosynth	1.1.1.86; 5.	TRUE	(S)-2-Aceto-2-hydroxybutanoate:NADP+	[c] : C00659 <==> C14463
R_R06926	0	1- and 2-Methylnaphthalene degradati	1.14.13.-	TRUE	.	[c] : C14098 + C00007 + C00004 + C00080 <==> C02909 + C00003 + C00001
R_R06927	0	1- and 2-Methylnaphthalene degradati	1.1.1.1	TRUE	alcohol:NAD+ oxidoreductase	[c] : C02909 + C00003 <==> C14099 + C00004 + C00080
R_R05066	0	Valine, leucine and isoleucine degradat	1.1.1.35; 1.	TRUE	3-Hydroxy-2-methylpropanoate:NAD+ o	[c] : C06001 + C00003 <==> C06002 + C00004 + C00080
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00011[e] --> C00011[b]
R_AMPTAS	0	Glutathione metabolism	3.4.11.2; 3.	FALSE	membrane alanyl aminopeptidase	[c] : C01419 + C00001 --> C00097 + C00037
R_METS	11.0547	Methionine metabolism; One carbon po	2.1.1.13	FALSE	5-Methyltetrahydrofolate:L-homocystein	[c] : C00440 + C05330 --> C00080 + C00073 + C00101
R_PTPAT	0	Pantothenate and CoA biosynthesis	2.7.7.3	TRUE	ATP:pantetheine-4'-phosphate adenylylt	[c] : C00002 + C00080 + C01134 <==> C00882 + C00013
R_cu2t	0.549348	Transport Database	.	FALSE	cu2transport	C00070[e] --> C00070[c]
R_GLNTRA	0	Glutamate metabolism	6.3.5.7	FALSE	Glu-tRNA(Gln):L-glutamine amido-ligase	[c] : C00002 + C00064 + glutrna_LPAREN_gln_RPAREN_ + C00001 --> C00008 + C02282 + C
R_FMNATr	0.549348	Riboflavin metabolism	2.7.7.2	FALSE	ATP:FMN adenylyltransferase	[c] : C00002 + C00061 + C00080 --> C00016 + C00013
R_so4t	0.549348	Transport Database	.	FALSE	so4transport	C00059[e] --> C00059[c]
R_SUCOAS	503.5043	Reductive carboxylate cycle (CO2 fixat	6.2.1.5	TRUE	Succinate:CoA ligase (ADP-forming)	[c] : C00002 + C00010 + C00042 <==> C00008 + C00009 + C00091
R_ASPCTn	20.65581	Pyrimidine metabolism; Alanine and as	2.1.3.2	FALSE	carbamoyl-phosphate:L-aspartate carba	[c] : C00049 + C00169 --> C00438 + C00080 + C00009
R_BG_CELL	0	.	.	FALSE	.	[c] : C00185 + C00001 --> 2 C00267
R_nh4t	-88.2704	Transport Database	.	TRUE	nh4transport	C01342[c] <==> C01342[e]
R_UAAGDS	0	Peptidoglycan biosynthesis; Lysine bio	6.3.2.13	FALSE	UDP-N-acetylmuramoyl-L-alanyl-D-glut	[c] : C00680 + C00002 + C00692 --> C00008 + C00080 + C00009 + C04877
R_PSP_L	0	Glycine, serine and threonine metaboli	3.1.3.3	FALSE	L-O-Phosphoserine phosphohydrolase	[c] : C00001 + C01005 --> C00009 + C00716
R_R06447	0	Terpenoid biosynthesis	2.5.1.31	TRUE	di-trans,poly-cis-Decaprenyl-diphosphat	[c] : ttc-ggdp + 7 C00129 <==> C04574 + 7 C00013
R_ADNUC	1000	Purine metabolism	3.2.2.8; 3.2	FALSE	Adenosine ribohydrolase	[c] : C00212 + C00001 --> C00147 + C00121
R_ICDHyr	567.9467	Reductive carboxylate cycle (CO2 fixat	1.1.1.42	TRUE	Isocitrate:NADP+ oxidoreductase (decar	[c] : C00311 + C00006 <==> C00026 + C00011 + C00005
R_SRC_C00	0	SourceFlux	.	FALSE	. source flux	C00007[b] --> C00007[e]
R_vitd2t	0	Transport Database	.	FALSE	vitd2transport	vitd2[e] --> vitd2[c]
R_R01070	332.6792	Fructose and mannose metabolism; Gly	4.1.2.13	TRUE	beta-D-fructose-1,6-bisphosphate D-glyc	[c] : C05378 <==> C00111 + C00118
R_OHPBAT	0	Vitamin B6 metabolism	2.6.1.52	TRUE	O-Phospho-4-hydroxy-L-threonine:2-ox	[c] : C00025 + C06054 <==> C00026 + C06055
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00163[e] --> C00163[b]
R_GLUDx	-783.388	Glutamate metabolism; Nitrogen metal	1.4.1.3; 1.4	TRUE	L-Glutamate:NAD+ oxidoreductase (deal	[c] : C00025 + C00001 + C00003 <==> C00026 + C00080 + C00004 + C01342

R_R06895	0	Porphyrin and chlorophyll metabolism	1.3.99.22	TRUE	coproporphyrinogen-III:S-adenosyl-L-m	[c] : C03263 + 2 C00019 <==> C01079 + 2 C00011 + 2 C00073 + 2 C05198
R_DHORTS	-20.6558	Pyrimidine metabolism	3.5.2.3	TRUE	(S)-dihydroorotate amidohydrolase	[c] : C00337 + C00001 <==> C00438 + C00080
R_PHETA1	-12.7016	Phenylalanine metabolism; Phenylalan	2.6.1.9; 2.6	TRUE	L-Phenylalanine:2-oxoglutarate aminotr	[c] : C00026 + C00079 <==> C00025 + C00166
R_DCTPD	0	Pyrimidine metabolism	3.5.4.13	FALSE	dCTP aminohydrolase	[c] : C00458 + C00080 + C00001 --> C00460 + C01342
R_HACD9n	0	Valine, leucine and isoleucine degradat	1.1.1.35; 1.	TRUE	(2S,3S)-3-hydroxy-2-methylbutanoyl-Co	[c] : C04405 + C00003 <==> C03344 + C00080 + C00004
R_SRC_C14	0.549348	SourceFlux	.	FALSE	. source flux	C14819[b] --> C14819[e]
R_METTRS	0	Methionine metabolism	6.1.1.10	FALSE	L-Methionine:tRNAMet ligase (AMP-forn	[c] : C00002 + C00073 + C01647 --> C00020 + C02430 + C00013
R_R04137	0	Valine, leucine and isoleucine degradat	4.2.1.17	TRUE	3-Hydroxyisopentyl-CoA hydro-lyase	[c] : C05998 <==> C03069 + C00001
R_PPND	9.443836	Phenylalanine, tyrosine and tryptopha	1.3.1.12	FALSE	Prephenate:NAD+ oxidoreductase(decar	[c] : C00003 + C00254 --> C01179 + C00011 + C00004
R_TMPPP	0	Thiamine metabolism	2.5.1.3	FALSE	2-Methyl-4-amino-5-hydroxymethylpyri	[c] : C04752 + C04327 + C00080 --> C00013 + C01081
R_QULNS	1.098696	Nicotinate and nicotinamide metabolis	.	FALSE	.	[c] : C00111 + C05840 --> C00080 + 2 C00001 + C00009 + C03722
R_R02073	-82.3041	Fructose and mannose metabolism	2.7.1.90	TRUE	diphosphate:beta-D-fructose-6-phospha	[c] : C00013 + f6p-B <==> C00009 + C05378
R_MTHFR3	11.0547	Methane metabolism; One carbon pool	1.5.1.20	FALSE	5-methyltetrahydrofolate:NADP+ oxidor	[c] : 2 C00080 + C00143 + C00005 --> C00440 + C00006
R_R07411	0	Porphyrin and chlorophyll metabolism	2.5.1.-	TRUE	.	[c] : C00032 <==> C15672
R_R04573	0	Peptidoglycan biosynthesis	6.3.2.10	TRUE	UDP-N-acetylmuramoyl-L-alanyl-D-glut	[c] : C00002 + C05892 + C00993 <==> C00008 + C00009 + C04702
R_R07412	0	Porphyrin and chlorophyll metabolism	.	TRUE	.	[c] : C15672 <==> hemeA_1
R_TYRTRS	0	Phenylalanine, tyrosine and tryptopha	6.1.1.1	FALSE	L-Tyrosine:tRNA(Tyr) ligase (AMP-form	[c] : C00002 + C00787 + C00082 --> C00020 + C00013 + C02839
R_R04572	0	Peptidoglycan biosynthesis	6.3.2.10	TRUE	UDP-N-acetylmuramoyl-L-alanyl-D-glut	[c] : C00002 + C04700 + C00993 <==> C00008 + C00009 + C04846
R_nadt	0	Transport Database	.	FALSE	nadtransport	C00003[e] --> C00003[c]
R_UAGCVT	0	Aminosugars metabolism	2.5.1.7	FALSE	Phosphoenolpyruvate:UDP-N-acetyl-D-g	[c] : C00074 + C00043 --> C00009 + C04631
R_a_D_gluc	0	Transport Database	.	FALSE	a-D-glucosetransport	C00267[e] --> C00267[c]
R_R03172	0	Valine, leucine and isoleucine degradat	1.3.99.12;	TRUE	(S)-2-methylbutanoyl-CoA:acceptor 2,3-	[c] : C15980 + C00028 <==> C03345 + C00030
R_R04960	-0.54935	Fatty acid biosynthesis	2.3.1.41; 2.	TRUE	Octanoyl-[acyl-carrier protein]:malonyl-	[c] : C05752 + C01209 <==> C05753 + C00011 + apoACP_ACP
R_R05219	0	Porphyrin and chlorophyll metabolism	2.1.1.152	TRUE	.	[c] : C06320 + C00033 + C00021 <==> C06416 + C00019 + C00001
R_R05218	0	Porphyrin and chlorophyll metabolism	1.16.8.1	TRUE	cob(II)yrinic acid-a,c-diamide:FMN oxid	[c] : 2 C06504 + C01847 <==> 2 C06505 + C00061 + 2 C00080
R_XPPT	0	Purine metabolism	2.4.2.22; 2.	FALSE	XMP:pyrophosphate phosphoribosyltran	[c] : C00119 + C00385 --> C00013 + C00655
R_ncamt	0	Transport Database	.	FALSE	ncamtransport	C00153[e] --> C00153[c]
R_NDPK3n	-0.82633	Pyrimidine metabolism	2.7.4.6	TRUE	ATP:CDP phosphotransferase	[c] : C00002 + C00112 <==> C00008 + C00063
R_PMANM	0	Fructose and mannose metabolism	5.4.2.8	TRUE	D-Mannose 6-phosphate 1,6-phosphomu	[c] : C00636 <==> C00275
R_R08089	0	Geraniol degradation	1.3.99.-	TRUE	.	[c] : C16464 + C00028 <==> C01920 + C00030
R_MTHFD	61.05511	One carbon pool by folate; Glyoxylate a	1.5.1.5	TRUE	5,10-methylenetetrahydrofolate:NADP+	[c] : C00143 + C00006 <==> C00445 + C00005
R_ribflvt	1.098696	Transport Database	.	FALSE	ribflvtransport	C00255[e] --> C00255[c]
R_R05217	0	Porphyrin and chlorophyll metabolism	1.14.13.83	TRUE	precorrin-3A,NADH:oxygen oxidoreduct	[c] : C05772 + C00007 + C00004 + C00080 <==> C06406 + C00003 + C00001
R_SCPx	0	Bile acid biosynthesis	2.3.1.16	FALSE	Propanoyl-CoA:acetyl-CoA C-acyltransfe	[c] : cholcoaone + C00010 --> cholcoa + C00100
R_R07954	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07481 + C00004 + C00080 + C00007 <==> C13747 + C00003 + C00067 + C00001
R_PGCD	0	Glycine, serine and threonine metaboli	1.1.1.95	FALSE	3-Phospho-D-glycerate:NAD+ 2-oxidore	[c] : C00197 + C00003 --> C03232 + C00080 + C00004
R_R07956	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07481 + C00005 + C00080 + C00007 <==> C07480 + C00006 + C00067 + C00001
R_R07957	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C13747 + C00004 + C00080 + C00007 <==> C16353 + C00003 + C00067 + C00001
R_R07950	0	Biosynthesis of unsaturated fatty acids	1.3.3.6	TRUE	.	[c] : C16172 + C00016 <==> C16387 + C01352
R_COCHL	0	Porphyrin and chlorophyll metabolism	6.6.1.2	FALSE	hydrogenobyrinic-acid-a,c-diamide:coba	[c] : C00002 + C00175 + C00001 + C06503 --> C00008 + C06504 + 2 C00080 + C00009
R_ACYP_2	0	Pyruvate metabolism	3.6.1.7	FALSE	Acetyl phosphate phosphohydrolase	[c] : C00227 + C00001 --> C00033 + C00080 + C00009
R_R07958	-1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C13747 + C00005 + C00080 + C00007 <==> C16353 + C00006 + C00067 + C00001
R_MECDPS	0	Biosynthesis of steroids	4.6.1.12	FALSE	2-Phospho-4-(cytidine 5'-diphospho)-2-	[c] : C11436 --> C11453 + C00055
R_R05071	1000	Valine, leucine and isoleucine biosynth	1.1.1.86; 5.	TRUE	(S)-2-Acetolactate methylmutase	[c] : C06010 <==> C04181
R_R01827	-194.561	Pentose phosphate pathway	2.2.1.2	TRUE	sedoheptulose-7-phosphate:D-glycerald	[c] : C05382 + C00118 <==> C00279 + f6p-B
R_HEXTT	0	Biosynthesis of steroids	2.5.1.30	FALSE	.	[c] : C01230 + C00129 --> C04216 + C00013
R_MDHm	-1000	Pyruvate metabolism; Citrate cycle (TC	1.1.1.37	TRUE	(S)-malate:NAD+ oxidoreductase	[c] : C00711 + C00003 <==> C00080 + C00004 + C00036
R_pydxt	0	Transport Database	.	FALSE	pydxtransport	C00250[e] --> C00250[c]
R_R00802	0	Starch and sucrose metabolism	3.2.1.26; 3.	TRUE	alpha-D-Glucoside glucohydrolase	[c] : C00089 + C00001 <==> C02336 + C00267
R_R01858	-1000	Purine metabolism	2.7.1.40	TRUE	dGTP:pyruvate 2-O-phosphotransferase	[c] : C00286 + C00022 <==> C00361 + C00074
R_CYSSr	-1000	Cysteine metabolism; Sulfur metabolis	2.5.1.65; 2.	TRUE	O3-Acetyl-L-serine acetate-lyase (adding	[c] : C00979 + C00297 <==> C00033 + C00097 + C00080
R_R01411	0	Pyrimidine metabolism	3.5.4.1	TRUE	5-Methylcytosine aminohydrolase	[c] : C02376 + C00001 <==> C00178 + C01342
R_R05177	0	Porphyrin and chlorophyll metabolism	5.4.1.2	TRUE	Precorrin 8X 11,12-methylmutase	[c] : C06408 <==> C06399
R_GLYTRS	0	Glycine, serine and threonine metaboli	6.1.1.14	FALSE	Glycine:tRNA(Gly) ligase (AMP-forming)	[c] : C00002 + C00037 + C01642 --> C00020 + C02412 + C00013
R_ARGN	0	Urea cycle and metabolism of amino gr	3.5.3.1	FALSE	L-Arginine amidinohydrolase	[c] : C00062 + C00001 --> C00077 + C00086
R_R00416	0	Aminosugars metabolism	2.7.7.23	TRUE	UTP:N-acetyl-alpha-D-glucosamine-1-ph	[c] : C00075 + C04501 <==> C00013 + C00043

R_ESC_C01	124.5222	EscapeFlux	.	FALSE	. escape flux	C01089[c] --> C01089[b]
R_R00412	-949.669	Benzoate degradation via CoA ligation;	1.3.99.1	TRUE	Succinate:(acceptor) oxidoreductase	[c] : C00042 + C00028 <==> C00122 + C00030
R_T2M26D	0	Limonene and pinene degradation	4.2.1.17	TRUE	trans-2-Methyl-5-isopropylhexa-2,5-die	[c] : C00001 + t2m26dcoa <==> 3h26dm5coa
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00064[c] --> C00064[b]
R_phemet	0	Transport Database	.	FALSE	phemetransport	C00032[e] --> C00032[c]
R_clt	0.549348	Transport Database	.	FALSE	cltransport	C00698[e] --> C00698[c]
R_ADOCBI	0	Porphyrin and chlorophyll metabolism	2.7.1.156	FALSE	.	[c] : C06508 + C00002 --> C06509 + C00008 + C00080
R_G1SATi	0	Porphyrin and chlorophyll metabolism	5.4.3.8	FALSE	(S)-4-Amino-5-oxopentanoate 4,5-amino	[c] : C03741 --> C00430
R_PPAKr	0	Propanoate metabolism	2.7.2.1; 2.7	TRUE	ATP:propanoate phosphotransferase	[c] : C00008 + C02876 <==> C00002 + C00163
R_GLNS	138.1552	Glutamate metabolism; Nitrogen metal	6.3.1.2	FALSE	L-Glutamate:ammonia ligase (ADP-form	[c] : C00002 + C00025 + C01342 --> C00008 + C00064 + C00080 + C00009
R_ergstt	0	Transport Database	.	FALSE	ergsttransport	C01694[e] --> C01694[c]
R_R01557	-888.115	Starch and sucrose metabolism	5.4.99.16	TRUE	Maltose alpha-D-glucosylmutase	[c] : C00208 <==> C01083
R_R08255	0	Drug metabolism - other enzymes	3.1.1.1	TRUE	.	[c] : C16641 + C00001 <==> C11173 + C16836
R_GLYCDx	0	Glycerolipid metabolism	1.1.1.6	FALSE	glycerol:NAD+ 2-oxidoreductase	[c] : C00116 + C00003 --> C01227 + C00080 + C00004
R_R00891	24.12176	Glycine, serine and threonine metaboli	4.2.1.22	TRUE	L-Serine hydro-lyase (adding homocyste	[c] : C00716 + C00297 <==> C00097 + C00001
R_R02670	0	Tryptophan metabolism	1.11.1.6	TRUE	Hydorogen-peroxide:hydrogen-peroxide	[c] : 2 C00632 + 4 C00007 <==> C05640 + 2 C00704 + 2 C00027 + 2 C00080
R_MI1PS	0	Streptomycin biosynthesis	5.5.1.4	FALSE	1L-myo-Inositol-1-phosphate lyase (isor	[c] : C00668 --> C01177
R_R05134	0	Glycolysis / Gluconeogenesis	3.2.1.86	TRUE	Salicin 6-phosphate glucohydrolase	[c] : C06188 + C00001 <==> 2hymeph + C01172
R_ME1	95.85013	Pyruvate metabolism	4.1.1.3; 1.1	FALSE	(S)-Malate:NADP+ oxidoreductase(oxalo	[c] : C00711 + C00003 --> C00011 + C00004 + C00022
R_adnt	0	Transport Database	.	FALSE	adntransport	C00212[e] --> C00212[c]
R_hco3t	0	Transport Database	.	TRUE	hco3transport	C01353[c] <==> C01353[e]
R_SRC_C00	0.549348	SourceFlux	.	FALSE	. source flux	C00059[b] --> C00059[e]
R_malttrt	0	Transport Database	.	FALSE	malttrtransport	C01835[e] --> C01835[c]
R_PHCDm	0	Arginine and proline metabolism	1.5.1.12	FALSE	L-1-Pyrroline-3-hydroxy-5-carboxylate:	[c] : C04281 + 2 C00001 + C00003 --> e4hglu + C00080 + C00004
R_IPPMIa	0	Valine, leucine and isoleucine biosynth	4.2.1.33	TRUE	3-Isopropylmalate hydro-lyase	[c] : C04411 <==> C02631 + C00001
R_IPPMIb	0	Valine, leucine and isoleucine biosynth	4.2.1.33	TRUE	2-Isopropylmalate hydro-lyase	[c] : C02631 + C00001 <==> C02504
R_ECOAH1	0	Valine, leucine and isoleucine degradat	4.2.1.17	TRUE	(S)-3-Hydroxyisobutyryl-CoA hydro-lyas	[c] : C03460 + C00001 <==> C04047
R_GHMT2r	72.68765	Methane metabolism; One carbon pool	2.1.2.1	TRUE	5,10-Methylenetetrahydrofolate:glycine	[c] : C00716 + C00101 <==> C00037 + C00001 + C00143
R_GAPD	0	Glycolysis / Gluconeogenesis	1.2.1.12; 1.	TRUE	D-glyceraldehyde-3-phosphate:NAD+ ox	[c] : C00118 + C00003 + C00009 <==> C00236 + C00080 + C00004
R_SSALy	0	Butanoate metabolism; Tyrosine metal	1.2.1.16	FALSE	Succinate-semialdehyde:NADP+ oxidore	[c] : C00001 + C00006 + C00232 --> 2 C00080 + C00005 + C00042
R_HSERTA	-964.824	Methionine metabolism; Sulfur metabo	2.3.1.31	TRUE	Acetyl-CoA:L-homoserine O-acetyltransf	[c] : C00024 + C00263 <==> C01077 + C00010
R_SSALx	0	Butanoate metabolism; Tyrosine metal	1.2.1.24; 1.	FALSE	Succinate-semialdehyde:NAD+ oxidored	[c] : C00001 + C00003 + C00232 --> 2 C00080 + C00004 + C00042
R_DHORD	20.65581	Pyrimidine metabolism	1.3.3.1	TRUE	(S)-Dihydroorotate:oxygen oxidoreducta	[c] : C00337 + C00007 <==> C00027 + C00295
R_TKT2	552.9957	Carbon fixation in photosynthetic orga	2.2.1.1	TRUE	D-Fructose 6-phosphate:D-glyceraldehy	[c] : C00279 + C00231 <==> C05345 + C00118
R_sucrt	0	Transport Database	.	FALSE	sucrtransport	C00089[e] --> C00089[c]
R_SRC_C00	198.4127	SourceFlux	.	FALSE	. source flux	C00001[b] --> C00001[e]
R_DHAD1	0	Valine, leucine and isoleucine biosynth	4.2.1.9	FALSE	(R)-2,3-Dihydroxy-3-methylbutanoate h	[c] : C04039 --> C00141 + C00001
R_UPP3S	0	Porphyrin and chlorophyll metabolism	4.2.1.75	FALSE	Hydroxymethylbilane hydro-lyase(cycliz	[c] : C01024 --> C00001 + C01051
R_UPPDC2	0	Porphyrin and chlorophyll metabolism	4.1.1.37	FALSE	Uroporphyrinogen I carboxy-lyase	[c] : 4 C00080 + C05766 --> 4 C00011 + C05768
R_UPPDC1	0	Porphyrin and chlorophyll metabolism	4.1.1.37	FALSE	Uroporphyrinogen-III carboxy-lyase	[c] : 4 C00080 + C01051 --> 4 C00011 + C03263
R_PPCOAO	0	beta-Alanine metabolism	1.3.99.3	FALSE	Propanoyl-CoA:(acceptor) 2,3-oxidoredu	[c] : C00016 + C00100 --> C01352 + prpncoa
R_R01786	1000	Glycolysis / Gluconeogenesis; Starch a	2.7.1.1; 2.7	TRUE	ATP:alpha-D-glucose 6-phosphotransfer	[c] : C00002 + C00267 <==> C00008 + C00668
R_R02071	0	Fructose and mannose metabolism	2.7.1.56	TRUE	ATP:D-fructose-1-phosphate 6-phospho	[c] : C00002 + C01094 <==> C00008 + C05378
R_R05449	0	1,4-Dichlorobenzene degradation	1.14.13.-	TRUE	.	[c] : C07098 + 2 C00004 + C00007 <==> C07097 + 2 C00003 + C01328 + C00698
R_acact	0	Transport Database	.	FALSE	acactransport	C00164[c] --> C00164[e]
R_DRBK	0	Pentose phosphate pathway	2.7.1.15	FALSE	.	[c] : C00002 + C01801 --> C00673 + C00008 + C00080
R_OMPDC	20.65581	Pyrimidine metabolism	4.1.1.23	FALSE	orotidine-5'-phosphate carboxy-lyase (U	[c] : C00080 + C01103 --> C00011 + C00105
R_arg_Lt	0	Transport Database	.	FALSE	arg-Ltransport	C00062[e] --> C00062[c]
R_FTHFLi	0	Glyoxylate and dicarboxylate metaboli	6.3.4.3	FALSE	Formate:tetrahydrofolate ligase (ADP-fo	[c] : C00002 + C00058 + C00101 --> C00234 + C00008 + C00009
R_NNAMrr	0	Nicotinate and nicotinamide metabolis	3.5.1.19	TRUE	Nicotinamide amidohydrolase	[c] : C00001 + C00153 <==> C11486 + C01342
R_R01641	194.5606	Pentose phosphate pathway; Carbon fi	2.2.1.1	TRUE	Sedoheptulose-7-phosphate:D-glyceralde	[c] : C05382 + C00118 <==> C03736 + C00231
R_spmdt	0	Transport Database	.	FALSE	spmdtransport	C00315[e] --> C00315[c]
R_HXPRT	0	Purine metabolism	2.4.2.8	FALSE	IMP:diphosphate phospho-D-ribosyltran	[c] : C00262 + C00119 --> C00130 + C00013
R_ACGSm	0	Urea cycle and metabolism of amino gr	2.3.1.1	FALSE	Acetyl-CoA:L-glutamate N-acetyltransfer	[c] : C00024 + C00025 --> C00624 + C00010 + C00080
R_ACOAD1	0	Butanoate metabolism	1.3.1.44; 1.	TRUE	Butanoyl-CoA:(acceptor) 2,3-oxidoreduc	[c] : b2coa + C00080 + C00004 <==> C00136 + C00003
R_MI1PP	0	Streptomycin biosynthesis; Inositol ph	3.1.3.25	FALSE	1D-myo-Inositol 1-phosphate phosphoh	[c] : C00001 + C01177 --> C00137 + C00009

R_HACD1	0	Butanoate metabolism; Lysine degrada	1.1.1.35	TRUE	(S)-3-Hydroxybutanoyl-CoA:NAD+ oxidd	[c] : C00332 + C00080 + C00004 <==> 3hbcoa + C00003
R_HACD2	0	Fatty acid elongation in mitochondria	1.1.1.211;	TRUE	(S)-hydroxyhexanoyl-CoA:NAD+ oxidore	[c] : C05269 + C00080 + C00004 <==> C05268 + C00003
R_R01600	-140.289	Glycolysis / Gluconeogenesis	2.7.1.2; 2.7	TRUE	ATP:beta-D-glucose 6-phosphotransfera	[c] : C00002 + C00221 <==> C00008 + C01172
R_SADT	0	Sulfur metabolism; Purine metabolism	2.7.7.4	FALSE	ATP:sulfate adenylyltransferase	[c] : C00002 + C00080 + C00059 --> C00224 + C00013
R_chsterol	0	Transport Database	.	FALSE	chsteroltransport	C00187[e] --> C00187[c]
R_lctst	0	Transport Database	.	FALSE	lctstransport	C00243[e] --> C00243[c]
R_BDHm	-124.522	Butanoate metabolism; Synthesis and d	1.1.1.30	TRUE	(R)-3-Hydroxybutanoate:NAD+ oxidored	[c] : C01089 + C00003 <==> C00164 + C00080 + C00004
R_GAPD_LI	1000	Glycolysis / Gluconeogenesis	1.2.1.13; 1.	TRUE	D-glyceraldehyde-3-phosphate:NADP+ d	[c] : C00118 + C00006 + C00009 <==> C00236 + C00080 + C00005
R_ADK1	-1000	Purine metabolism	2.7.4.3	TRUE	ATP:AMP phosphotransferase	[c] : C00020 + C00002 <==> 2 C00008
R_NTPP2	0	Purine metabolism	3.6.1.8; 3.6	FALSE	Guanosine 5'-triphosphate pyrophospho	[c] : C00044 + C00001 --> C00144 + C00080 + C00013
R_PPPGOm	0	Porphyrin and chlorophyll metabolism	1.3.3.4	FALSE	Protoporphyrinogen-IX:oxygen oxidored	[c] : 3 C00007 + 2 C01079 --> 6 C00001 + 2 C02191
R_ANS2	3.880026	Phenylalanine, tyrosine and tryptopha	4.1.3.27	FALSE	chorismate pyruvate-lyase (amino-accep	[c] : C00251 + C01342 --> C00108 + C00080 + C00001 + C00022
R_PYLALD	0	Limonene and pinene degradation	1.2.1.3	FALSE	Aldehyde:NAD+ oxidoreductase	[c] : C00001 + C00003 + pylald --> 2 C00080 + C00004 + peracd
R_BETALD	0	Glycine, serine and threonine metaboli	1.2.1.8	FALSE	p-Cumic alcohol:NADP+ oxidoreductase	[c] : C00576 + C00001 + C00006 --> C00719 + 2 C00080 + C00005
R_trp_Lt	0	Transport Database	.	FALSE	trp-Ltransport	C00078[e] --> C00078[c]
R_ASP1DC	759.9417	Alanine and aspartate metabolism; bet	4.1.1.11; 4.	FALSE	L-Aspartate 1-carboxy-lyase	[c] : C00049 + C00080 --> C00099 + C00011
R_R03824	0	Carotenoid biosynthesis	.	TRUE	.	[c] : C05435 <==> caro
R_R07700	0	Naphthalene and anthracene degradat	1.14.-.-	TRUE	aniline dioxygenase	[c] : C00292 + C00007 <==> C00090 + C01342
R_R06977	0	Glycine, serine and threonine metaboli	2.6.1.76	TRUE	L-2,4-diaminobutyrate:2-oxoglutarate 4-	[c] : C00025 + C00441 <==> C00026 + C03283
R_R06979	0	Glycine, serine and threonine metaboli	4.2.1.108	TRUE	Ectoine hydro-lyase	[c] : C06442 <==> C00001 + C06231
R_R06978	0	Glycine, serine and threonine metaboli	2.3.1.178	TRUE	L-2,4-diaminobutyrate acetyltransferase	[c] : C03283 + C00024 <==> C06442 + C00010
R_NTPP1	0	Purine metabolism	3.6.1.19	FALSE	2'-Deoxyguanosine 5'-triphosphate diph	[c] : C00286 + C00001 --> C00362 + C00080 + C00013
R_R07709	-1000	Naphthalene and anthracene degradat	1.14.13.-	TRUE	.	[c] : C00805 + C00004 + C00007 + C00080 <==> C00628 + C00003 + C00001
R_GCCa	0.248494	Glycine, serine and threonine metaboli	1.4.4.2	FALSE	glycine:lipoylprotein oxidoreductase (de	[c] : C00037 + C00080 + C02051 --> C01242 + C00011
R_KAS14	0	Fatty acid biosynthesis	2.3.1.41; 2.	FALSE	Acyl-[acyl-carrier-protein]:malonyl-[acy	[c] : C03939 + C00080 + C01209 --> C00229 + C05744 + C00011
R_glyt	0	Transport Database	.	FALSE	glytransport	C00037[e] --> C00037[c]
R_ORPT	-20.6558	Pyrimidine metabolism	2.4.2.10	TRUE	Orotidine-5'-phosphate:diphosphate pho	[c] : C01103 + C00013 <==> C00295 + C00119
R_CELBpts	0	.	.	FALSE	.	[c] : C00074 + C00185 --> C04534 + C00022
R_R03132	0	Cysteine metabolism	2.5.1.48; 2.	TRUE	O3-Acetyl-L-serine acetate-lyase (adding	[c] : C00979 + C05529 <==> C05824 + C00033
R_rib_Dt	0	Transport Database	.	FALSE	rib-Dtransport	C00121[e] --> C00121[c]
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00158[c] --> C00158[b]
R_R04445	0	Arginine and proline metabolism	1.5.1.12	TRUE	L-1-Pyrroline-3-hydroxy-5-carboxylate:	[c] : C04281 + C00006 + 2 C00001 <==> e4hglu + C00005 + C00080
R_fe3t	0.549348	Transport Database	.	FALSE	fe3transport	C14819[e] --> C14819[c]
R_R02991	0	Benzoate degradation via hydroxylatio	3.1.1.24	TRUE	4-Carboxymethylbut-3-en-4-olide enol-l	[c] : C03586 + C00001 <==> C00846
R_SELCYST	0	Selenoamino acid metabolism	4.2.1.22	FALSE	L-Serine hydro-lyase (adding homocyste	[c] : selhcys + C00716 --> C00001 + selcyst
R_AMID2	0	Phenylalanine metabolism; Styrene de	3.5.1.4	FALSE	2-phenylacetamide amidohydrolase	[c] : C00001 + C02505 --> C01342 + C07086
R_R00708	-15.1541	Arginine and proline metabolism; Glut	1.5.1.12	TRUE	L-1-Pyrroline-5-carboxylate:NAD+ oxidd	[c] : C03912 + C00006 + 2 C00001 <==> C00025 + C00005 + C00080
R_R03509	3.880026	Phenylalanine, tyrosine and tryptopha	5.3.1.24	TRUE	N-(5-Phospho-beta-D-ribosyl)anthranila	[c] : C04302 <==> C01302
R_R03508	3.880026	Phenylalanine, tyrosine and tryptopha	4.1.1.48	TRUE	1-(2-Carboxyphenylamino)-1-deoxy-D-r	[c] : C01302 <==> C03506 + C00011 + C00001
R_ME2	0	Pyruvate metabolism	4.1.1.3; 1.1	FALSE	(S)-Malate:NADP+ oxidoreductase(oxalo	[c] : C00711 + C00006 --> C00011 + C00005 + C00022
R_ASNS1	16.50841	Alanine and aspartate metabolism; Nit	6.3.5.4	FALSE	L-aspartate:L-glutamine amido-ligase (A	[c] : C00049 + C00002 + C00064 + C00001 --> C00020 + C00152 + C00025 + C00080 + C00(
R_ALAD_L	0	Reductive carboxylate cycle (CO2 fixati	1.4.1.1	FALSE	L-Alanine:NAD+ oxidoreductase (deamir	[c] : C00041 + C00001 + C00003 --> C00080 + C00004 + C01342 + C00022
R_ORNTAC	20.27863	Urea cycle and metabolism of amino gr	2.3.1.35	FALSE	N2-Acetyl-L-ornithine:L-glutamate N-ac	[c] : C00437 + C00025 --> C00624 + C00077
R_R08359	0	Glutathione metabolism	2.5.1.16	TRUE	S-adenosylmethioninamine:cadaverine 3	[c] : C01137 + C01672 <==> C00170 + C16565
R_R04385	-0.54935	Fatty acid biosynthesis	6.3.4.14	TRUE	biotin-carboxyl-carrier-protein:carbon-d	[c] : C00002 + C06250 + C01353 <==> C00008 + C00009 + C04419
R_R04386	-0.54935	Fatty acid biosynthesis	6.4.1.2	TRUE	Acetyl-CoA:carbon-dioxide ligase (ADP-f	[c] : C00024 + C04419 <==> C00083 + C06250
R_NMNATr	0	Nicotinate and nicotinamide metabolis	2.7.7.1; 2.7	FALSE	ATP:nicotinamide-nucleotide adenylyltr	[c] : C00002 + C00080 + C00455 --> C00003 + C00013
R_R05258	0	gamma-Hexachlorocyclohexane degrad	1.14.13.-	TRUE	.	[c] : C00472 + C00088 + C00006 + C00001 <==> 4nph + C00007 + C00005 + C00080
R_R07706	0	Naphthalene and anthracene degradat	1.14.-.-	TRUE	nitrobenzene 1,2-dioxygenase	[c] : C06813 + C00007 <==> C00090 + C00088
R_R01770	1000	Purine metabolism	3.2.2.8; 3.2	TRUE	Inosine ribohydrolase	[c] : C00294 + C00001 <==> C00262 + C00121
R_R04773	0	Selenoamino acid metabolism	6.1.1.10	TRUE	Selenomethionine:tRNAMet ligase (AMP	[c] : C00002 + C05335 + C01647 <==> C00020 + C00013 + C05336
R_R00935	0	Valine, leucine and isoleucine degradat	1.2.1.27	TRUE	(S)-Methylmalonate semialdehyde:NAD-	[c] : C06002 + C00010 + C00003 <==> C00100 + C00011 + C00004 + C00080
R_R07663	0	Toluene and xylene degradation	1.14.13.-	TRUE	.	[c] : 2 C06677 + C00007 + 2 C00080 <==> 2 C01468 + 2 C11481
R_R04672	-1000	Valine, leucine and isoleucine biosynth	2.2.1.6	TRUE	(S)-2-Acetolactate pyruvate-lyase (carbo	[c] : C06010 + C00068 <==> C05125 + C00022
R_ptrct	0	Transport Database	.	FALSE	ptrctransport	C00134[e] --> C00134[c]
R_glu_Lt	0	Transport Database	.	FALSE	glu-Ltransport	C00025[e] --> C00025[c]

R_R00028	888.1152	Starch and sucrose metabolism	3.2.1.20	TRUE	alpha-D-Glucoside glucohydrolase	[c] : C00208 + C00001 <==> 2 C00267
R_R04958	0	Fatty acid biosynthesis	2.3.1.86; 1.	TRUE	Octanoyl-[acyl-carrier protein]:malonyl-	[c] : C05752 + C00003 <==> C05751 + C00004 + C00080
R_R05132	0	Glycolysis / Gluconeogenesis	2.7.1.69	TRUE	Protein-N(pai)-phosphohistidine:sugar I	[c] : C04261 + C06186 <==> C00615 + C06187
R_UDPGDr	0	Nucleotide sugars metabolism; Ascorb	1.1.1.22	TRUE	UDPglucose:NAD+ oxidoreductase	[c] : C00001 + 2 C00003 + C00029 <==> 3 C00080 + 2 C00004 + C00167
R_R04955	0	Fatty acid biosynthesis	2.3.1.86; 1.	TRUE	Hexanoyl-[acyl-carrier protein]:malonyl	[c] : C05749 + C00003 <==> C05748 + C00004 + C00080
R_R04957	0	Fatty acid biosynthesis	2.3.1.41; 2.	TRUE	hexanoyl-[acyl-carrier protein]:malonyl-	[c] : C05749 + C01209 <==> C05750 + C00011 + apoACP_ACP
R_R00022	0	Aminosugars metabolism	3.2.1.52	TRUE	.	[c] : C01674 + C00001 <==> 2 C00140
R_R04951	0	Glutathione metabolism	3.4.11.2; 3.	TRUE	.	[c] : C05729 + C00001 <==> C05726 + C00037
R_R05133	0	Glycolysis / Gluconeogenesis	3.2.1.86	TRUE	Arbutin 6-phosphate glucohydrolase	[c] : C06187 + C00001 <==> C02389 + C01172
R_R04952	0	Fatty acid biosynthesis	2.3.1.41; 2.	TRUE	butyryl-[acyl-carrier protein]:malonyl-[a	[c] : C05745 + C01209 <==> C05746 + C00011 + apoACP_ACP
R_ACKr	-552.996	Pyruvate metabolism; Taurine and hyp	2.7.2.1; 2.7	TRUE	ATP:acetate phosphotransferase	[c] : C00033 + C00002 <==> C00227 + C00008
R_CYSTRS	0	Cysteine metabolism	6.1.1.16	FALSE	L-Cysteine:tRNA(Cys) ligase (AMP-formi	[c] : C00002 + C00097 + C01639 --> C00020 + C03125 + C00013
R_GLUSy	0	Glutamate metabolism; Nitrogen metal	1.4.1.13	FALSE	L-Glutamate:NADP+ oxidoreductase (tra	[c] : C00026 + C00064 + C00080 + C00005 --> 2 C00025 + C00006
R_GLUSx	0	Glutamate metabolism; Nitrogen metal	1.4.1.14	FALSE	L-glutamate:NAD+ oxidoreductase (tran	[c] : C00026 + C00064 + C00080 + C00004 --> 2 C00025 + C00003
R_TRSAR	0	Glyoxylate and dicarboxylate metaboli	1.1.1.60	FALSE	(R)-Glycerate:NAD+ oxidoreductase	[c] : 2h3oppan + C00080 + C00004 --> C00258 + C00003
R_val_Lt	0	Transport Database	.	FALSE	val-Ltransport	C00183[e] --> C00183[c]
R_R08310	0	Drug metabolism - cytochrome P450	1.1.1.1	TRUE	4-hydroxy-5-phenyltetrahydro-1,3-oxaz	[c] : C16595 + C00003 <==> C16596 + C00004 + C00080
R_ADPT	0	Purine metabolism	2.4.2.8; 2.4	FALSE	AMP:pyrophosphate phosphoribosyltrar	[c] : C00147 + C00119 --> C00020 + C00013
R_dribt	0	Transport Database	.	FALSE	dribtransport	C01801[e] --> C01801[c]
R_FBA	0	Carbon fixation in photosynthetic orga	4.1.2.13	TRUE	D-fructose-1,6-bisphosphate D-glyceralc	[c] : C00354 <==> C00111 + C00118
R_DPCOAK	0	Pantothenate and CoA biosynthesis	2.7.1.24	FALSE	ATP:dephospho-CoA 3'-phosphotransfer	[c] : C00002 + C00882 --> C00008 + C00010 + C00080
R_4HGLSD	0	Arginine and proline metabolism	1.5.99.8; 1.	FALSE	L-erythro-4-Hydroxyglutamate:NAD+ ox	[c] : C05938 + C00001 + C00003 <==> e4hglu + 2 C00080 + C00004
R_PNTK	0	Pantothenate and CoA biosynthesis	2.7.1.33	FALSE	ATP:pantothenate 4'-phosphotransferas	[c] : C00002 + C00864 --> C03492 + C00008 + C00080
R_ca2t	0.549348	Transport Database	.	FALSE	ca2transport	C00076[e] --> C00076[c]
R_ADNCYC	0	Purine metabolism	4.6.1.1	FALSE	ATP pyrophosphate-lyase (cyclizing)	[c] : C00002 --> C00575 + C00013
R_R00236	-1000	Pyruvate metabolism	6.2.1.1	TRUE	Acetyl adenylate:CoA ligase (AMP-formi	[c] : C05993 + C00010 <==> C00020 + C00024
R_cys_Lt	17.31399	Transport Database	.	FALSE	cys-Ltransport	C00097[e] --> C00097[c]
R_R05220	0	Porphyrin and chlorophyll metabolism	2.5.1.17	TRUE	ATP:cob(I)yrinic acid-a,c-diamide Cobet	[c] : C06505 + C00002 <==> C06506 + C00536
R_SRC_C00	0.549348	SourceFlux	.	FALSE	. source flux	C00698[b] --> C00698[e]
R_R05224	0	Porphyrin and chlorophyll metabolism	6.3.5.9	TRUE	.	[c] : C06399 + 2 C00064 + 2 C00002 + 2 C00001 <==> C06503 + 2 C00009 + 2 C00025 + 2 C
R_leu_Lt	1000	Transport Database	.	FALSE	leu-Ltransport	C00123[e] --> C00123[c]
R_R05653	0	Naphthalene and anthracene degradat	1.14.13.-	TRUE	phenanthrene 9,10-monooxygenase	[c] : C11422 + C00007 + C00004 + C00080 <==> C11429 + C00001 + C00003
R_R07456	0.549348	Vitamin B6 metabolism	.	TRUE	.	[c] : C00118 + C00199 + C00064 <==> C00018 + C00025
R_R05655	0	Naphthalene and anthracene degradat	1.14.13.-	TRUE	.	[c] : C11422 + C00007 + C00004 + C00080 <==> C11432 + C00001 + C00003
R_R05654	0	Naphthalene and anthracene degradat	1.14.13.-	TRUE	phenanthrene 1,2-monooxygenase	[c] : C11422 + C00007 + C00004 + C00080 <==> C11431 + C00001 + C00003
R_R05657	0	Naphthalene and anthracene degradat	2.1.1.-	TRUE	.	[c] : C11432 + C05694 <==> C11433 + C05693
R_R05048	0	Folate biosynthesis	6.-.-.-; 3.5.4	TRUE	GTP 7,8-8,9-dihydrolase	[c] : C05923 <==> C06148
R_R08281	0	Drug metabolism - cytochrome P450	1.1.1.1	TRUE	alcophosphamide:NAD+ oxidoreductase	[c] : C07645 + C00004 + C00080 <==> C16551 + C00003
R_SRC_C00	0.2	SourceFlux	.	FALSE	. source flux	C00185[b] --> C00185[e]
R_R02026	-964.824	Methionine metabolism	.	TRUE	O-acetyl-L-homoserine acetate-lyase (L-	[c] : C01077 + C05529 + C00342 + C00080 <==> C05330 + C00094 + C00343 + C00033
R_acaldt	0	Transport Database	.	FALSE	acaldtransport	C00084[c] --> C00084[e]
R_RPE	137.8491	Pentose phosphate pathway; Pentose a	5.1.3.1	TRUE	D-Ribulose-5-phosphate 3-epimerase	[c] : C00199 <==> C00231
R_MAN1PT	0	Fructose and mannose metabolism	2.7.7.13	FALSE	GTP:alpha-D-mannose-1-phosphate gua	[c] : C00044 + C00080 + C00636 --> C00096 + C00013
R_R02383	0	Tyrosine metabolism	1.14.13.-; 1	TRUE	Monophenol,L-dopa:oxygen oxidoreduct	[c] : C00483 + C00007 + C00004 + C00080 <==> C03758 + C00003 + C00001
R_R01342	0	Nitrogen metabolism	1.4.99.1	TRUE	D-Amino-acid:(acceptor) oxidoreductase	[c] : C05167 + C00001 + C00028 <==> C00161 + C01342 + C00030
R_R05046	0	Folate biosynthesis	3.5.4.16	TRUE	Formamidopyrimidine nucleoside triph	[c] : C05922 + C00001 <==> C05923 + C00058
R_R00296	0	Methane metabolism	1.2.99.2	TRUE	Carbon-monoxide:(acceptor) oxidoredu	[c] : C00237 + C00001 + C00028 <==> C00011 + C00030
R_PSD_SA	0	Glycerophospholipid metabolism; Glyc	4.1.1.65	FALSE	Phsophatidyl-L-serine carboxy-lyase	[c] : C00080 + 0.02 ps_SA --> C00011 + 0.02 pe_SA
R_ACACT1	0	Valine, leucine and isoleucine degradat	2.3.1.16	TRUE	Propanoyl-CoA:acetyl-CoA C-acyltransfe	[c] : C03344 + C00010 <==> C00024 + C00100
R_LYSTRS	0	Lysine biosynthesis	6.1.1.6	FALSE	L-Lysine:tRNALys ligase (AMP-forming)	[c] : C00002 + C00047 + C01646 --> C00020 + C01646 + C00013
R_ureat	0	Transport Database	.	FALSE	ureatransport	C00086[c] --> C00086[e]
R_PRAGS	30.52756	Purine metabolism	6.3.4.13	FALSE	5-Phospho-D-ribosylamine:glycine ligas	[c] : C00002 + C00037 + C03090 --> C00008 + C03838 + C00080 + C00009
R_R04566	0	Fatty acid biosynthesis	1.1.1.100; 1	TRUE	(3R)-3-Hydroxytetradecanoyl-[acyl-carr	[c] : 3hmrsACP + C00006 <==> C05759 + C00005 + C00080
R_o2t	0	Transport Database	.	FALSE	o2transport	C00007[e] --> C00007[c]
R_SRC_C00	23.46317	SourceFlux	.	FALSE	. source flux	C00047[b] --> C00047[e]
R_adet	0	Transport Database	.	FALSE	adetransport	C00147[e] --> C00147[c]

R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00078[c] --> C00078[b]
R_hxant	0	Transport Database	.	FALSE	hxantransport	C00262[e] --> C00262[c]
R_GALCTN	0	Galactose metabolism	4.2.1.6	FALSE	D-Galactonate hydro-lyase	[c] : C00880 --> C01216 + C00001
R_HSDy	951.719	Lysine biosynthesis; Glycine, serine an	1.1.1.3	TRUE	L-Homoserine:NADP+ oxidoreductase	[c] : C00263 + C00006 <==> C00441 + C00080 + C00005
R_gthrdt	0	Transport Database	.	FALSE	gthrdtransport	C00051[e] --> C00051[c]
R_ascb_Lt	0	Transport Database	.	FALSE	ascb-Ltransport	C00072[e] --> C00072[c]
R_fort	0	Transport Database	.	FALSE	fortransport	C00058[c] --> C00058[e]
R_CPC8MM	0	Porphyrin and chlorophyll metabolism	5.4.1.2	TRUE	.	[c] : C11545 <==> C05773
R_R05628	0	Peptidoglycan biosynthesis	2.7.8.13	TRUE	UDPMurAc(oyl-L-Ala-D-gamma-Glu-L-Ly	[c] : C04846 + C17556 <==> C00105 + C05888
R_R05030	0	Peptidoglycan biosynthesis	6.3.1.2	TRUE	Undecaprenyl-diphospho-N-acetylmura	[c] : C00002 + C05893 + C01342 <==> C00008 + C00009 + C05894
R_R05033	0	Peptidoglycan biosynthesis	6.3.1.2	TRUE	Undecaprenyl-diphospho-N-acetylmura	[c] : C00002 + C05898 + C01342 <==> C00008 + C00009 + C05899
R_R05032	0	Peptidoglycan biosynthesis	2.4.1.227	TRUE	.	[c] : C05897 + C00043 <==> C05898 + C00015
R_ESC_C00	446.1651	EscapeFlux	.	FALSE	. escape flux	C00042[e] --> C00042[b]
R_R03316	-503.504	Citrate cycle (TCA cycle)	1.2.4.2	TRUE	.	[c] : C05381 + C15972 <==> C16254 + C00068
R_NDPK9n	-589.701	Purine metabolism	2.7.4.6	TRUE	ATP:IDP phosphotransferase	[c] : C00002 + C00104 <==> C00008 + C00081
R_R02241	0	Glycerolipid metabolism; Glycerophosp	2.3.1.51	TRUE	acyl-CoA:1-acyl-sn-glycerol-3-phosphate	[c] : pa_Hp_pa_hs_pa_SC_pa_EC_pa_SA + C00010 <==> 1ag3p_SC + C00040
R_R02569	496.4957	Glycolysis / Gluconeogenesis; Pyruvate	2.3.1.12	TRUE	acetyl-CoA:enzyme N6-(dihydrolipoyl)ly	[c] : C00024 + C15973 <==> C00010 + C16255
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00037[c] --> C00037[b]
R_PEPCK	0	Glycolysis / Gluconeogenesis; Pyruvate	4.1.1.32	FALSE	GTP:oxaloacetate carboxy-lyase (transpl	[c] : C00044 + C00036 --> C00011 + C00035 + C00074
R_TDPm	0	Thiamine metabolism	3.6.1.15	FALSE	Thiamin diphosphate phosphohydrolase	[c] : C00001 + C00068 --> C00080 + C00009 + C01081
R_R07939	1000	Caffeine metabolism	1.14.14.1;	TRUE	.	[c] : C07481 + C00005 + C00007 + C00080 <==> C13747 + C00006 + C00067 + C00001
R_HSDxi	0	Lysine biosynthesis; Glycine, serine an	1.1.1.3	FALSE	L-Homoserine:NAD+ oxidoreductase	[c] : C00441 + C00080 + C00004 --> C00263 + C00003
R_PRASCS	30.52756	Purine metabolism	6.3.2.6	TRUE	1-(5-Phosphoribosyl)-5-amino-4-carbox	[c] : C04751 + C00049 + C00002 <==> C04823 + C00008 + C00080 + C00009
R_R08555	0	Aminosugars metabolism	4.2.-.-	TRUE	N-acetylmuramic acid 6-phosphate ethe	[c] : C16698 + C00001 <==> C00357 + C00256
R_ADCYRS	0	Porphyrin and chlorophyll metabolism	6.3.5.10	FALSE	.	[c] : C06506 + 4 C00002 + 4 C00064 + 4 C00001 --> C06507 + 4 C00008 + 4 C00025 + 4 C00
R_R07463	0	Thiamine metabolism	1.4.3.19	TRUE	glycine oxidase	[c] : C00037 <==> C15809
R_PRFGS	30.52756	Purine metabolism	6.3.5.3	FALSE	5'-Phosphoribosylformylglycinamide:L-g	[c] : C00002 + C04376 + C00064 + C00001 --> C00008 + C04640 + C00025 + C00080 + C00(
R_R08559	0	Aminosugars metabolism	2.7.1.69	TRUE	Protein-N(pai)-phosphohistidine:sugar I	[c] : C02713 + C04261 <==> C16698 + C00615
R_DADK	0	Purine metabolism	2.7.4.11; 2.	TRUE	ATP:dAMP phosphotransferase	[c] : C00002 + C00360 <==> C00008 + C00206
R_CYTK2n	0	Pyrimidine metabolism	2.7.4.14	TRUE	ATP:dCMP phosphotransferase	[c] : C00002 + C00239 <==> C00008 + C00705
R_R05238	0	3-Chloroacrylic acid degradation	1.2.1.3	TRUE	.	[c] : C16348 + C00001 <==> C06615 + 2 C00080
R_R03869	0	Valine, leucine and isoleucine degradat	1.2.1.3	TRUE	(S)-Methylmalonate semialdehyde:NAD-	[c] : C06002 + C00003 + C00001 <==> C02170 + C00004 + C00080
R_R07839	0	Benzoate degradation via hydroxylatio	5.3.3.10	TRUE	.	[c] : C04434 <==> C04451
R_NABTNC	0	Urea cycle and metabolism of amino gr	1.2.1.3	FALSE	N4-Acetylaminobutanal:NAD+ oxidored	[c] : C00001 + C05936 + C00003 --> C02946 + 2 C00080 + C00004
R_ALAALA	0	Peptidoglycan biosynthesis; D-Alanine	6.3.2.4	TRUE	D-alanine:D-alanine ligase (ADP-forming	[c] : 2 C00133 + C00002 <==> C00008 + C00993 + C00080 + C00009
R_GLUPRT	30.52756	Glutamate metabolism; Purine metabo	2.4.2.14	FALSE	5-phosphoribosylamine:diphosphate ph	[c] : C00064 + C00001 + C00119 --> C00025 + C00013 + C03090
R_ADSL1	14.99205	Alanine and aspartate metabolism; Pur	4.3.2.2	FALSE	N6-(1,2-dicarboxyethyl)AMP AMP-lyase	[c] : C03794 --> C00020 + C00122
R_ESC_C00	1000	EscapeFlux	.	FALSE	. escape flux	C00033[c] --> C00033[b]
R_SHCHF	0	Porphyrin and chlorophyll metabolism	4.99.1.4	FALSE	S-Adenosyl-L-methionine:uroporphyrin-	[c] : C14818 + C05778 --> 3 C00080 + C00748
R_CITL	432.0533	Citrate cycle (TCA cycle)	4.1.3.6	FALSE	Citrate oxaloacetate-lyase ((pro-3S)-CH2	[c] : C00158 --> C00033 + C00036
R_R03943	0	Tyrosine metabolism	2.1.1.-	TRUE	.	[c] : C02442 + C00019 <==> C06199 + C00021
R_PPDK	0	Pyruvate metabolism; Carbon fixation	2.7.9.1	FALSE	ATP:pyruvate,orthophosphate phosphot	[c] : C00002 + C00009 + C00022 --> C00020 + C00080 + C00074 + C00013
R_R07687	0	Naphthalene and anthracene degradat	1.14.-.-	TRUE	.	[c] : C14315 + C00007 + 2 C00080 + 2 C05359 <==> C16205
R_ornt	0	Transport Database	.	FALSE	orntransport	C00077[e] --> C00077[c]
R_PNP	1000	Nicotinate and nicotinamide metabolis	2.4.2.1	TRUE	N-Ribosylnicotinamide:orthophosphate	[c] : C00009 + C03150 <==> C00080 + C00153 + C00620
R_SHSL1	0	Methionine metabolism	2.5.1.48	FALSE	O-Succinyl-L-homoserine succinate-lyas	[c] : C00097 + C01118 --> cyst-L + C00080 + C00042
R_R03948	0	Porphyrin and chlorophyll metabolism	2.1.1.130	TRUE	S-Adenosyl-L-methionine:precorrin-4 C2	[c] : C00019 + dscl <==> C00021 + C05772 + C00080
R_R07962	1000	Caffeine metabolism	1.13.12.-	TRUE	.	[c] : C07480 + C00005 + C00080 + C00007 <==> C16353 + C00006 + C00067 + C00001
R_R02143	-1000	Purine metabolism	3.2.2.1	TRUE	Xanthosine ribohydrolase	[c] : C01762 + C00001 <==> C00385 + C00121
R_maltt	0	Transport Database	.	FALSE	malttransport	C00208[e] --> C00208[c]
R_ITCOALr	0	C5-Branched dibasic acid metabolism	6.2.1.5	TRUE	Itaconate:CoA ligase (ADP-forming)	[c] : C00002 + C00010 + C00490 <==> C00008 + C00531 + C00009
R_RBFK	0.549348	Riboflavin metabolism	2.7.1.26	FALSE	ATP:riboflavin 5'-phosphotransferase	[c] : C00002 + C00255 --> C00008 + C00061 + C00080
R_DHDPS	0	Lysine biosynthesis	4.2.1.52	FALSE	L-Aspartate-4-semialdehyde hydro-lyas	[c] : C00441 + C00022 --> C03340 + C00080 + 2 C00001
R_NBAH	0	Phenylalanine metabolism	3.5.1.32	TRUE	N-Benzoylglycine amidohydrolase	[c] : C01586 + C00001 <==> C00180 + C00037
R_b_D_gluc	0	Transport Database	.	FALSE	b-D-glucosetransport	C00221[e] --> C00221[c]
R_GTPCII	0	Riboflavin metabolism	3.5.4.25	FALSE	GTP 7,8-8,9-dihydrolase (pyrophosphate	[c] : C00044 + 3 C00001 --> 25dhpp + C00058 + 2 C00080 + C00013

R_ARGSL	0	Alanine and aspartate metabolism; Ure	4.3.2.1	TRUE	2-(Nomega-L-arginino)succinate arginin	[c] : C03406 <==> C00062 + C00122
R_LYSAM	0	Lysine degradation	5.4.3.2	TRUE	L-Lysine 2,3-aminomutase	[c] : C00047 <==> C01142
R_ILETA	-19.876	Valine, leucine and isoleucine degradat	2.6.1.42	TRUE	L-Isoleucine:2-oxoglutarate aminotransf	[c] : C00026 + C00407 <==> C03465 + C00025
R_GTHPe	0	Glutathione metabolism	1.11.1.9	TRUE	glutathione:hydrogen-peroxide oxidorec	[e] : 2 C00051 + C00027 <==> C00127 + 2 C00001
R_ACOATA	0	Fatty acid biosynthesis	2.3.1.85; 2.	TRUE	acetyl-CoA:[acyl-carrier-protein] S-acety	[c] : C00229 + C00024 <==> C03939 + C00010
R_R01163	0	Histidine metabolism	1.1.1.23	TRUE	L-Histidinal:NAD+ oxidoreductase	[c] : C01929 + C00001 + C00003 <==> C00135 + C00004 + C00080
R_ICHORSi	0	Ubiquinone and menaquinone biosynt	5.4.4.2	FALSE	Chorismate hydroxymutase	[c] : C00251 --> C00885
R_cellulose	0	Transport Database	.	FALSE	cellulosetransport	C00760[e] --> C00760[c]
R_CYSTS	0	Methionine metabolism; Glycine, serin	4.2.1.22	FALSE	L-serine hydro-lyase (adding homocyste	[c] : C05330 + C00716 --> cyst-L + C00001
R_HACD4p	0	Fatty acid elongation in mitochondria	1.1.1.211;	TRUE	(S)-hydroxydecanoyl-CoA:NAD+ oxidore	[c] : C05265 + C00080 + C00004 <==> 3hdcoa + C00003
R_R08258	0	Drug metabolism - other enzymes	3.1.1.1	TRUE	.	[c] : C16543 + C00001 <==> C11173 + C16837
R_PDX5PO	0	Vitamin B6 metabolism	1.4.3.5	TRUE	Pyridoxine 5-phosphate:oxygen oxidore	[c] : C00007 + C00627 <==> C00027 + C00018
R_R07888	0	alpha-Linolenic acid metabolism	1.3.3.6	TRUE	.	[c] : C16327 + C00016 <==> C16328 + C01352
R_xyl_Dt	0	Transport Database	.	FALSE	xyl-Dtransport	C01394[e] --> C01394[c]
R_HISTRS	0	Histidine metabolism	6.1.1.21	FALSE	L-Histidine:tRNA(His) ligase (AMP-form	[c] : C00002 + C00135 + C01643 --> C00020 + C02988 + C00013
R_R04639	0	Folate biosynthesis	3.5.4.16	TRUE	2-Amino-4-hydroxy-6-(erythro-1,2,3-tri	[c] : C04895 + C00001 <==> C06148
R_ESC_C00	0	EscapeFlux	.	FALSE	. escape flux	C00246[e] --> C00246[b]
R_R06941	0	Caprolactam degradation	1.1.1.35	TRUE	(S)-3-hydroxyacyl-CoA:NAD+ oxidoredu	[c] : C14145 + C00003 <==> C02232 + C00004 + C00080
R_R06942	0	Caprolactam degradation	4.2.1.17	TRUE	(3S)-3-hydroxyacyl-CoA hydro-lyase	[c] : C14144 + C00001 <==> C14145
R_R04534	0.549348	Fatty acid biosynthesis	1.1.1.100; 1	TRUE	(3R)-3-Hydroxydecanoyl-[acyl-carrier-p	[c] : C04619 + C00006 <==> C05753 + C00005
R_R04533	0	Fatty acid biosynthesis	1.1.1.100; 1	TRUE	(3R)-3-Hydroxybutanoyl-[acyl-carrier p	[c] : C04618 + C00006 <==> C05744 + C00005 + C00080
R_CSND	0	Pyrimidine metabolism	3.5.4.1	FALSE	Cytosine aminohydrolase	[c] : C00380 + C00080 + C00001 --> C01342 + C00106
R_R07464	0	Thiamine metabolism	.	TRUE	.	[c] : C15815 + C11437 + C00082 <==> C04327
R_R07465	0	Thiamine metabolism	.	TRUE	.	[c] : C15815 + C00082 + C15809 <==> C04327
R_R05662	0	Peptidoglycan biosynthesis	2.4.1.227	TRUE	.	[c] : C04851 + C00043 <==> C05893 + C00015
R_FOLD3m	0	Folate biosynthesis	2.5.1.15	FALSE	2-Amino-4-hydroxy-6-hydroxymethyl-7	[c] : 2ahhmd + C00568 --> C00921 + C00013
R_R07461	0	Thiamine metabolism	.	TRUE	.	[c] : C15812 + C15813 <==> C15814
R_R04440	-1000	Valine, leucine and isoleucine biosynth	1.1.1.86	TRUE	(R)-2,3-Dihydroxy-3-methylbutanoate:N	[c] : C04039 + C00006 <==> C04181 + C00005 + C00080
R_R07541	0	Carotenoid biosynthesis	.	TRUE	.	[c] : C05435 <==> C15908
R_R00069	0	Histidine metabolism	1.14.13.-	TRUE	.	[c] : 2 C05565 <==> C00007 + 2 C03680
R_SHSL2r	975.8782	Methionine metabolism	2.5.1.-; 2.5.	TRUE	O4-succinyl-L-homoserine:hydrogen sul	[c] : C00297 + C01118 <==> C00080 + C05330 + C00042
R_R04198	27.7166	Lysine biosynthesis	1.3.1.26	TRUE	2,3,4,5-Tetrahydrodipicolinate:NAD+ ox	[c] : C03972 + C00003 <==> C03340 + C00004 + C00080
R_R04212	0	Alanine and aspartate metabolism	6.3.5.6	TRUE	Asp-tRNA(Asn):L-glutamine amido-ligas	[c] : C03402 + C00025 + C00009 + C00008 <==> C06113 + C00064 + C00002 + C00001
R_HPPKm	0	Folate biosynthesis	2.7.6.3	FALSE	ATP:2-amino-4-hydroxy-6-hydroxymeth	[c] : 2ahhmp + C00002 --> 2ahhmd + C00020 + C00080
R_MCOATA	-0.54935	Fatty acid biosynthesis	2.3.1.85; 2.	TRUE	Malonyl-CoA:[acyl-carrier-protein] S-ma	[c] : C00229 + C00083 <==> C00010 + C01209
R_XYLI1	0	Pentose and glucuronate interconversi	5.3.1.5	TRUE	D-xylose aldose-ketose-isomerase	[c] : C01394 <==> C00310
R_ni2t	0	Transport Database	.	FALSE	ni2transport	C00291[e] --> C00291[c]
R_R05181	0	Porphyrin and chlorophyll metabolism	2.1.1.133	TRUE	S-adenosyl-L-methionine:precorrin-4 C1	[c] : C00019 + C06407 <==> C00021 + C06416
R_R05180	0	Porphyrin and chlorophyll metabolism	2.1.1.131	TRUE	S-Adenosyl-L-methionine:precorrin-3B (	[c] : C00019 + C06406 <==> C00021 + C06407
R_NNDPR	1.098696	Nicotinate and nicotinamide metabolis	2.4.2.19	FALSE	Nicotinate-nucleotide:pyrophosphate ph	[c] : 2 C00080 + C00119 + C03722 --> C00011 + C01185 + C00013
R_R05265	0	gamma-Hexachlorocyclohexane degrad	1.14.-.-	TRUE	.	[c] : C02235 + C00007 + 3 C00080 <==> C02814 + C00088 + C00001
R_sprmt	0	Transport Database	.	FALSE	sprmtransport	C00750[e] --> C00750[c]
R_DXPRIi	0	Biosynthesis of steroids	1.1.1.267	FALSE	1-Deoxy-D-xylulose-5-phosphate isomer	[c] : C11437 + C00080 + C00005 --> C11434 + C00006
R_PHETRS	0	Phenylalanine, tyrosine and tryptopha	6.1.1.20	FALSE	L-Phenylalanine:tRNA(Ala) ligase (AMP-	[c] : C00002 + C00079 + C01648 --> C00020 + C03511 + C00013
R_GARFT	30.52756	One carbon pool by folate; Purine meta	2.1.2.2	TRUE	10-Formyltetrahydrofolate:5'-phosphor	[c] : C00234 + C03838 <==> C04376 + C00080 + C00101
R_PGLer	0	Pentose phosphate pathway	3.1.1.31	FALSE	6-Phospho-D-glucono-1,5-lactone lacton	[c] : C01236 + C00001 --> C00345 + C00080
R_R05341	0	Carotenoid biosynthesis	.	TRUE	.	[c] : C05432 <==> C05435
R_PRATPP	0	Histidine metabolism	3.6.1.31	FALSE	Phosphoribosyl-ATP pyrophosphohydro	[c] : C00001 + C02739 --> C00080 + C00013 + C02741
R_act	0	Transport Database	.	TRUE	actransport	C00033[c] <==> C00033[e]
R_PRAIS	30.52756	Purine metabolism	6.3.3.1	FALSE	2-(Formamido)-N1-(5-phosphoribosyl)a	[c] : C00002 + C04640 --> C00008 + C03373 + 2 C00080 + C00009
R_ASPK	-951.719	Lysine biosynthesis; Glycine, serine an	2.7.2.4	TRUE	ATP:L-aspartate 4-phosphotransferase	[c] : C00049 + C00002 <==> C03082 + C00008
R_R04745	0	Fatty acid elongation in mitochondria	1.1.1.211;	TRUE	(S)-hydroxyoctanoyl-CoA:NAD+ oxidore	[c] : C05266 + C00003 <==> C05267 + C00004 + C00080
R_ALCD2if	0	Glycolysis / Gluconeogenesis	1.1.1.71; 1.	FALSE	Ethanol:NAD+ oxidoreductase	[c] : C00469 + C00003 --> C00084 + C00080 + C00004
R_ASAD	951.719	Lysine biosynthesis; Glycine, serine an	1.2.1.11	TRUE	L-Aspartate-4-semialdehyde:NADP+ oxi	[c] : C00441 + C00006 + C00009 <==> C03082 + C00080 + C00005
R_ORNTAr	0	Arginine and proline metabolism	2.6.1.13	TRUE	L-Ornithine:2-oxo-acid aminotransferas	[c] : C00026 + C00077 <==> C00025 + C01165

Appendix - A - Tfu_v3 - Proteomics Model With Constraints

ID	Flux	Pathways	ECs	Reversible	Name	Equation
R_NACHEX20ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg37 --> C00140 + ksi_deg38
R_GALASE16ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : 2 C00001 + ksii_core2_deg2 --> 2 C00124 + ksii_core2_deg3
R_R07263	0	Ubiquinone and other terpenoid-q	4.1.3.36	TRUE	4-(2-carboxyphenyl)-4-oxobutanoyl-CoA dehydr	[c] : C03160 <==> C15547 + C00001
R_FAOXC226205	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : c226coa + C00010 + C00001 + C00003 --> C00024 + C00080 + C00004 + t
R_ALDD2x	0	Glycolysis/Gluconeogenesis	1.2.1.3	FALSE	aldehydedehydrogenase(acetaldehyde,NAD)	[c] : C00084 + C00001 + C00003 --> C00033 + 2 C00080 + C00004
R_MME	0	Alternate Carbon Metabolism	5.1.99.1	TRUE	methylmalonyl-CoAepimerase	[c] : C01213 <==> C00683
R_GLACOm	0	Ascorbate and Aldarate Metabolisr	1.2.1.3	FALSE	D-Glucuronolactone:NAD+oxidoreductase,mitocl	[m] : glac + 2 C00001 + C00003 --> C00818 + 3 C00080 + C00004
R_GALASE3ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : 2 C00001 + ksi_deg5 --> 2 C00124 + ksi_deg6
R_IZPN	0	Histidine Metabolism	3.5.2.7	FALSE	imidazolonepropionase	[c] : C03680 + C00001 --> C00439 + C00080
R_PRPPS	0.2	Pentose Phosphate Pathway	2.7.6.1	TRUE	phosphoribosylpyrophosphatesynthetase	[c] : C00002 + C03736 <==> C00020 + C00080 + C00119
R_HPROb	0	Arginine and Proline Metabolism	1.5.1.2	FALSE	L-hydroxyprolinereductase(NADP)	[c] : C04281 + 2 C00080 + C00005 --> C01157 + C00006
R_HPROa	0	Arginine and Proline Metabolism	1.5.1.2	FALSE	L-hydroxyprolinereductase(NAD)	[c] : C04281 + 2 C00080 + C00004 --> C01157 + C00003
R_DASYN_EC	0	Membrane Lipid Metabolism	2.7.7.41	TRUE	CDP-Diacylglycerolsynthetase(Ecoli)	[c] : C00063 + C00080 + 0.02 pa_ec <==> 0.02 cdpdag_ec + C00013
R_FAOXC226205	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : c226coa + C00010 + C00001 + C00003 --> C00024 + C00080 + C00004 +
R_IPMD	0	Valine, Leucine and Isoleucine Met	1.1.1.85	FALSE	3-isopropylmalatedehydrogenase	[c] : C04411 + C00003 --> C04236 + C00080 + C00004
R_THRTRSm	0	Threonine and Lysine Metabolism	6.1.1.3	FALSE	threonyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C00188 + C01651 --> C00020 + C00013 + C02992
R_ESC_C00042_c	1000	EscapeFlux	.	FALSE	. escape flux	C00042[c] --> C00042[b]
R_mg2t	0.0038	Transport Database	.	FALSE	mg2transport	C00305[e] --> C00305[c]
R_BETALDHxm	0	Glycine, Serine, and Threonine Me	1.2.1.8	FALSE	betaine-aldehydedehydrogenase,mitochondrial	[m] : C00576 + C00001 + C00003 --> C00719 + 2 C00080 + C00004
R_FBA4	0	Glyoxylate and Dicarboxylate Meta	4.1.2.13	TRUE	D-Fructose1-phosphateD-glyceraldehyde-3-phos	[c] : xu1p-D <==> C00111 + C00266
R_PYDXNO	0	Pyridoxine Metabolism	1.4.3.5	TRUE	pyridoxineoxidase	[c] : C00007 + C00314 <==> C00027 + C00250
R_EXCH_C00186_	0	ExchangeFlux	.	TRUE	. exchange flux	C00186[c] <==> C00186[b]
R_GALASE12ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg32 --> C00124 + ksi_deg33
R_FBA2	0	Fructose and Mannose Metabolism	4.1.2.13	TRUE	D-Fructose1-phosphateD-glyceraldehyde-3-phos	[c] : C01094 <==> C00111 + C00577
R_FBA3	0	Glycolysis/Gluconeogenesis	4.1.2.13	TRUE	Sedoheptulose1,7-bisphosphateD-glyceraldehyd	[c] : C00447 <==> C00111 + C00279
R_CTPS2	0	Pyrimidine Biosynthesis	6.3.4.2	FALSE	CTPsynthase(glutamine)	[c] : C00002 + C00064 + C00001 + C00075 --> C00008 + C00063 + C00025 + 2
R_G6PDH2	0	Pentose Phosphate Pathway	1.1.1.49	FALSE	glucose6-phosphatedehydrogenase	[c] : C00668 + C00006 --> C01236 + C00080 + C00005
R_G6PDH3	0	Central Metabolism	1.1.1.49	FALSE	glucose6-phosphatedehydrogenase(F420-Depen	[c] : f420-2 + C00668 --> C01236 + f420-2h2
R_TPIg	0	Glycolysis/Gluconeogenesis	5.3.1.1	TRUE	triose-phosphateisomerase,glycosome	[x] : C00111 <==> C00118
R_GLYCK	0	Glyoxylate Metabolism	2.7.1.31	FALSE	glyceratekinase	[c] : C00002 + C00258 --> C00197 + C00008 + C00080
R_NAPRTm	0	NAD Biosynthesis	2.4.2.11	FALSE	NAPRTase,mitochondrial	[m] : C00080 + C11486 + C00119 --> C01185 + C00013
R_R02111	-0.1373	Starch and Sucrose Metabolism	2.4.1.1	TRUE	1,4-alpha-D-Glucan:orthophosphate alpha-D-glu	[c] : strch2_strch1 + C00009 <==> C00718 + C00103
R_CTPS1	0.069	Nucleotides	6.3.4.2	FALSE	CTPsynthase(NH3)	[c] : C00002 + C01342 + C00075 --> C00008 + C00063 + 2 C00080 + C00009
R_EXCH_C00033_	0	ExchangeFlux	.	TRUE	. exchange flux	C00033[c] <==> C00033[b]
R_ABTArm	0	Glutamate Metabolism	2.6.1.19	TRUE	4-aminobutyratetransaminase,reversible(mitoch	[m] : C00334 + C00026 <==> C00025 + C00232
R_EXCH_C00022_	0	ExchangeFlux	.	TRUE	. exchange flux	C00022[c] <==> C00022[b]
R_SRC_C00062_e	0.1404	SourceFlux	.	FALSE	. source flux	C00062[b] --> C00062[e]
R_DHPS2	0	Cofactor and Prosthetic Group Bio	2.5.1.15	FALSE	dihydropteroatesynthase	[c] : C00568 + C04807 --> C00921 + C00080 + C00013
R_urit	0	Transport Database	.	FALSE	uritransport	C00299[e] --> C00299[c]
R_FAOXC16180m	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationfattyacid	[m] : 4 C00010 + 3 C00016 + 4 C00001 + C05272 + 4 C00003 --> 4 C00024 + 3
R_EXCH_h2o_e	1000	ExchangeFlux	.	TRUE	. exchange flux	C00001[e] <==> C00001[b]
R_SELADT	0	Selenoamino Acid Metabolism	2.7.7.4	FALSE	selenateadenylyltransferase	[c] : C00002 + C00080 + sel --> adsel + C00013
R_DHPSm	0	Folate Metabolism	2.5.1.15	FALSE	dihydropteroatesynthase,mitochondrial	[m] : 2ahhmp + C00568 --> C00921 + C00001
R_FCLT	0	Cofactor and Prosthetic Group Bio	4.99.1.1	FALSE	Ferrochelatase	[c] : C14818 + C02191 --> 2 C00080 + C00032
R_GALASE9ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg23 --> C00124 + ksi_deg24
R_VALTAm	0	Valine, Leucine and Isoleucine Met	2.6.1.42	TRUE	valinetransaminase,mitochondiral	[m] : C00026 + C00183 <==> C00141 + C00025
R_SUCD3_DASH_	0	Oxidative Phosphorylation	1.3.5.1	TRUE	succinatedehydrogenase(ubiquinone-6),mitocho	[m] : C01352 + C17568 <==> C00016 + C00390
R_CAT	500	Glyoxylate and Dicarboxylate Meta	1.11.1.6	FALSE	catalase	[c] : 2 C00027 --> 2 C00001 + C00007
R_MMMm	0	Valine, Leucine and Isoleucine Met	5.4.99.2	TRUE	methylmalonyl-CoAmutase	[m] : C01213 <==> C00091
R_HPPK	0	Folate Biosynthesis	2.7.6.3	FALSE	2-amino-4-hydroxy-6-hydroxymethyldihydropte	[c] : 2ahhmp + C00002 --> 2ahhmd + C00020 + C00080
R_PPA_1	0	Transport, Extracellular	3.6.1.1	FALSE	inorganicdiphosphatase(oneprotontranslocation	C00001[c] + C00013[c] --> C00080[e] + 2 C00009[c]

R_NNATn	0	NAD Metabolism	2.7.7.18	FALSE	nicotinate-nucleotideadenylyltransferase	[n] : C00002 + C00080 + C01185 --> C00857 + C00013
R_SERTRS	0	Glycine and Serine Metabolism	6.1.1.11	FALSE	Seryl-tRNAsynthetase	[c] : C00002 + C00716 + C01650 --> C00020 + C00013 + C02553
R_NNATr	-1000	NAD Metabolism	2.7.7.18	TRUE	nicotinate-nucleotideadenylyltransferase	[c] : C00002 + C00080 + C01185 <==> C00857 + C00013
R_NACHEX4ly	0	Chondroitin Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : cs_c_deg1 + C00001 --> C01132 + cs_c_deg2
R_GHMT2rm	0	Glycine, Serine, and Threonine Me	2.1.2.1	TRUE	glycinehydroxymethyltransferase,reversible,mit	[m] : C00716 + C00101 <==> C00037 + C00001 + C00143
R_FBAg	0	Glycolysis/Gluconeogenesis	4.1.2.13	TRUE	fructose-bisphosphatealdolase,glycosome	[x] : C00354 <==> C00111 + C00118
R_EDA	0	Pentose Phosphate Pathway	4.1.2.14	FALSE	2-dehydro-3-deoxy-phosphogluconatealdolase	[c] : C04442 --> C00118 + C00022
R_EXCH_pyr_c	0	ExchangeFlux	.	TRUE	. exchange flux	C00022[c] <==> C00022[b]
R_AHEXASE2ly	0	N-Glycan Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : 3 C00001 + n2m2nmn --> 3 C00140 + m2mn
R_ACS2	0	Propanoate Metabolism	6.2.1.1	FALSE	acetyl-CoAsynthase(propionate)	[c] : C00002 + C00010 + C00163 --> C00020 + C00100 + C00013
R_lac_Dt	0	Transport Database	.	TRUE	lac-Dtransport	C00256[c] <==> C00256[e]
R_PUNP1m	0	NAD Biosynthesis	2.4.2.1	TRUE	purine-nucleosidephosphorylase(Adenosine),mi	[m] : C00212 + C00009 <==> C00147 + C00620
R_GNKg	0	Pentose Phosphate Pathway	2.7.1.12	TRUE	gluconatekinase,glycosomal	[x] : C00002 + glcn_d <==> C00345 + C00008 + C00080
R_mn2t	0.0038	Transport Database	.	FALSE	mn2transport	C00034[e] --> C00034[c]
R_PDHcr	500.02	.	1.8.1.4	TRUE	Pyruvatedehydrogenase(dihydrolipoamidedehy	[c] : C00579 + C00003 <==> C00080 + C15972 + C00004
R_DGK1	0	Nucleotides	2.7.4.8	TRUE	deoxyguanylatekinase(dGMP:ATP)	[c] : C00002 + C00362 <==> C00008 + C00361
R_SHK3Dr	-1000	Tyrosine, Tryptophan and Phenyla	1.1.1.25	TRUE	shikimatedehydrogenase	[c] : C02637 + C00080 + C00005 <==> C00006 + C00493
R_ADSELK	0	Selenoamino Acid Metabolism	2.7.1.25	FALSE	adenylyl-selenatekinase	[c] : adsel + C00002 --> 3padsel + C00008 + C00080
R_KARA1im	0	Valine, Leucine and Isoleucine Met	1.1.1.86	FALSE	acetohydroxyacidisomeroreductase,mitochondri	[m] : C06010 + C00080 + C00005 --> C04039 + C00006
R_TRDRm	0	Nucleotides	1.8.1.9	FALSE	thioredoxinreductase(NADPH)	[m] : C00080 + C00005 + C00343 --> C00006 + C00342
R_FDHr	-1000	Glyoxylate Metabolism	1.2.1.2	TRUE	formatedehydrogenase	[c] : C00058 + C00003 <==> C00011 + C00004
R_ESC_C01342_e	1000	EscapeFlux	.	FALSE	. escape flux	C01342[e] --> C01342[b]
R_ESC_C00199_c	0.4	EscapeFlux	.	FALSE	. escape flux	C00199[c] --> C00199[b]
R_ICDHyrm	-1000	Citric Acid Cycle	1.1.1.42	TRUE	Isocitratedehydrogenase(NADP+)	[m] : C00311 + C00006 <==> C00026 + C00011 + C00005
R_SPODM	0	ROS Detoxification	1.15.1.1	FALSE	superoxidedismutase	[c] : 2 C00080 + 2 C00704 --> C00027 + C00007
R_UDPGDr	-1000	Central Metabolism	1.1.1.22	TRUE	UDPglucose6-dehydrogenase	[c] : C00001 + 2 C00003 + C00029 <==> 3 C00080 + 2 C00004 + C00167
R_avite1t	0	Transport Database	.	FALSE	avite1transport	avite1[e] --> avite1[c]
R_gthrdt	0	Transport Database	.	FALSE	gthrdtransport	C00051[e] --> C00051[c]
R_ESC_C00266_c	0	EscapeFlux	.	FALSE	. escape flux	C00266[c] --> C00266[b]
R_NACHEX21ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg39 --> C00140 + ksi_deg40
R_ACACT7r	0	Fatty Acid Degradation	2.3.1.16	TRUE	acetyl-CoAC-acyltransferase(tetradecanoyl-CoA)	[c] : C00024 + C02593 <==> C05259 + C00010
R_CYOO_HP	0	Respiration chain 4	1.9.3.1	FALSE	cytochromec553oxidase,Hpylori	4 focytcc553[c] + 5.98 C00080[c] + C00007[c] --> 4 ficytcc553[c] + 2 C00080[
R_PDH	0	Glycolysis/Gluconeogenesis	1.2.4.1	FALSE	pyruvatedehydrogenase	[c] : C00010 + C00003 + C00022 --> C00024 + C00011 + C00004
R_SUCOASm	0	Citric Acid Cycle	6.2.1.5	TRUE	Succinate--CoAligase(ADP-forming)	[m] : C00002 + C00010 + C00042 <==> C00008 + C00009 + C00091
R_GLUTRS_LPAR	0	Glutamine Metabolism	6.1.1.17	FALSE	Glutamyl-tRNAsynthetase(Gln)	[c] : C00002 + C00025 + C01640 --> C00020 + glutrna_lparen_gln_rparen_ + C
R_ACACT1	1000	Cholesterol Metabolism	2.3.1.9	FALSE	acetyl-CoAC-acetyltransferase	[c] : 2 C00024 --> C00332 + C00010
R_ACSp	0	Pyruvate Metabolism	6.2.1.1	FALSE	acetyl-CoAsynthetase	[x] : C00033 + C00002 + C00010 --> C00024 + C00020 + C00013
R_TMPPP	0	Cofactor and Prosthetic Group Bio	2.5.1.3	FALSE	thiamine-phosphatediphosphorylase	[c] : C04752 + C04327 + C00080 --> C00013 + C01081
R_GUAPRT	0	Salvage Pathway	2.4.2.8	FALSE	guaninephosphoribosyltransferase	[c] : C00242 + C00119 --> C00144 + C00013
R_PGSA_SA	0	.	2.7.8.5	TRUE	Phosphatidylglycerolsynthase(Saureus)	[c] : 0.02 cdpdag_sa + C00623 <==> C00055 + C00080 + 0.02 pgp_sa
R_DHAK	0	Glycerolipid Metabolism	2.7.1.29	FALSE	dihydroxyacetonekinase	[c] : C00002 + C01227 --> C00008 + C00111 + C00080
R_NADH2_DASH_	0	Oxidative Phosphorylation	1.6.99.3	FALSE	NADHdehydrogenase,mitochondrial	5 C00080[m] + C00004[m] + C17568[m] --> C00080[c] + C00003[m] + C0039
R_GALASE13ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg35 --> C00124 + ksi_deg36
R_nh4t	499.3	Transport Database	.	TRUE	nh4transport	C01342[c] <==> C01342[e]
R_GLUDx	499.59	Nitrogen Metabolism	1.4.1.2	TRUE	glutamatedehydrogenase(NAD)	[c] : C00025 + C00001 + C00003 <==> C00026 + C00080 + C00004 + C01342
R_FAOXC224204	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : adrncoa + C00010 + C00001 + C00003 + C00007 --> C00024 + arachdcoa
R_FAOXC18480x	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : 5 C00010 + 5 C00001 + 5 C00003 + C00007 + strdnccoa --> 5 C00024 + 5
R_mant	0	Transport Database	.	FALSE	mantransport	C00936[e] --> C00936[c]
R_GLUSx	0	Glutamate Metabolism	1.4.1.14	FALSE	glutamatesynthase(NADH2)	[c] : C00026 + C00064 + C00080 + C00004 --> 2 C00025 + C00003
R_GALASE7ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg17 --> C00124 + ksi_deg18
R_PRAMPC	0	Histidine Metabolism	3.5.4.19	FALSE	phosphoribosyl-AMPcyclohydrolase	[c] : C00001 + C02741 --> C04896
R_NAPRT	521.56	NAD Biosynthesis	2.4.2.11	FALSE	NAPRTase	[c] : C00080 + C11486 + C00119 --> C01185 + C00013
R_5HOXINDACTC	0	Tryptophan Metabolism	1.2.1.3	FALSE	5-Hydroxyindoleacetaldehyde:NAD+oxidoreduct	[m] : 5hoxindact + C00001 + C00003 --> 5hoxindoa + 2 C00080 + C00004
R_FAOXC18480m	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoffattyacid	[m] : 5 C00010 + C00016 + 5 C00001 + 5 C00003 + strdnccoa --> 5 C00024 + C
R_TRDR2	0	Miscellaneous	1.8.1.9	FALSE	Thioredoxin(ubiquinone10)reductase(NADPH)	[c] : C00080 + C00005 + q10 --> C00006 + q10h2
R_TRDR3	0	Miscellaneous	1.8.1.9	FALSE	Thioredoxin(ubiquinone10)reductase(NADH)	[c] : C00080 + C00004 + q10 --> C00003 + q10h2

R_ASPTAm	0	Alanine and Aspartate Metabolism	2.6.1.1	TRUE	aspartatetransaminase	[m] : C00026 + C00049 <==> C00025 + C00036
R_EHGLATm	0	Arginine and Proline Metabolism	2.6.1.1	FALSE	L-erythro-4-Hydroxyglutamate:2-oxoglutaratear	[m] : C00026 + e4hglu --> C05946 + C00025
R_btnt	0	Transport Database	.	FALSE	btntransport	C00120[e] --> C00120[c]
R_PGDH	0	Pentose Phosphate Pathway	1.1.1.44	FALSE	phosphogluconatedehydrogenase	[c] : C00345 + C00006 --> C00011 + C00005 + C00199
R_NACHEX24ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksii_core2_deg7 --> C00140 + ksii_core2_deg8
R_GK1m	0	Nucleotides	2.7.4.8	TRUE	guanylatekinase(GMP:ATP),mitochondrial	[m] : C00002 + C00144 <==> C00008 + C00035
R_cd2t	0	Transport Database	.	FALSE	cd2transport	C01413[e] --> C01413[c]
R_NTPP11	0	Nucleotides	3.6.1.19	FALSE	Nucleosidetriphosphatepyrophosphorylase(xtp)	[c] : C00001 + C00700 --> C00080 + C00013 + C00655
R_ASP1DC	0	beta-Alanine Metabolism	4.1.1.11	FALSE	aspartate1-decarboxylase	[c] : C00049 + C00080 --> C00099 + C00011
R_PANTS	0	Cofactor and Prosthetic Group Bio	6.3.2.1	FALSE	pantothenatesynthase	[c] : C00099 + C00002 + C00522 --> C00020 + C00080 + C00864 + C00013
R_DHORD7	0	Nucleotide Metabolism	1.3.3.1	TRUE	dihydrooroticaciddehydrogenase(f420)	[c] : C00337 + f420-2 <==> f420-2h2 + C00295
R_EHGLATp	0	Arginine and Proline Metabolism	2.6.1.1	FALSE	L-erythro-4-Hydroxyglutamate:2-oxoglutaratear	[x] : C00026 + e4hglu --> C05946 + C00025
R_ASPTAp	0	Alanine and Aspartate Metabolism	2.6.1.1	TRUE	aspartatetransaminase,peroxisomal	[x] : C00026 + C00049 <==> C00025 + C00036
R_MDHi2	0	Vitamins and Cofactor Biosynthesi	1.1.1.37	FALSE	malatedehydrogenase(otherdirection)	[c] : C00080 + C00004 + C00036 --> C00711 + C00003
R_FMETTRS	0	Methionine Metabolism	2.1.2.9	FALSE	Methionyl-tRNAformyltransferase	[c] : C00234 + C02430 --> C03294 + C00080 + C00101
R_LACZe	0	Galactose Metabolism	3.2.1.23	FALSE	b-galactosidase,extracellular	[e] : C00001 + C00243 --> C00124 + C00267
R_GLUTRS	0	Cofactor and Prosthetic Group Bio	6.1.1.17	FALSE	Glutamyl-tRNAsynthetase	[c] : C00002 + C00025 + C01641 --> C00020 + C02987 + C00013
R_PFK_3	0	Glycolysis/Gluconeogenesis	2.7.1.11	FALSE	phosphofructokinase(s7p)	[c] : C00002 + C05382 --> C00008 + C00080 + C00447
R_PPA2m	0	Others	3.6.1.1	FALSE	inorganictriphosphatase,mitochondrial	[m] : C00001 + C00536 --> C00080 + C00009 + C00013
R_DHORD3	0	Pyrimidine Metabolism	1.3.3.1	TRUE	dihydrooroticaciddehydrogenase(menaquinone(	[c] : C00337 + mqn6 <==> mql6 + C00295
R_ASPCT	0	Purine and Pyrimidine Biosynthes	2.1.3.2	FALSE	aspartatecarbamoyltransferase	[c] : C00049 + C00169 --> C00438 + C00080 + C00009
R_G5SD	0	Arginine and Proline Metabolism	1.2.1.41	FALSE	glutamate-5-semialdehydedehydrogenase	[c] : C03287 + C00080 + C00005 --> C01165 + C00006 + C00009
R_xyltt	0	Transport Database	.	FALSE	xylttransport	C00379[e] --> C00379[c]
R_ANS	0	Tyrosine, Tryptophan and Phenyla	4.1.3.27	FALSE	anthranilatesynthase	[c] : C00251 + C00064 --> C00108 + C00025 + C00080 + C00022
R_GHMT3	0	Lysine Metabolism	2.1.2.1	FALSE	glycinehydroxymethyltransferase	[c] : 3htmelys + C00080 --> 4tmeabut + C00037
R_HSTPT	0	Histidine Metabolism	2.6.1.9	FALSE	histidinol-phosphatetransaminase	[c] : C00025 + C01267 --> C00026 + C01100
R_R05627	-0.0451	Peptidoglycan Biosynthesis	3.6.1.27	TRUE	Undecaprenyl-diphosphate phosphohydrolase	[c] : C04574 + C00001 <==> C17556 + C00009
R_MMSAD3m	0	Propanoate Metabolism	1.2.1.27	FALSE	methylmalonate-semialdehydedehydrogenase(n	[m] : C00010 + C00222 + C00003 --> C00024 + C00011 + C00004
R_ile_Lt	0.1376	Transport Database	.	FALSE	ile-Ltransport	C00407[e] --> C00407[c]
R_GLU5Km	0	Urea cycle/amino group Metabolis	2.7.2.11	FALSE	glutamate5-kinase(m)	[m] : C00002 + C00025 --> C00008 + C03287
R_ADSL2r	-1000	Purine and Pyrimidine Biosynthes	4.3.2.2	TRUE	adenylosuccinatelyase	[c] : C04823 <==> C04677 + C00122
R_MI3PP	0	Inositol Phosphate Metabolism	3.1.3.25	FALSE	myo-inositol3-phosphatase	[c] : C00001 + C04006 --> C00137 + C00009
R_METTRSm	0	Methionine Metabolism	6.1.1.10	FALSE	methionyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C00073 + C01647 --> C00020 + C02430 + C00013
R_NACHEX2ly	0	Chondroitin Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : cs_a_deg4 + C00001 --> C01132 + cs_a_deg5
R_TKT1g	0	Pentose Phosphate Pathway	2.2.1.1	TRUE	transketolase,glycosomal	[x] : C03736 + C00231 <==> C00118 + C05382
R_GLU5K	0	Arginine and Proline Metabolism	2.7.2.11	FALSE	glutamate5-kinase	[c] : C00002 + C00025 --> C00008 + C03287
R_RNDR1n	0	Nucleotide Salvage Pathway	1.17.4.1	FALSE	ribonucleoside-diphosphatereductase,nuclear	[n] : C00008 + C00342 --> C00206 + C00001 + C00343
R_SRC_C00097_e	0.0433	SourceFlux	.	FALSE	. source flux	C00097[b] --> C00097[e]
R_PSD_EC	0	Membrane Lipid Metabolism	4.1.1.65	FALSE	Phosphatidylserinedecarboxylase(Ecoli)	[c] : C00080 + 0.02 C02737 --> C00011 + 0.02 C00350
R_GLCP	0	Glycolysis/Gluconeogenesis	2.4.1.1	FALSE	glycogenphosphorylase	[c] : C00182 + C00009 --> C00103
R_SRC_C00047_e	0.1625	SourceFlux	.	FALSE	. source flux	C00047[b] --> C00047[e]
R_DPCOAK	0	CoA Biosynthesis	2.7.1.24	FALSE	dephospho-CoAkinase	[c] : C00002 + C00882 --> C00008 + C00010 + C00080
R_NDPK1n	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:GDP),nuclea	[n] : C00002 + C00035 <==> C00008 + C00044
R_NDPK1m	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:GDP),mitoch	[m] : C00002 + C00035 <==> C00008 + C00044
R_EXCH_C00042_	-0.299	ExchangeFlux	.	TRUE	. exchange flux	C00042[c] <==> C00042[b]
R_KYN	0	Tryptophan Metabolism	3.7.1.3	FALSE	kynureninase	[c] : lkynr + C00001 --> C00041 + C00108 + C00080
R_AMID	0	Arginine and Proline Metabolism	3.5.1.4	FALSE	amidase	[c] : C03078 + C00001 --> 4gudbutn + C01342
R_ASPTRSm	0	Alanine and Aspartate Metabolism	6.1.1.12	FALSE	Aspartyl-tRNAsynthetase,mitochondrial	[m] : C00049 + C00002 + C01638 --> C00020 + C02984 + C00013
R_EXCH_h_e	0	ExchangeFlux	.	TRUE	. exchange flux	C00080[e] <==> C00080[b]
R_ALDD2xm	0	Glycolysis/Gluconeogenesis	1.2.1.3	FALSE	aldehydedehydrogenase(acetylaldehyde,NAD),m	[m] : C00084 + C00001 + C00003 --> C00033 + 2 C00080 + C00004
R_SRC_C00007_e	0	SourceFlux	.	FALSE	. source flux	C00007[b] --> C00007[e]
R_GALUi	0	Cell Envelope Biosynthesis	2.7.7.9	FALSE	UTP-glucose-1-phosphateuridylyltransferase(irr	[c] : C00103 + C00080 + C00075 --> C00013 + C00029
R_galt	0	Transport Database	.	FALSE	galtransport	C00124[e] --> C00124[c]
R_pro_Lt	0.1049	Transport Database	.	FALSE	pro-Ltransport	C00148[e] --> C00148[c]
R_ESC_C00469_c	0	EscapeFlux	.	FALSE	. escape flux	C00469[c] --> C00469[b]
R_HACD7p	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxohexade	[x] : C05259 + C00080 + C00004 <==> C05258 + C00003

R_guat	0	Transport Database	.	FALSE	guatransport	C00242[e] --> C00242[c]
R_ECOAH7p	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxyhexad	[x] : C05258 <==> C00001 + C05272
R_SRC_C00238_e	0.0038	SourceFlux	.	FALSE	. source flux	C00238[b] --> C00238[e]
R_NACHEX25ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksii_core2_deg9 --> C00140 + f1a
R_GF6PTA	0	Aminosugar Metabolism	2.6.1.16	FALSE	glutamine-fructose-6-phosphatetransaminase	[c] : C05345 + C00064 --> C00352 + C00025
R_glc_Dt	0	Transport Database	.	FALSE	glc-Dtransport	C00267[e] --> C00267[c]
R_SRC_C00255_e	0.0038	SourceFlux	.	FALSE	. source flux	C00255[b] --> C00255[e]
R_GHMT2	0	Glycine and Serine Metabolism	2.1.2.1	FALSE	glycinehydroxymethyltransferase	[c] : C00716 + C00101 --> C00037 + C00001 + C00143
R_GLBRAN	0	Starch and Sucrose Metabolism	2.4.1.18	FALSE	1,4-alpha-glucanbranchingenzyme(glygn1->glyg	[c] : glygn1 --> glygn2
R_PROTRS	0	Arginine and Proline Metabolism	6.1.1.15	FALSE	Prolyl-tRNAsynthetase	[c] : C00002 + C00148 + C01649 --> C00020 + C00013 + C02702
R_SRC_C00647_c	0.0038	SourceFlux	.	FALSE	. source flux	C00647[b] --> C00647[c]
R_HSK	0.1202	Threonine and Lysine Metabolism	2.7.1.39	FALSE	homoserinekinase	[c] : C00002 + C00263 --> C00008 + C00080 + C01102
R_AKGDb	500.02	Citric Acid Cycle	2.3.1.61	FALSE	oxoglutaratedehydrogenase(dihydrolipoamideS-	[c] : C00010 + C16254 --> C00579 + C00091
R_AKGDa	500.02	Citric Acid Cycle	1.2.4.2	TRUE	oxoglutaratedehydrogenase(lipoamide)	[c] : C00026 + C00080 + C15972 <==> C00011 + C16254
R_GCCam	0	Glycine, Serine, and Threonine Me	1.4.4.2	TRUE	glycine-cleavagecomplex(lipoylprotein),mitocho	[m] : C00037 + C00080 + C02051 <==> C01242 + C00011
R_SRC_C14819_e	0.0038	SourceFlux	.	FALSE	. source flux	C14819[b] --> C14819[e]
R_ICDHy	1000	Citric Acid Cycle	1.1.1.42	FALSE	isocitratedehydrogenase(NADP)	[c] : C00311 + C00006 --> C00026 + C00011 + C00005
R_NACHEX23ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksii_core2_deg4 --> C00140 + ksii_core2_deg5
R_FMETTRSm	0	Folate Metabolism	2.1.2.9	FALSE	Methionyl-tRNAformyltransferase,mitochondria	[m] : C00234 + C02430 --> C03294 + C00080 + C00101
R_HACD7	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxohexade	[c] : C05259 + C00080 + C00004 <==> C05258 + C00003
R_TPI	0	Glycolysis/Gluconeogenesis	5.3.1.1	TRUE	triose-phosphateisomerase	[c] : C00111 <==> C00118
R_pyrt	0	Transport Database	.	TRUE	pyrtransport	C00022[c] <==> C00022[e]
R_2OXOADOXm	0	Lysine Metabolism	1.2.4.2	FALSE	2-Oxoadipate:lipoamde2-oxidoreductase(decarb	[m] : C00322 + C00010 + C00003 --> C00011 + C00527 + C00004
R_AKGDm	0	Citric Acid Cycle	1.2.4.2	FALSE	2-oxoglutaratedehydrogenase	[m] : C00026 + C00010 + C00003 --> C00011 + C00004 + C00091
R_FAOXC160	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : 7 C00010 + 7 C00016 + 7 C00001 + 7 C00003 + C00154 --> 8 C00024 + 7
R_FAOXC183806	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoffattyacid	[m] : 5 C00010 + 5 C00001 + lnlncgcoa + 5 C00003 + 2 C00007 --> 5 C00024 +
R_EXCH_etoh_c	0	ExchangeFlux	.	TRUE	. exchange flux	C00469[c] <==> C00469[b]
R_GNDer	0	Pentose Phosphate Pathway	1.1.1.44	FALSE	phosphogluconatedehydrogenase,endoplasmicre	[r] : C00345 + C00006 --> C00011 + C00005 + C00199
R_ASPTA	999.67	Alanine and Aspartate Metabolism	2.6.1.1	TRUE	aspartatetransaminase	[c] : C00026 + C00049 <==> C00025 + C00036
R_NDPK9	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:IDP)	[c] : C00002 + C00104 <==> C00008 + C00081
R_NDPK8	-999.89	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dADP)	[c] : C00002 + C00206 <==> C00008 + C00131
R_NDPK7	0.0057	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dCDP)	[c] : C00002 + C00705 <==> C00008 + C00458
R_NDPK6	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dUDP)	[c] : C00002 + C01346 <==> C00008 + C00460
R_NDPK5	0.0057	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dGDP)	[c] : C00002 + C00361 <==> C00008 + C00286
R_NDPK4	0.0057	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dTDP)	[c] : C00002 + C00363 <==> C00008 + C00459
R_NDPK3	-0.0057	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:CDP)	[c] : C00002 + C00112 <==> C00008 + C00063
R_zn2t	0.0038	Transport Database	.	FALSE	zn2transport	C00038[e] --> C00038[c]
R_CDSm	0	Glycerophospholipid Metabolism	2.7.7.41	FALSE	phosphatidatecytidylyltransferase	[m] : C00063 + C00080 + pa_hs --> cdpdag_hs + C00013
R_DUTPDP	0	Nucleotide Salvage Pathway	3.6.1.23	FALSE	dUTPdiphosphatase	[c] : C00460 + C00001 --> C00365 + C00080 + C00013
R_FAOXC183806	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : 5 C00010 + 5 C00001 + lnlncgcoa + 5 C00003 + 2 C00007 --> 5 C00024 +
R_fe2t	0.0038	Transport Database	.	FALSE	fe2transport	C14818[e] --> C14818[c]
R_SRC_C01342_e	0	SourceFlux	.	FALSE	. source flux	C01342[b] --> C01342[e]
R_AHEXASEly	0	N-Glycan Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : 2 C00001 + n2m2mn --> 2 C00140 + m2mn
R_NACHEX27ly	0	Hyaluronan Metabolism	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ha_deg1 --> C00140 + ha_pre1
R_LEUTAi	0	Valine, Leucine and Isoleucine Met	2.6.1.42	FALSE	leucinetransaminase(irreversible)	[c] : C00233 + C00025 --> C00026 + C00123
R_SRC_C00010_e	0.0038	SourceFlux	.	FALSE	. source flux	C00010[b] --> C00010[e]
R_PDX5PO	0	Vitamin B6 Metabolism	1.4.3.5	TRUE	pyridoxine5'-phosphateoxidase	[c] : C00007 + C00627 <==> C00027 + C00018
R_PYAM5POr	-1000	Vitamin B6 Metabolism	1.4.3.5	TRUE	pyridoxamine5'-phosphateoxidase	[c] : C00001 + C00007 + C00647 <==> C00027 + C01342 + C00018
R_ala_Lt	0.2436	Transport Database	.	FALSE	ala-Ltransport	C00041[e] --> C00041[c]
R_LACZ	0	Alternate Carbon Metabolism	3.2.1.23	FALSE	b-galactosidase	[c] : C00001 + C00243 --> C00124 + C00267
R_ENO	-0.3022	Glycolysis/Gluconeogenesis	4.2.1.11	TRUE	enolase	[c] : C00631 <==> C00001 + C00074
R_NACHEX11ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg10 --> C00140 + ksi_deg11
R_DDPGA	0	Glyoxylate Biosynthesis	4.1.2.14	TRUE	2-dehydro-3-deoxy-phosphogluconatealdolase	[c] : C05946 <==> C00048 + C00022
R_PUNP3m	0	NAD Biosynthesis	2.4.2.1	TRUE	purine-nucleosidephosphorylase(Guanosine),mi	[m] : C00387 + C00009 <==> C00242 + C00620
R_cellobioset	0.2	Transport Database	.	FALSE	cellobiosetransport	C00185[e] --> C00185[c]
R_PPK2	999.93	Oxidative phosphorylation	2.7.4.1	FALSE	polyphosphatekinase	[c] : C00002 + C00013 --> C00008 + C00536

R_ACACT8p	0	Fatty Acid Metabolism	2.3.1.16	FALSE	acetyl-CoAacyltransferase(hexadecanoyl-CoA),p	[x] : C16216 + C00010 --> C00024 + C00154
R_ASAD	-0.1202	Threonine and Lysine Metabolism	1.2.1.11	TRUE	aspartate-semialdehydededehydrogenase	[c] : C00441 + C00006 + C00009 <==> C03082 + C00080 + C00005
R_KARA1i	1000	Valine, Leucine and Isoleucine Met	1.1.1.86	FALSE	acetohydroxyacidisomeroreductase	[c] : C06010 + C00080 + C00005 --> C04039 + C00006
R_FAOXC225183	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoffattyacid	[m] : 2 C00010 + dcsptn1coa + 2 C00001 + 2 C00003 --> 2 C00024 + 2 C00080
R_EXCH_C00011_	500.33	ExchangeFlux	.	TRUE	. exchange flux	C00011[e] <==> C00011[b]
R_THFATm	0	Folate Metabolism	2.1.2.10	FALSE	tetrahydrofolateaminomethyltransferase,mitoch	[m] : C00001 + C00445 --> C03479 + C00080
R_SPODMn	0	ROS Detoxification	1.15.1.1	FALSE	superoxidedismutase,nuclear	[n] : 2 C00080 + 2 C00704 --> C00027 + C00007
R_SPODMm	0	ROS Detoxification	1.15.1.1	FALSE	superoxidedismutase	[m] : 2 C00080 + 2 C00704 --> C00027 + C00007
R_FAOXC225183	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : 2 C00010 + dcsptn1coa + 2 C00001 + 2 C00003 --> 2 C00024 + 2 C00080
R_GALASE1ly	0	N-Glycan Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : 2 C00001 + l2n2m2mn --> 2 C00124 + n2m2mn
R_FAOXC180	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : C00010 + C00016 + C00001 + C00003 + C00412 --> C00024 + C01352 +
R_ACACT3r	0	Fatty Acid Degradation	2.3.1.16	TRUE	acetyl-CoAC-acyltransferase(hexanoyl-CoA)(r)	[c] : C00024 + C05270 <==> C05267 + C00010
R_DHQTi	1000	Tyrosine, Tryptophan and Phenyla	4.2.1.10	FALSE	3-dehydroquinatedehydratase,irreversible	[c] : C00944 --> C02637 + C00001
R_SPODMx	0	ROS Detoxification	1.15.1.1	FALSE	superoxidedismutase,peroxisome	[x] : 2 C00080 + 2 C00704 --> C00027 + C00007
R_PYDXO	0	Pyridoxine Metabolism	1.4.3.5	TRUE	pyridoxaloxidase	[c] : 2 C00001 + C01342 + 0.5 C00007 + C00250 <==> 2 C00027 + C00534
R_5HOXINDACTC	0	Tryptophan Metabolism	1.2.1.3	FALSE	5-Hydroxyindoleacetaldehyde:NAD+oxidoreduct	[c] : 5hoxindact + C00001 + C00003 --> 5hoxindoa + 2 C00080 + C00004
R_BDG2HCGHD	0	Stilbene, coumarine and lignin Bio	3.2.1.21	FALSE	beta-D-Glucosyl-2-coumarinateglucohydrolase	[c] : bdg2hc + C00001 --> 2coum + C00267 + C00080
R_TKT2g	0	Pentose Phosphate Pathway	2.2.1.1	TRUE	transketolase,glycosomal	[x] : C00279 + C00231 <==> C05345 + C00118
R_amett	0	Transport Database	.	FALSE	amettransport	C00019[e] --> C00019[c]
R_IMACTD_m	0	Histidine Metabolism	1.2.1.3	FALSE	Imidazoleacetaldeydededehydrogenase(mito)	[m] : C00001 + im4act + C00003 --> 2 C00080 + im4ac + C00004
R_CDGGGPP3	0	Lipid and Cell Wall Metabolism	2.7.8.5	FALSE	CDP-alcoholphosphatidyltransferase(glycerol1-p	[c] : cdgggp + glyc1p --> C00055 + dggpgp + C00080
R_HACD10p	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxohexacos	[x] : 3hxccoa + C00003 <==> 3ohxccoa + C00080 + C00004
R_ADSL1r	-999.91	Purine and Pyrimidine Biosynthes	4.3.2.2	TRUE	adenylsuccinatelyase	[c] : C03794 <==> C00020 + C00122
R_NAMNPP	478.44	Cofactor and Prosthetic Group Bio	2.4.2.11	FALSE	nicotinicacidmononucleotidepyrophosphorylase	[c] : C00002 + C00001 + C11486 + C00119 --> C00008 + C01185 + C00009 + C
R_inostt	0	Transport Database	.	FALSE	inosttransport	C00137[e] --> C00137[c]
R_OCBT	-1000	Arginine and Proline Metabolism	2.1.3.3	TRUE	ornithinecarbamoyltransferase	[c] : C00169 + C00077 <==> C00327 + C00080 + C00009
R_DTMPK	0.0057	Nucleotides	2.7.4.9	TRUE	dTMPkinase	[c] : C00002 + C00364 <==> C00008 + C00363
R_NDPK1	1000	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:GDP)	[c] : C00002 + C00035 <==> C00008 + C00044
R_SRC_C00038_e	0.0038	SourceFlux	.	FALSE	. source flux	C00038[b] --> C00038[e]
R_NDPK2	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:UDP)	[c] : C00002 + C00015 <==> C00008 + C00075
R_ALARi	1000	Alanine and Aspartate Metabolism	5.1.1.1	FALSE	alanineracemase(irreversible)	[c] : C00041 --> C00133
R_DAAD	0	Alanine and Aspartate Metabolism	1.4.99.1	FALSE	D-Aminoaciddehydrogenase	[c] : C00133 + C00016 + C00001 --> C01352 + C01342 + C00022
R_ASPK	0.1202	Threonine and Lysine Metabolism	2.7.2.4	TRUE	aspartatekinase	[c] : C00049 + C00002 <==> C03082 + C00008
R_NDPK5n	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dGDP),nucle	[n] : C00002 + C00361 <==> C00008 + C00286
R_NDPK5m	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dGDP),mitoc	[m] : C00002 + C00361 <==> C00008 + C00286
R_st	0	Transport Database	.	FALSE	stransport	C00087[e] --> C00087[c]
R_GBEZ	0	Alternate Carbon Metabolism	2.4.1.18	FALSE	1,4-alpha-glucanbranchingenzyme	[c] : C00718 --> C00182 + C00001
R_EXCH_C00080_	-1000	ExchangeFlux	.	TRUE	. exchange flux	C00080[c] <==> C00080[b]
R_P5CRm	0	Arginine and Proline Metabolism	1.5.1.2	FALSE	pyrroline-5-carboxylatereductase(m)	[m] : C03912 + 2 C00080 + C00005 --> C00006 + C00148
R_EXCH_C00080_	0	ExchangeFlux	.	TRUE	. exchange flux	C00080[e] <==> C00080[b]
R_ESC_C00186_c	0	EscapeFlux	.	FALSE	. escape flux	C00186[c] --> C00186[b]
R_GCCbim	0	Glycine, Serine, and Threonine Me	2.1.2.10	FALSE	glycine-cleavagecomplex(lipoylprotein)irreversi	[m] : C01242 + C00101 --> C02972 + C00143 + C01342
R_OCBTm	0	Urea cycle/amino group Metabolis	2.1.3.3	FALSE	ornithinecarbamoyltransferase,irreversible	[m] : C00169 + C00077 --> C00327 + C00080 + C00009
R_na1t	0	Transport Database	.	FALSE	na1transport	C01330[e] --> C01330[c]
R_OCBTi	1000	Arginine and Proline Metabolism	2.1.3.3	FALSE	ornithinecarbamoyltransferase,irreversible	[c] : C00169 + C00077 --> C00327 + C00080 + C00009
R_ICL	0	Anaplerotic reactions	4.1.3.1	FALSE	Isocitratelyase	[c] : C00311 --> C00048 + C00042
R_ABTA	1000	Arginine and Proline Metabolism	2.6.1.19	FALSE	4-aminobutyratetransaminase	[c] : C00334 + C00026 --> C00025 + C00232
R_NACHEX17ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg28 --> C00140 + ksi_deg29
R_AHCi	1000	Methionine Metabolism	3.3.1.1	FALSE	adenosylhomocysteinase	[c] : C00021 + C00001 --> C00212 + C05330
R_FAOXC205184	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoffattyacid	[m] : C00010 + C00001 + C00003 + tmndnccoa --> C00024 + C00080 + C0000
R_IMACTD	0	Histidine Metabolism	1.2.1.3	FALSE	Imidazoleacetaldeydededehydrogenase	[c] : C00001 + im4act + C00003 --> 2 C00080 + im4ac + C00004
R_NPHSr	-1000	Vitamins and Cofactor Biosynthesi	4.1.3.36	TRUE	naphthoatesynthase(reversible)	[c] : C03160 <==> C00010 + C03657
R_TMPKr	0	Cofactor and Prosthetic Group Bio	2.7.4.16	TRUE	thiamine-phosphatekinase	[c] : C00002 + C01081 <==> C00008 + C00068
R_FCLTm	0	Heme Biosynthesis	4.99.1.1	FALSE	Ferrochelatase,mitochondrial	[m] : C14818 + C02191 --> 2 C00080 + C00032
R_NDPK4m	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dTDP),mitoc	[m] : C00002 + C00363 <==> C00008 + C00459
R_urat	0	Transport Database	.	FALSE	uratransport	C00106[e] --> C00106[c]

R_THDPS	0	Threonine and Lysine Metabolism	2.3.1.117	FALSE	tetrahydrodipicolinatesuccinylase	[c] : C00001 + C00091 + C03972 --> C00010 + C04462
R_FOLD3	0	Folate Biosynthesis	2.5.1.15	FALSE	dihydropteroatesynthase	[c] : 2ahhmd + C00568 --> C00921 + C00013
R_NDPK4n	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dTDP),nucle	[n] : C00002 + C00363 <==> C00008 + C00459
R_SRC_C00123_e	0.2137	SourceFlux	.	FALSE	. source flux	C00123[b] --> C00123[e]
R_FDH	1000	Fatty Acid Metabolism	1.2.1.2	FALSE	formatedehydrogenase	[c] : C00058 + C00003 --> C00011 + C00004
R_NADK	0.0038	NAD Metabolism	2.7.1.23	FALSE	NADkinase	[c] : C00002 + C00003 --> C00008 + C00080 + C00006
R_SSALy	0	Arginine and Proline Metabolism	1.2.1.16	FALSE	succinate-semialdehydedehydrogenase(NADP)	[c] : C00001 + C00006 + C00232 --> 2 C00080 + C00005 + C00042
R_SRC_C00262_e	0.2	SourceFlux	.	FALSE	. source flux	C00262[b] --> C00262[e]
R_SELMETAT	0	Selenoamino Acid Metabolism	2.5.1.6	FALSE	selenomethionineadenosyltransferase	[c] : C00002 + C00001 + C05335 --> C00009 + C00013 + C05691
R_gsnt	0	Transport Database	.	FALSE	gsntransport	C00387[e] --> C00387[c]
R_FAOXC204	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : arachdcoa + 9 C00010 + 5 C00016 + 9 C00001 + 9 C00003 --> 10 C00024
R_FAOXC203183	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoffattyacid	[m] : C00010 + dlnlcgcoa + C00016 + C00001 + C00003 --> C00024 + C01352
R_VALTA	0	Valine, Leucine and Isoleucine Met	2.6.1.42	TRUE	valinetransaminase	[c] : C00026 + C00183 <==> C00141 + C00025
R_PPAKr	0	Alternate Carbon Metabolism	2.7.2.1	TRUE	Propionatekinase	[c] : C00008 + C02876 <==> C00002 + C00163
R_ILETRS	0	Valine, Leucine and Isoleucine Met	6.1.1.5	FALSE	Isoleucyl-tRNAsynthetase	[c] : C00002 + C00407 + C01644 --> C00020 + C03127 + C00013
R_SEAHCYSHYD	0	Selenoamino Acid Metabolism	3.3.1.1	FALSE	Se-Adenosylselenohomocysteinehydrolase	[c] : C00001 + seahcys --> C00212 + selhcys
R_MCOATAm	0	Fatty Acid Metabolism	2.3.1.39	TRUE	Malonyl-CoA-ACPtransacylase,mitochondrial	[m] : C00229 + C00083 <==> C00010 + C01209
R_IGPS	0	Tyrosine, Tryptophan and Phenyla	4.1.1.48	FALSE	indole-3-glycerol-phosphatesynthase	[c] : C01302 + C00080 --> C03506 + C00011 + C00001
R_PGKg	0	Glycolysis/Gluconeogenesis	2.7.2.3	TRUE	phosphoglyceratekinase	[x] : C00236 + C00008 <==> C00197 + C00002
R_PDHm	0	Glycolysis/Gluconeogenesis	1.2.4.1	FALSE	pyruvatedehydrogenase	[m] : C00010 + C00003 + C00022 --> C00024 + C00011 + C00004
R_cytdt	0	Transport Database	.	FALSE	cytdtransport	cytd[e] --> cytd[c]
R_SRC_C00135_e	0.0451	SourceFlux	.	FALSE	. source flux	C00135[b] --> C00135[e]
R_PPBNGS	0	Heme Biosynthesis	4.2.1.24	FALSE	porphobilinogensynthase	[c] : 2 C00430 --> C00080 + 2 C00001 + C00931
R_PDHam2m	0	Pyruvate Metabolism	1.2.4.2	TRUE	pyruvatedehydrogenase(lipoamide)	[m] : 2ahethmpp + C15972 <==> C16255 + C00068
R_GCC2bim	0	Glycine, Serine, and Threonine Me	2.1.2.10	FALSE	glycine-cleavagesystem(lipoamide)irreversible,r	[m] : alpam + C00101 --> C00579 + C00143 + C01342
R_SRC_C00078_e	0.0269	SourceFlux	.	FALSE	. source flux	C00078[b] --> C00078[e]
R_GALASE4ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg8 --> C00124 + ksi_deg9
R_SRC_C00305_e	0.0038	SourceFlux	.	FALSE	. source flux	C00305[b] --> C00305[e]
R_PGSA_HP	0	Glycerolipid Synthesis	2.7.8.5	TRUE	PhosphatidylglycerolsynthaseHpspecific	[c] : cdpdag_hp + C00623 <==> C00055 + C00080 + pgp_hp
R_ECOAH9m	0	Valine, Leucine and Isoleucine Met	4.2.1.17	TRUE	2-Methylprop-2-enoyl-CoA(2-Methylbut-2-enoyl	[m] : C03345 + C00001 <==> C04405
R_HEXTT	0	Sterol Biosynthesis	2.5.1.30	FALSE	trans-hexaprenyltranstransferase	[c] : C01230 + C00129 --> C04216 + C00013
R_phe_Lt	0.088	Transport Database	.	FALSE	phe-Ltransport	C00079[e] --> C00079[c]
R_CBLATm	0	Vitamin B12 Metabolism	2.5.1.17	TRUE	cob(I)alaminadenosyltransferase,mitochondrial	[m] : C00002 + C00853 + C00080 <==> C00194 + C00536
R_NP1	0	NAD Metabolism	2.4.2.1	FALSE	nucleotidephosphatase	[c] : C00080 + C11486 + C00620 --> nicrns + C00009
R_FAOXC183803	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoffattyacid	[m] : 5 C00010 + 2 C00016 + 5 C00001 + lnlncacoa + 5 C00003 --> 5 C00024 +
R_PGL	0	Pentose Phosphate Pathway	3.1.1.31	FALSE	6-phosphogluconolactonase	[c] : C01236 + C00001 --> C00345 + C00080
R_PGK	0.2	Glycolysis/Gluconeogenesis	2.7.2.3	TRUE	phosphoglyceratekinase	[c] : C00197 + C00002 <==> C00236 + C00008
R_PGI	0.4	Glycolysis/Gluconeogenesis	5.3.1.9	TRUE	glucose-6-phosphateisomerase	[c] : C00668 <==> C05345
R_ADK1m	1000	Nucleotides	2.7.4.3	TRUE	adenylatekinase,mitochondrial	[m] : C00020 + C00002 <==> 2 C00008
R_ARGDr	-1000	Arginine and Proline Metabolism	3.5.3.6	TRUE	argininedeiminase	[c] : C00062 + C00001 <==> C00327 + C01342
R_NDPK2m	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:UDP),mitoch	[m] : C00002 + C00015 <==> C00008 + C00075
R_TRPS3	0	Tyrosine, Tryptophan and Phenyla	4.2.1.20	FALSE	tryptophansynthase(indoleglycerolphosphate)	[c] : C03506 --> C00118 + C00463
R_TRPS2	0	Tyrosine, Tryptophan and Phenyla	4.2.1.20	FALSE	tryptophansynthase(indole)	[c] : C00463 + C00716 --> C00001 + C00078
R_ADK1g	0	Purine Metabolism	2.7.4.3	TRUE	adenylatekinase,glycosome	[x] : C00020 + C00002 <==> 2 C00008
R_zymstt	0	Transport Database	.	FALSE	zymsttransport	C05437[e] --> C05437[c]
R_GALASE8ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg20 --> C00124 + ksi_deg21
R_biomass_target	0.4872	BiomassObjective	.	FALSE	BiomassRxn	[c] : 34.7964804614 C00001 + 40.1701382876 C00002 + 0.00780937124549
R_PPDKgr	0	Glycolysis/Gluconeogenesis	2.7.9.1	TRUE	Pyruvate,phosphatedikinase.,glycosome	[x] : C00002 + C00009 + C00022 <==> C00020 + C00080 + C00074 + C00013
R_folt	0	Transport Database	.	FALSE	foltransport	C00504[e] --> C00504[c]
R_KATp	0	Fatty Acid Biosynthesis	2.3.1.16	FALSE	3-ketoacyl-CoAthiolase,peroxisomal	[x] : C00264 + C00010 --> C00024 + C00040
R_AMALT1	0	Alternate Carbon Metabolism	2.4.1.25	FALSE	Amylomaltase(maltotriose)	[c] : C00208 + C01835 --> C00267 + C02052
R_GMPS2	0.1076	Nucleotides	6.3.5.2	FALSE	GMPsynthase	[c] : C00002 + C00064 + C00001 + C00655 --> C00020 + C00025 + C00144 + 2
R_AGPR	0	Arginine and Proline Metabolism	1.2.1.38	TRUE	N-acetyl-g-glutamyl-phosphatereductase	[c] : C01250 + C00006 + C00009 <==> C04133 + C00080 + C00005
R_EXCH_mal_DAS	-0.0983	ExchangeFlux	.	TRUE	. exchange flux	C00711[c] <==> C00711[b]
R_SRC_C00016_c	0.0038	SourceFlux	.	FALSE	. source flux	C00016[b] --> C00016[c]
R_nact	0	Transport Database	.	FALSE	nactransport	C11486[e] --> C11486[c]

R_SHKK	0	Tyrosine, Tryptophan and Phenyla	2.7.1.71	FALSE	shikimatekinase	[c] : C00002 + C00493 --> C00008 + C00080 + C03175
R_KARA2i	1000	Valine, Leucine and Isoleucine Met	1.1.1.86	FALSE	ketol-acidreductoisomerase(2-Aceto-2-hydroxyb	[c] : C00659 + C00080 + C00005 --> C04104 + C00006
R_TRDR	0.0172	Nucleotides	1.8.1.9	FALSE	thioredoxinreductase(NADPH)	[c] : C00080 + C00005 + C00343 --> C00006 + C00342
R_GLACO	0	Ascorbate and Aldarate Metabolisı	1.2.1.3	FALSE	D-Glucuronolactone:NAD+oxidoreductase	[c] : glac + 2 C00001 + C00003 --> C00818 + 3 C00080 + C00004
R_GLYKm	0	Glycerophospholipid Metabolism	2.7.1.30	FALSE	glycerolkinase	[m] : C00002 + C00116 --> C00008 + C00623 + C00080
R_GLYKg	0	Glycolysis/Gluconeogenesis	2.7.1.30	TRUE	glycerolkinase(reversible),glycosome	[x] : C00002 + C00116 <==> C00008 + C00623 + C00080
R_ATPasel	0	Transport, Lysosomal	3.6.3.14	FALSE	V-typeATPase,H+transporting,lysosomal	C00002[c] + 3 C00080[c] + C00001[c] --> C00008[c] + 4 C00080[l] + C00009[
R_xant	0	Transport Database	.	FALSE	xantransport	C00385[e] --> C00385[c]
R_EHGLAT	0	Arginine and Proline Metabolism	2.6.1.1	FALSE	L-erythro-4-Hydroxyglutamate:2-oxoglutaratear	[c] : C00026 + e4hglu --> C05946 + C00025
R_TRPTRSm	0	Tyrosine, Tryptophan and Phenyla	6.1.1.2	FALSE	Tryptophanyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C01652 + C00078 --> C00020 + C00013 + C03512
R_MECOALm	0	C5-Branched dibasic Acid Metabol	6.2.1.5	TRUE	mesaconate--CoAligase(ADP-forming),mitochon	[m] : C00002 + C00010 + mescon <==> C00008 + mescoa + C00009
R_UDPGD	1000	Starch and Sucrose Metabolism	1.1.1.22	FALSE	UDPglucose6-dehydrogenase	[c] : C00001 + 2 C00003 + C00029 --> 3 C00080 + 2 C00004 + C00167
R_NADH2_DASH	0	Oxidative Phosphorylation	1.6.99.3	FALSE	NADHdehydrogenase,mitochondrial	[m] : C00080 + C00004 + C17568 --> C00003 + C00390
R_NACHEX13ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg16 --> C00140 + ksi_deg17
R_ASPTRS	0	Alanine and Aspartate Metabolism	6.1.1.12	FALSE	Aspartyl-tRNAsynthetase	[c] : C00049 + C00002 + C01638 --> C00020 + C02984 + C00013
R_thft	0	Transport Database	.	FALSE	thftransport	C00101[e] --> C00101[c]
R_DASYNm_SC	0	Phospholipid Biosynthesis	2.7.7.41	TRUE	CDP-Diacylglycerolsynthetase,yeast-specific,mit	[m] : C00063 + C00080 + 0.01 C00416 <==> 0.01 cdpdag_sc + C00013
R_GLUDxi	1000	Glutamate Metabolism	1.4.1.2	FALSE	glutamatedehydrogenase(NAD)	[c] : C00025 + C00001 + C00003 --> C00026 + C00080 + C00004 + C01342
R_GALCTND	0	Alternate Carbon Metabolism	4.2.1.6	FALSE	galactonatedehydratase	[c] : C00880 --> C01216 + C00001
R_ASPKi	0	Alanine and Aspartate Metabolism	2.7.2.4	FALSE	aspartatekinase,irreversible	[c] : C00049 + C00002 --> C03082 + C00008
R_TRPTRS	0	Tyrosine, Tryptophan and Phenyla	6.1.1.2	FALSE	Tryptophanyl-tRNAsynthetase	[c] : C00002 + C01652 + C00078 --> C00020 + C00013 + C03512
R_NDPK2n	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:UDP),nuclea	[n] : C00002 + C00015 <==> C00008 + C00075
R_CBLAT_DELET	0	Cofactor and Prosthetic Group Bio	2.5.1.17	TRUE	cob(I)alaminadenosyltransferase	[c] : C00002 + C00853 + C00001 <==> C00194 + C00009 + C00013
R_pnto_Rt	0	Transport Database	.	FALSE	pnto-Rtransport	C00864[e] --> C00864[c]
R_SRC_C14818_e	0.0038	SourceFlux	.	FALSE	. source flux	C14818[b] --> C14818[e]
R_thymt	0	Transport Database	.	FALSE	thymtransport	C00178[e] --> C00178[c]
R_NACHEX19ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg34 --> C00140 + ksi_deg35
R_G5SD2	0	Arginine and Proline Metabolism	1.2.1.41	FALSE	glutamate-5-semialdehydedehydrogenase	[c] : C03287 + C00080 + C00004 --> C01165 + C00003 + C00009
R_CBPSn	0	Arginine and Proline Metabolism	6.3.5.5	FALSE	carbamoyl-phosphatesynthase(glutamine-hydro	[n] : 2 C00002 + C00064 + C00001 + C01353 --> 2 C00008 + C00169 + C0002
R_DHAD1m	0	Valine, Leucine and Isoleucine Met	4.2.1.9	FALSE	dihydroxy-aciddehydratase(2,3-dihydroxy-3-me	[m] : C04039 --> C00141 + C00001
R_GLUDxm	0	Glutamate Metabolism	1.4.1.2	TRUE	glutamatedehydrogenase(NAD)(mitochondrial)	[m] : C00025 + C00001 + C00003 <==> C00026 + C00080 + C00004 + C01342
R_SRC_C00080_c	0	SourceFlux	.	FALSE	. source flux	C00080[b] --> C00080[c]
R_ECOAH6p	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxytetrad	[x] : C05260 <==> C00001 + C05273
R_NADS1	0	Cofactor and Prosthetic Group Bio	6.3.1.5	FALSE	NADsynthase(nh3)	[c] : C00002 + C00857 + C01342 --> C00020 + C00080 + C00003 + C00013
R_csnt	0	Transport Database	.	FALSE	csntransport	C00380[e] --> C00380[c]
R_AGMT	0	Arginine and Proline Metabolism	3.5.3.11	FALSE	agmatinase	[c] : C00179 + C00001 --> C00134 + C00086
R_PDHcm	0	Glycolysis/Gluconeogenesis	1.8.1.4	FALSE	pyruvatedehydrogenase(dihydrolipoamidedehy	[m] : C00579 + C00003 --> C00080 + C15972 + C00004
R_PSERT	0.1022	Glycine, Serine, and Threonine Me	2.6.1.52	FALSE	phosphoserinetransaminase	[c] : C03232 + C00025 --> C00026 + C01005
R_HACD6p	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-Hydroxyacyl-CoAdehydrogenase(3-oxotetrade	[x] : C05261 + C00080 + C00004 <==> C05260 + C00003
R_R07618	0	Citric Acid Cycle	1.8.1.4	TRUE	enzyme N6-(dihydrolipoyl)lysine:NAD+ oxidored	[c] : C15973 + C00003 <==> C15972 + C00004 + C00080
R_PGLg	0	Pentose Phosphate Pathway	3.1.1.31	FALSE	6-phosphogluconolactonase,glycosomal	[x] : C01236 + C00001 --> C00345 + C00080
R_MALT	0	Starch and Sucrose Metabolism	3.2.1.20	FALSE	alpha-glucosidase	[c] : C00001 + C00208 --> 2 C00267
R_ILETAm	0	Valine, Leucine and Isoleucine Met	2.6.1.42	TRUE	isoleucinetransaminase,mitochondrial	[m] : C00026 + C00407 <==> C03465 + C00025
R_IMPD	0.1076	Nucleotides	1.1.1.205	FALSE	IMPdehydrogenase	[c] : C00001 + C00130 + C00003 --> C00080 + C00004 + C00655
R_ADSL2	1000	IMP Biosynthesis	4.3.2.2	FALSE	adenylosuccinatelyase	[c] : C04823 --> C04677 + C00122
R_PRO1x	1000	Arginine and Proline Metabolism	1.5.1.2	FALSE	prolineoxidase(L-proline,NAD)	[c] : C00003 + C00148 --> C03912 + 2 C00080 + C00004
R_AGMTm	0	Arginine and Proline Metabolism	3.5.3.11	FALSE	agmatinase(m)	[m] : C00179 + C00001 --> C00134 + C00086
R_ht	0	Transport Database	.	FALSE	htransport	C00080[c] --> C00080[e]
R_DUTPDPm	0	Nucleotides	3.6.1.23	FALSE	dUTPdiphosphatase	[m] : C00460 + C00001 --> C00365 + C00080 + C00013
R_DHORTS	0	Pyrimidine Biosynthesis	3.5.2.3	TRUE	dihydroorotase	[c] : C00337 + C00001 <==> C00438 + C00080
R_MMSAD1m	0	Valine, Leucine and Isoleucine Met	1.2.1.27	FALSE	methylmalonate-semialdehydedehydrogenase	[m] : C00349 + C00010 + C00003 --> C00011 + C00004 + C00100
R_DUTPDPn	0	Nucleotides	3.6.1.23	FALSE	dUTPdiphosphatase,nuclear	[n] : C00460 + C00001 --> C00365 + C00080 + C00013
R_ACONT	0	Citric Acid Cycle	4.2.1.3	TRUE	aconitase	[c] : C00158 <==> C00311
R_AMPTASECGe	0	Glutathione Metabolism	3.4.11.2	FALSE	alanylaminopeptidase(cys-gly)(e)	[e] : C01419 + C00001 --> C00097 + C00037
R_PPNDH	0	Tyrosine, Tryptophan and Phenyla	4.2.1.51	FALSE	prephenatedehydratase	[c] : C00080 + C00254 --> C00011 + C00001 + C00166
R_DCTPD2	0	N - others	3.5.4.13	FALSE	dCTPdeaminase	[c] : C00063 + C00080 + C00001 --> C01342 + C00075

R_UAMAS	0	Cell Envelope Biosynthesis	6.3.2.8	FALSE	UDP-N-acetylmuramoyl-L-alaninesynthetase	[c] : C00041 + C00002 + C01050 --> C00008 + C00080 + C00009 + C01212
R_ASADi	0	Alanine and Aspartate Metabolism	1.2.1.11	FALSE	aspartate-semialdehydedehydrogenase,irreversi	[c] : C03082 + C00080 + C00005 --> C00441 + C00006 + C00009
R_ACACT1rm	-1000	Tryptophan Metabolism	2.3.1.9	TRUE	acetyl-CoAC-acetyltransferase,mitochondrial	[m] : 2 C00024 <==> C00332 + C00010
R_PUNP5	0	Purine Catabolism	2.4.2.1	TRUE	purine-nucleosidephosphorylase(Inosine)	[c] : C00294 + C00009 <==> C00262 + C00620
R_PUNP4	0	Purine Catabolism	2.4.2.1	TRUE	purine-nucleosidephosphorylase(Deoxyguanosir	[c] : C00330 + C00009 <==> C00672 + C00242
R_FAOXC181160	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationfattyacid	[m] : 5 C00010 + 4 C00016 + 5 C00001 + 5 C00003 + odecoa --> 5 C00024 + 4
R_PUNP6	0	Purine Catabolism	2.4.2.1	TRUE	purine-nucleosidephosphorylase(Deoxyinosine)	[c] : C05512 + C00009 <==> C00672 + C00262
R_PDHe3	1000	Pyruvate Metabolism	1.8.1.4	FALSE	pyruvatedehydrogenase(dihydrolipoamidedehy	[m] : C00579 + C00003 --> C00080 + C15972 + C00004
R_PDHe2	0	Pyruvate Metabolism	2.3.1.61	FALSE	pyruvatedehydrogenase(dihydrolipoamideS-ace	[m] : C16255 + C00010 + C00080 --> C00024 + C00579
R_PUNP3	0	Purine Catabolism	2.4.2.1	TRUE	purine-nucleosidephosphorylase(Guanosine)	[c] : C00387 + C00009 <==> C00242 + C00620
R_PUNP2	0	Purine Catabolism	2.4.2.1	TRUE	purine-nucleosidephosphorylase(Deoxyadenosir	[c] : C00559 + C00009 <==> C00672 + C00147
R_SRC_C00175_c	0.0038	SourceFlux	.	FALSE	. source flux	C00175[b] --> C00175[c]
R_SPODMe	0	ROS Detoxification	1.15.1.1	FALSE	superoxidedismutase,extracellular	[e] : 2 C00080 + 2 C00704 --> C00027 + C00007
R_ACACT6p	0	Fatty Acid Metabolism	2.3.1.16	FALSE	acetyl-CoAC-acetyltransferase(dodecanoyl),pero	[x] : C05261 + C00010 --> C00024 + ddcacoa
R_ACACT6r	0	.	2.3.1.16	TRUE	acetyl-CoAC-acyltransferase(dodecanoyl-CoA)(r	[c] : C00024 + ddcacoa <==> C05261 + C00010
R_ILETRSm	0	Valine, Leucine and Isoleucine Met	6.1.1.5	FALSE	isoleucyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C00407 + C01644 --> C00020 + C03127 + C00013
R_G3PD2	0.2575	Alternate Carbon Metabolism	1.1.1.94	TRUE	glycerol-3-phosphatedehydrogenase(NADP)	[c] : C00623 + C00006 <==> C00111 + C00080 + C00005
R_MI4PP	0	Inositol Phosphate Metabolism	3.1.3.25	FALSE	myo-inositol4-phosphatase	[c] : C00001 + C03546 --> C00137 + C00009
R_TALA	-0.2	Pentose Phosphate Pathway	2.2.1.2	TRUE	transaldolase	[c] : C00118 + C05382 <==> C00279 + C05345
R_DGK2m	0	Nucleotides	2.7.4.8	TRUE	deoxyguanylatekinase(dGMP:dATP)(mitochondr	[m] : C00131 + C00362 <==> C00206 + C00361
R_C2M26DCOAH	0	Limonene and pinene Degradation	4.2.1.17	TRUE	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoAhy	[x] : c2m26dcoa + C00001 <==> 3h26dm5coa
R_SRC_C00070_e	0.0038	SourceFlux	.	FALSE	. source flux	C00070[b] --> C00070[e]
R_UAMAGS	0	Cell Envelope Biosynthesis	6.3.2.9	FALSE	UDP-N-acetylmuramoyl-L-alanyl-D-glutamatesyr	[c] : C00002 + C00217 + C01212 --> C00008 + C00080 + C00009 + C00692
R_GALASE6ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg14 --> C00124 + ksi_deg15
R_NDPK10m	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dIDP),mitocl	[m] : C00002 + C01344 <==> C00008 + C01345
R_NDPK10n	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dIDP),nuclea	[n] : C00002 + C01344 <==> C00008 + C01345
R_ATPS4m	0	Oxidative Phosphorylation	3.6.3.14	FALSE	ATPsynthase(fourprotonsforoneATP)	C00008[m] + 4 C00080[c] + C00009[m] --> C00002[m] + 3 C00080[m] + C000
R_ESC_C03688_c	0.0038	EscapeFlux	.	FALSE	. escape flux	C03688[c] --> C03688[b]
R_DASYN	0	Glycerophospholipid Metabolism	2.7.7.41	TRUE	CTP:phosphatidate cytidyltransferase	[c] : C00063 + C00080 + 0.01 pa <==> 0.01 C00269 + C00013
R_SRC_C00076_e	0.0038	SourceFlux	.	FALSE	. source flux	C00076[b] --> C00076[e]
R_retinolt	0	Transport Database	.	FALSE	retinoltransport	C00473[e] --> C00473[c]
R_fumt	0	Transport Database	.	TRUE	fumtransport	C00122[c] <==> C00122[e]
R_ATPS4r	0	Oxidative Phosphorylation	3.6.3.14	TRUE	ATPsynthase(fourprotonsforoneATP)	C00008[c] + 4 C00080[e] + C00009[c] <==> C00002[c] + 3 C00080[c] + C000
R_AKGDam	0	Citric Acid Cycle	1.2.4.2	TRUE	oxoglutaratedehydrogenase(lipoamide)	[m] : C00026 + C00080 + C15972 <==> C00011 + C16254
R_ARGSSr	-1000	Arginine and Proline Metabolism	6.3.4.5	TRUE	argininosuccinatesynthase,reversible	[c] : C00049 + C00002 + C00327 <==> C00020 + C03406 + C00080 + C00013
R_NDPK9n	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:IDP),nuclear	[n] : C00002 + C00104 <==> C00008 + C00081
R_NADH2_DASH_	0	Oxidative Phosphorylation	1.6.99.3	FALSE	NADHdehydrogenase,mitochondrial	5 C00080[m] + C00004[m] + q10[m] --> 4 C00080[c] + C00003[m] + q10h2[m
R_FAOXC150m	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid(oddchain)	[m] : 6 C00010 + 6 C00016 + 6 C00001 + 6 C00003 + ptdcacoa --> 6 C00024 +
R_PRPNCOAHYDi	0	beta-Alanine Metabolism	4.2.1.17	FALSE	Propenoyl-CoAhydrolase(m)	[m] : C00001 + prpncoa --> 3hpcoa
R_CLPNSm_SC	0	Phospholipid Biosynthesis	2.7.8.5	FALSE	cardiolipinsynthase,yeast-specific,mitochondrial	[m] : 0.01 cdpdag_sc + 0.01 pg_sc --> 0.01 clpn_sc + C00055 + C00080
R_asn_Lt	0.1143	Transport Database	.	FALSE	asn-Ltransport	C00152[e] --> C00152[c]
R_GAPD	-0.2	Glycolysis/Gluconeogenesis	1.2.1.12	TRUE	glyceraldehyde-3-phosphatedehydrogenase	[c] : C00118 + C00003 + C00009 <==> C00236 + C00080 + C00004
R_PRPNCOAHYDi	0	beta-Alanine Metabolism	4.2.1.17	FALSE	Propenoyl-CoAhydrolase(x)	[x] : C00001 + prpncoa --> 3hpcoa
R_NACHEX8ly	0	Chondroitin Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : cs_e_deg2 + C00001 --> C01132 + cs_e_deg3
R_METAT	0.0038	Methionine Metabolism	2.5.1.6	FALSE	methionineadenosyltransferase	[c] : C00002 + C00001 + C00073 --> C00019 + C00009 + C00013
R_NTPP9	0	Nucleotides	3.6.1.19	FALSE	Nucleosidetriphosphatepyrophosphorylase(itp)	[c] : C00001 + C00081 --> C00080 + C00130 + C00013
R_RNDR4	0	Nucleotides	1.17.4.1	FALSE	ribonucleoside-diphosphatereductase(UDP)	[c] : C00342 + C00015 --> C01346 + C00001 + C00343
R_FAOXC245225	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : C00010 + C00001 + C00003 + C00007 + tetpent6coa --> C00024 + dcsptn
R_ORPT	0	Pyrimidine Biosynthesis	2.4.2.10	TRUE	orotatephosphoribosyltransferase	[c] : C01103 + C00013 <==> C00295 + C00119
R_RNDR3	0.0057	Nucleotides	1.17.4.1	FALSE	ribonucleoside-diphosphatereductase(CDP)	[c] : C00112 + C00342 --> C00705 + C00001 + C00343
R_MDH	-999.87	Citric Acid Cycle	1.1.1.37	TRUE	malatedehydrogenase	[c] : C00711 + C00003 <==> C00080 + C00004 + C00036
R_SELCYSTGL	0	Selenoamino Acid Metabolism	4.4.1.1	FALSE	selanocystathionineg-Lyase	[c] : C00001 + selcyst --> C00109 + C01342 + C05688
R_ser_Lt	0	Transport Database	.	FALSE	ser-Ltransport	C00716[e] --> C00716[c]
R_GARFTi	1000	Purine and Pyrimidine Biosynthes	2.1.2.2	FALSE	phosphoribosylglycinamideformyltransferase,in	[c] : C00234 + C03838 --> C04376 + C00080 + C00101
R_COKECBESr	0	Alkaloid Biosynthesis II	3.1.1.1	FALSE	Carboxylesterase(cocaine)(er)	[r] : coke + C00001 --> C00180 + egme + C00080
R_PYK	999.04	Glycolysis/Gluconeogenesis	2.7.1.40	FALSE	pyruvatekinase	[c] : C00008 + C00080 + C00074 --> C00002 + C00022

R_NACHEX6ly	0	Chondroitin Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : cs_d_deg1 + C00001 --> C01132 + cs_d_deg2
R_CHORS	0	Tyrosine, Tryptophan and Phenyla	4.2.3.5	FALSE	chorismatesynthase	[c] : C01269 --> C00251 + C00009
R_DDPGAm	0	Arginine and Proline Metabolism	4.1.2.14	TRUE	2-dehydro-3-deoxy-phosphogluconatealdolase,n	[m] : C05946 <==> C00048 + C00022
R_ACGK	0	Arginine and Proline Metabolism	2.7.2.8	FALSE	acetylglutamatekinase	[c] : C00624 + C00002 --> C04133 + C00008
R_PGAMT	0	Cell Envelope Biosynthesis	5.4.2.10	TRUE	phosphoglucosaminemutase	[c] : C06156 <==> C00352
R_thmt	0	Transport Database	.	FALSE	thmtransport	C00378[e] --> C00378[c]
R_ACGS	0	Arginine and Proline Metabolism	2.3.1.1	FALSE	N-acetylglutamatesynthase	[c] : C00024 + C00025 --> C00624 + C00010 + C00080
R_FAOXC11	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : C00010 + dmnoncoa + C00001 + C00003 --> C00024 + dmhptcoa + C000
R_ATPPRT	0	Histidine Metabolism	2.4.2.17	FALSE	ATPphosphoribosyltransferase	[c] : C00002 + C00119 --> C00013 + C02739
R_EXCH_succ_c	0.299	ExchangeFlux	.	TRUE	. exchange flux	C00042[c] <==> C00042[b]
R_GLUK	0.4	Glycolysis/Gluconeogenesis	2.7.1.2	FALSE	Glucokinase	[c] : C00002 + C00267 --> C00008 + C01172 + C00080
R_PGSA_EC	0	Membrane Lipid Metabolism	2.7.8.5	TRUE	Phosphatidylglycerolsynthase(Ecoli)	[c] : 0.02 cdpdag_ec + C00623 <==> C00055 + C00080 + 0.02 pgp_ec
R_ABTAr	-1000	.	2.6.1.19	TRUE	4-aminobutyratetransaminase	[c] : C00334 + C00026 <==> C00025 + C00232
R_MALTly	0	Starch and Sucrose Metabolism	3.2.1.20	FALSE	alpha-glucosidase,lysosomal	[l] : C00001 + C00208 --> 2 C00267
R_ACONTm	0	Citric Acid Cycle	4.2.1.3	TRUE	Aconitatehydratase	[m] : C00158 <==> C00311
R_SRC_C00052_c	0.1373	SourceFlux	.	FALSE	. source flux	C00052[b] --> C00052[c]
R_EXCH_pi_e	-0.6031	ExchangeFlux	.	TRUE	. exchange flux	C00009[e] <==> C00009[b]
R_FUM	-999.91	Citric Acid Cycle	4.2.1.2	TRUE	fumarase	[c] : C00122 + C00001 <==> C00711
R_PTPATi	1000	Cofactor and Prosthetic Group Bio	2.7.7.3	FALSE	pantetheine-phosphateadenylyltransferase	[c] : C00002 + C00080 + C01134 --> C00882 + C00013
R_P5CRxm	0	Arginine and Proline Metabolism	1.5.1.2	FALSE	pyrroline-5-carboxylatereductase(m)	[m] : C03912 + 2 C00080 + C00004 --> C00003 + C00148
R_xyl_Dt	0	Transport Database	.	FALSE	xyl-Dtransport	C01394[e] --> C01394[c]
R_PPC	1000	Anaplerotic reactions	4.1.1.31	FALSE	phosphoenolpyruvatecarboxylase	[c] : C00011 + C00001 + C00074 --> C00080 + C00036 + C00009
R_GTPCI	0	Tetrahydrobiopterin	3.5.4.16	FALSE	GTPcyclohydrolaseI	[c] : C00044 + C00001 --> C04895 + C00058 + C00080
R_PFKg	0	Glycolysis/Gluconeogenesis	2.7.1.11	FALSE	phosphofructokinase,glycosome	[x] : C00002 + C05345 --> C00008 + C00354 + C00080
R_frut	0	Transport Database	.	FALSE	frutransport	C10906[e] --> C10906[c]
R_kt	0.0038	Transport Database	.	FALSE	ktransport	C00238[e] --> C00238[c]
R_GALASE17ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksii_core2_deg5 --> C00124 + ksii_core2_deg6
R_his_Lt	0.0451	Transport Database	.	FALSE	his-Ltransport	C00135[e] --> C00135[c]
R_HKYNH	0	Tryptophan Metabolism	3.7.1.3	FALSE	3-Hydroxy-L-kynureninehydrolase	[c] : C00001 + C03227 --> C00632 + C00041
R_ALATRS	0	Alanine and Aspartate Metabolism	6.1.1.7	FALSE	Alanyl-tRNAsynthetase	[c] : C00041 + C00002 + C01635 --> C00886 + C00020 + C00013
R_ADSK	0	Nucleotides	2.7.1.25	FALSE	adenylyl-sulfatekinase	[c] : C00224 + C00002 --> C00008 + C00080 + C00053
R_G6PI	-1000	Glycolysis/Gluconeogenesis	5.3.1.9	TRUE	Glucose-6-phosphateisomerase	[c] : C00668 <==> C01172
R_RNDR4n	0	Nucleotide Salvage Pathway	1.17.4.1	FALSE	ribonucleoside-diphosphatereductase(UDP),nuc	[n] : C00342 + C00015 --> C01346 + C00001 + C00343
R_ADSS	0.0924	Nucleotides	6.3.4.4	FALSE	adenylosuccinatesynthase	[c] : C00049 + C00044 + C00130 --> C03794 + C00035 + 2 C00080 + C00009
R_hco3t	0	Transport Database	.	TRUE	hco3transport	C01353[c] <==> C01353[e]
R_VALTRSm	0	Valine, Leucine and Isoleucine Met	6.1.1.9	FALSE	valyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C01653 + C00183 --> C00020 + C00013 + C02554
R_SRC_C00003_e	0.0076	SourceFlux	.	FALSE	. source flux	C00003[b] --> C00003[e]
R_ergstt	0	Transport Database	.	FALSE	ergsttransport	C01694[e] --> C01694[c]
R_succt	0	Transport Database	.	TRUE	succtransport	C00042[c] <==> C00042[e]
R_ACOTA	0	Arginine and Proline Metabolism	2.6.1.11	TRUE	acetylornithinetransaminase	[c] : C00437 + C00026 <==> C01250 + C00025
R_rib_Dt	0	Transport Database	.	FALSE	rib-Dtransport	C00121[e] --> C00121[c]
R_uratet	0	Transport Database	.	FALSE	uratetransport	C00366[e] --> C00366[c]
R_TRE6PS	0	Alternate Carbon Metabolism	2.4.1.15	FALSE	alpha,alpha-trehalose-phosphatesynthase(UDP-f	[c] : C00668 + C00029 --> C00080 + C00689 + C00015
R_EXCH_C01342_	-1000	ExchangeFlux	.	TRUE	. exchange flux	C01342[e] <==> C01342[b]
R_DHQD	-1000	Tyrosine, Tryptophan and Phenyla	4.2.1.10	TRUE	3-dehydroquinatedehydratase	[c] : C00944 <==> C02637 + C00001
R_ESC_C00711_c	0	EscapeFlux	.	FALSE	. escape flux	C00711[c] --> C00711[b]
R_FAOXC244224	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : C00010 + C00001 + C00003 + C00007 + tettet6coa --> C00024 + adrncoa
R_CPC6R	0	Vitamins and Cofactor Biosynthesi	1.3.1.54	FALSE	precorrin-6Areductase	[c] : C11542 + C00080 + C00005 --> C11543 + C00006
R_MOHMT	0	Cofactor and Prosthetic Group Bio	2.1.2.11	FALSE	3-methyl-2-oxobutanoatehydroxymethyltransfer	[c] : C00141 + C00001 + C00143 --> C00966 + C00101
R_PPAg	0	Oxidative phosphorylation	3.6.1.1	FALSE	inorganicdiphosphatase	[x] : C00001 + C00013 --> C00080 + 2 C00009
R_ESC_C00080_e	0	EscapeFlux	.	FALSE	. escape flux	C00080[e] --> C00080[b]
R_ACACT5p	0	Fatty Acid Metabolism	2.3.1.16	FALSE	acetyl-CoAC-acyltransferase(decanoyl-CoA),perc	[x] : C05263 + C00010 --> C00024 + dcacoa
R_SRC_C00034_e	0.0038	SourceFlux	.	FALSE	. source flux	C00034[b] --> C00034[e]
R_ACACT5r	0	.	2.3.1.16	TRUE	acetyl-CoAC-acyltransferase(decanoyl-CoA)(r)	[c] : C00024 + dcacoa <==> C05263 + C00010
R_PPAm	0	Oxidative Phosphorylation	3.6.1.1	FALSE	inorganicdiphosphatase	[m] : C00001 + C00013 --> C00080 + 2 C00009
R_PPAn	0	Miscellaneous	3.6.1.1	FALSE	inorganicdiphosphatase,nuclear	[n] : C00001 + C00013 --> C00080 + 2 C00009

R_HACD1	0	.	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(acetoacetyl-C	[c] : C00332 + C00080 + C00004 <==> 3hbcoa + C00003
R_4abzt	0	Transport Database	.	FALSE	4abztransport	C00568[e] --> C00568[c]
R_ARGTRS	0	Arginine and Proline Metabolism	6.1.1.19	FALSE	Arginyl-tRNAsynthetase	[c] : C00062 + C00002 + C01636 --> C00020 + C02163 + C00013
R_GTPDPK	0	Purine and Pyrimidine Biosynthes	2.7.6.5	FALSE	GTPdiphosphokinase	[c] : C00002 + C00044 --> C00020 + C04494 + C00080
R_NABTNO	0	Arginine and Proline Metabolism	1.2.1.3	FALSE	N4-Acetylaminobutanal:NAD+oxidoreductase	[c] : C00001 + C05936 + C00003 --> C02946 + 2 C00080 + C00004
R_ACGKm	0	Arginine and Proline Metabolism	2.7.2.8	FALSE	acetylglutamatekinase,mitochondrial	[m] : C00624 + C00002 --> C04133 + C00008
R_PUNP7	0	Nucleotides	2.4.2.1	TRUE	purine-nucleosidephosphorylase(Xanthosine)	[c] : C00009 + C01762 <==> C00620 + C00385
R_GHMT3m	0	Lysine Metabolism	2.1.2.1	FALSE	glycinehydroxymethyltransferase,mitochondrial	[m] : 3htmelys + C00080 --> 4tmeabut + C00037
R_CYOO6m	0	Oxidative Phosphorylation	1.9.3.1	FALSE	cytochromecoxidase,mitochondrial	4 C01071[m] + 10 C00080[m] + C00007[m] --> 4 C01070[m] + 2 C00001[m] +
R_ECOAH11p	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxyhexac	[x] : C00001 + hxc2coa <==> 3hxccoa
R_h2ot	4.0417	Transport Database	.	TRUE	h2otransport	C00001[c] <==> C00001[e]
R_PUNP1	0	Nucleotides	2.4.2.1	TRUE	purine-nucleosidephosphorylase(Adenosine)	[c] : C00212 + C00009 <==> C00147 + C00620
R_PSERDg_SC	0	Phospholipid Biosynthesis	4.1.1.65	FALSE	phosphatidylserinedecarboxylase,yeast-specific,	[g] : C00080 + 0.01 ps_sc --> C00011 + 0.01 pe_sc
R_SRC_C00152_e	0.1143	SourceFlux	.	FALSE	. source flux	C00152[b] --> C00152[e]
R_fe3t	0.0038	Transport Database	.	FALSE	fe3transport	C14819[e] --> C14819[c]
R_ESC_C00080_c	0	EscapeFlux	.	FALSE	. escape flux	C00080[c] --> C00080[b]
R_MMM2	0	Alternate Carbon Metabolism	5.4.99.2	FALSE	Methylmalonyl-CoAmutase	[c] : C00091 --> C01213
R_PPA2	0	Others	3.6.1.1	FALSE	inorganictriphosphatase	[c] : C00001 + C00536 --> C00080 + C00009 + C00013
R_LYSTRSm	0	Threonine and Lysine Metabolism	6.1.1.6	FALSE	Lysyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C00047 + C01646 --> C00020 + C01646 + C00013
R_CATm	0	ROS Detoxification	1.11.1.6	FALSE	catalase	[m] : 2 C00027 --> 2 C00001 + C00007
R_ATPS3v	0	Oxidative Phosphorylation	3.6.3.14	FALSE	ATPsynthase,vacuole	C00008[v] + 3 C00080[c] + C00009[v] --> C00002[v] + 2 C00080[v] + C00001
R_PAPPT3	0	Cell Envelope Biosynthesis	2.7.8.13	FALSE	phospho-N-acetylmuramoyl-pentapeptide-trans	[c] : C17556 + C04882 --> C05897 + C00105
R_FAOXC225205	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : C00010 + dcsptn1coa + C00001 + C00003 + C00007 --> C00024 + C0008
R_ADK4m	-1000	Nucleotide Salvage Pathway	2.7.4.3	TRUE	adentylatekinase(ITP),mitochondrial	[m] : C00020 + C00081 <==> C00008 + C00104
R_ACOAD2	0	Fatty Acid Degradation	1.3.99.3	TRUE	acyl-CoAdehydrogenase(hexanoyl-CoA)	[c] : C00080 + C05271 + C00004 <==> C05270 + C00003
R_ACACT2r	0	Fatty Acid Degradation	2.3.1.16	TRUE	acetyl-CoAC-acyltransferase(butanoyl-CoA)(r)	[c] : C00024 + C00136 <==> C05269 + C00010
R_tcyntt	0	Transport Database	.	FALSE	tcynttransport	C01755[e] --> C01755[c]
R_FAOXC224204	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : adrncoa + C00010 + C00016 + C00001 + C00003 --> C00024 + arachdcoa
R_pydxnt	0	Transport Database	.	FALSE	pydxntransport	C00314[e] --> C00314[c]
R_asp_Lt	0	Transport Database	.	FALSE	asp-Ltransport	C00049[e] --> C00049[c]
R_CYOOm	0	Oxidative Phosphorylation	1.9.3.1	FALSE	cytochromecoxidase,mitochondrial	4 C01071[m] + 6 C00080[m] + C00007[m] --> 4 C01070[m] + 6 C00080[c] + 2
R_ATPS3m	0	Oxidative Phosphorylation	3.6.3.14	FALSE	ATPsynthase,mitochondrial	C00008[m] + 3 C00080[c] + C00009[m] --> C00002[m] + 2 C00080[m] + C000
R_UPP3MT	0	Cofactor and Prosthetic Group Bio	2.1.1.107	FALSE	uroporphyrinogenmethyltransferase	[c] : 2 C00019 + C01051 --> 2 C00021 + dscl + C00080
R_THRS	0.1202	Glycine, Serine, and Threonine Me	4.2.3.1	FALSE	threoninesynthase	[c] : C00001 + C01102 --> C00009 + C00188
R_R04949	0	.	3.2.1.21	TRUE	Cyanoglycoside glucohydrolase	[c] : C05713 + C00001 <==> C05712 + C00267
R_NDPK8m	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dADP),mitoc	[m] : C00002 + C00206 <==> C00008 + C00131
R_NDPK8n	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dADP),nucle	[n] : C00002 + C00206 <==> C00008 + C00131
R_P5CR	1000	Urea cycle/amino group Metabolis	1.5.1.2	FALSE	pyrroline-5-carboxylatereductase	[c] : C03912 + 2 C00080 + C00005 --> C00006 + C00148
R_leu_Lt	0.2137	Transport Database	.	FALSE	leu-Ltransport	C00123[e] --> C00123[c]
R_KARA1	1000	Valine, Leucine and Isoleucine Met	1.1.1.86	TRUE	ketol-acidreductoisomerase(2,3-dihydroxy-3-me	[c] : C04039 + C00006 <==> C06010 + C00080 + C00005
R_FAOXC246226	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : C00010 + C00001 + C00003 + C00007 + tethex3coa --> C00024 + c226coa
R_KARA2	-1000	Valine, Leucine and Isoleucine Met	1.1.1.86	TRUE	ketol-acidreductoisomerase(2-Acetolactate)	[c] : C00659 + C00080 + C00005 <==> C04104 + C00006
R_GLUKg	0	Glycolysis/Gluconeogenesis	2.7.1.2	FALSE	Glucokinase	[x] : C00002 + C00221 --> C00008 + C01172 + C00080
R_G3PD1	-0.2575	Glycerophospholipid Metabolism	1.1.1.94	TRUE	glycerol-3-phosphatedehydrogenase(NAD)	[c] : C00623 + C00003 <==> C00111 + C00080 + C00004
R_PNTKm	0	CoA Biosynthesis	2.7.1.33	FALSE	pantothenatekinase(mitochondrial)	[m] : C00002 + C00864 --> C03492 + C00008 + C00080
R_PYAM5PO	1000	Cofactor and Prosthetic Group Bio	1.4.3.5	FALSE	pyridoxamine5'-phosphateoxidase	[c] : C00001 + C00007 + C00647 --> C00027 + C01342 + C00018
R_FAOXC18280m	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoffattyacid	[m] : 5 C00010 + 3 C00016 + 5 C00001 + lneldccoa + 5 C00003 --> 5 C00024 +
R_PSDm_hs	0	Glycerophospholipid Metabolism	4.1.1.65	FALSE	Phosphatidylserinedecarboxylase	[m] : C00080 + ps_hs --> C00011 + pe_hs
R_ADAe	0	Nucleotides	3.5.4.4	FALSE	Adenosinedeaminase,extracellular	[e] : C00212 + C00080 + C00001 --> C00294 + C01342
R_GALASE11ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg29 --> C00124 + ksi_deg30
R_FAOXC204184	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationfattyacid	[m] : C00010 + eicostetcoa + C00016 + C00001 + C00003 --> C00024 + C0135
R_cholt	0	Transport Database	.	FALSE	choltransport	C00114[e] --> C00114[c]
R_PGI3	1000	Glycolysis/Gluconeogenesis	5.3.1.9	TRUE	glucose-6-phosphateisomerase,glycosome	[x] : g6p-a <==> C01172
R_PGI2	1000	Glycolysis/Gluconeogenesis	5.3.1.9	TRUE	glucose-6-phosphateisomerase,glycosome	[x] : C01172 <==> C05345
R_PGI1	-1000	Glycolysis/Gluconeogenesis	5.3.1.9	TRUE	glucose-6-phosphateisomerase,glycosome	[x] : g6p-a <==> C05345
R_G6PDHg	0	Pentose Phosphate Pathway	1.1.1.49	FALSE	glucose-6-phosphatedehydrogenase,glycosomal	[x] : C01172 + C00006 --> C01236 + C00080 + C00005

R_FAOXC225205	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : C00010 + dcsptn1coa + C00001 + C00003 + C00007 --> C00024 + C0008
R_GALU	-0.1373	Galactose Metabolism	2.7.7.9	TRUE	UTP-glucose-1-phosphateuridylyltransferase	[c] : C00103 + C00080 + C00075 <==> C00013 + C00029
R_SRC_C00009_e	0	SourceFlux	.	FALSE	. source flux	C00009[b] --> C00009[e]
R_lac_Lt	0	Transport Database	.	TRUE	lac-Ltransport	C00186[c] <==> C00186[e]
R_EXCH_C00001_	-995.96	ExchangeFlux	.	TRUE	. exchange flux	C00001[e] <==> C00001[b]
R_NNATm	0	NAD Metabolism	2.7.7.18	FALSE	nicotinate-nucleotideadenylyltransferase,mitoch	[m] : C00002 + C00080 + C01185 --> C00857 + C00013
R_met_Lt	0.0766	Transport Database	.	FALSE	met-Ltransport	C00073[e] --> C00073[c]
R_ACOTAim	0	Arginine and Proline Metabolism	2.6.1.11	FALSE	acteylornithinetransaminase,irreversible,mitoch	[m] : C01250 + C00025 --> C00437 + C00026
R_nmnt	0	Transport Database	.	FALSE	nmntransport	C00455[e] --> C00455[c]
R_DAPDC	0	Threonine and Lysine Metabolism	4.1.1.20	FALSE	diaminopimelatedecarboxylase	[c] : C00680 + C00080 --> C00011 + C00047
R_lys_Lt	0.1625	Transport Database	.	FALSE	lys-Ltransport	C00047[e] --> C00047[c]
R_EXCH_gcald_c	0	ExchangeFlux	.	TRUE	. exchange flux	C00266[c] <==> C00266[b]
R_LEUTRS	0	Valine, Leucine and Isoleucine Met	6.1.1.4	FALSE	Leucyl-tRNAsynthetase	[c] : C00002 + C00123 + C01645 --> C00020 + C02047 + C00013
R_PSERDv_SC	0	Phospholipid Biosynthesis	4.1.1.65	FALSE	phosphatidylserinedecarboxylase,yeast-specific,	[v] : C00080 + 0.01 ps_sc --> C00011 + 0.01 pe_sc
R_IGPDH	0	Histidine Metabolism	4.2.1.19	FALSE	imidazoleglycerol-phosphatedehydratase	[c] : C04666 --> C00001 + C01267
R_GK1	1000	Nucleotides	2.7.4.8	TRUE	guanylatekinase(GMP:ATP)	[c] : C00002 + C00144 <==> C00008 + C00035
R_GK2	-999.89	Purine and Pyrimidine Biosynthes	2.7.4.8	TRUE	guanylatekinase(GMP:dATP)	[c] : C00131 + C00144 <==> C00206 + C00035
R_APAT2rm	0	beta-Alanine Metabolism	2.6.1.19	TRUE	3-Aminopropanoate:2-oxoglutarateaminotransfe	[m] : C00026 + C00099 <==> C00025 + C00222
R_GLYTRS	0	Glycine and Serine Metabolism	6.1.1.14	FALSE	Glycyl-tRNAsynthetase	[c] : C00002 + C00037 + C01642 --> C00020 + C02412 + C00013
R_FAOXC16080m	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : 4 C00010 + 4 C00016 + 4 C00001 + 4 C00003 + C00154 --> 4 C00024 + 4
R_ECOAH5	0	.	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxydodec	[c] : C05262 <==> dd2coa + C00001
R_ECOAH4	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxydecan	[c] : 3hdcoa <==> C05275 + C00001
R_ECOAH7	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxyhexad	[c] : C05258 <==> C00001 + C05272
R_ECOAH6	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxytetrad	[c] : C05260 <==> C00001 + C05273
R_G6PI2	0	Glycolysis/Gluconeogenesis	5.3.1.9	TRUE	Glucose-6-phosphateisomerase	[c] : C01172 <==> f6p-b
R_AGDC_r	-1000	Carbohydrate Metabolism	3.5.1.25	TRUE	N-acetylglucosamine-6-phosphatedeacetylase(re	[c] : C00357 + C00001 <==> C00033 + C00352
R_ECOAH3	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxyoctan	[c] : C05266 <==> C00001 + C05276
R_ADSL1	1000	Nucleotides	4.3.2.2	FALSE	adenylosuccinatelyase	[c] : C03794 --> C00020 + C00122
R_FAOXC16080x	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : 4 C00010 + 4 C00001 + 4 C00003 + 4 C00007 + C00154 --> 4 C00024 + 4
R_SRC_C00082_e	0.0654	SourceFlux	.	FALSE	. source flux	C00082[b] --> C00082[e]
R_THRD_Lm	0	Threonine and Lysine Metabolism	4.3.1.19	FALSE	L-threoninedeaminase,mitochondrial	[m] : C00188 --> C00109 + C01342
R_DHORD	1000	Purine and Pyrimidine Biosynthes	1.3.3.1	TRUE	dihydooroticaciddehydrogenase	[c] : C00337 + C00007 <==> C00027 + C00295
R_FUMg	0	Glycolysis/Gluconeogenesis	4.2.1.2	TRUE	fumarase,glycosome	[x] : C00122 + C00001 <==> C00711
R_CATp	0	Miscellaneous	1.11.1.6	FALSE	catalaseA,peroxisomal	[x] : 2 C00027 --> 2 C00001 + C00007
R_OHPBAT	0	Cofactor and Prosthetic Group Bio	2.6.1.52	TRUE	O-Phospho-4-hydroxy-L-threonine:2-oxoglutara	[c] : C00025 + C06054 <==> C00026 + C06055
R_HACD9m	0	Valine, Leucine and Isoleucine Met	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(2-Methylacet	[m] : C04405 + C00003 <==> C03344 + C00080 + C00004
R_orott	0	Transport Database	.	TRUE	orottransport	C00295[c] <==> C00295[e]
R_FUMm	0	Citric Acid Cycle	4.2.1.2	TRUE	fumarase,mitochondrial	[m] : C00122 + C00001 <==> C00711
R_C2M26DCOAH	0	Limonene and pinene Degradation	4.2.1.17	TRUE	cis-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoAhy	[m] : c2m26dcoa + C00001 <==> 3h26dm5coa
R_NDPK6n	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dUDP),nucle	[n] : C00002 + C01346 <==> C00008 + C00460
R_RPEg	0	Pentose Phosphate Pathway	5.1.3.1	TRUE	ribulose5-phosphate3-epimerase,glycosomal	[x] : C00199 <==> C00231
R_lctst	0	Transport Database	.	FALSE	lctstransport	C00243[e] --> C00243[c]
R_NDPK6m	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dUDP),mitoc	[m] : C00002 + C01346 <==> C00008 + C00460
R_PGIg	0	Glycolysis/Gluconeogenesis	5.3.1.9	TRUE	glucose-6-phosphateisomerase,glycosome	[x] : C00668 <==> C05345
R_ECOAH5p	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxydodec	[x] : C05262 <==> dd2coa + C00001
R_R02736	-999.6	Glutathione metabolism	1.1.1.49	TRUE	beta-D-Glucose-6-phosphate:NADP+ 1-oxoreduc	[c] : C01172 + C00006 <==> C01236 + C00005 + C00080
R_arab_Dt	0	Transport Database	.	FALSE	arab-Dtransport	C00216[e] --> C00216[c]
R_ECOAH1	0	.	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxybutan	[c] : 3hbcoa <==> b2coa + C00001
R_fort	0	Transport Database	.	FALSE	fortransport	C00058[c] --> C00058[e]
R_PHETRSm	0	Tyrosine, Tryptophan and Phenyla	6.1.1.20	FALSE	phenylalanyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C00079 + C01648 --> C00020 + C03511 + C00013
R_DOLPMT_L	0	N-Glycan Biosynthesis	2.4.1.83	FALSE	Dolichyl-phosphateD-mannosyltransferase(liver	[c] : 0.1 dolp_l + C00096 --> 0.1 dolmanp_l + C00035
R_NACHEX10ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : 2 C00001 + ksi_deg7 --> 2 C00140 + ksi_deg8
R_ACSm	0	Glycolysis/Gluconeogenesis	6.2.1.1	FALSE	acetyl-CoAsynthetase	[m] : C00033 + C00002 + C00010 --> C00024 + C00020 + C00013
R_GLUTRSm	0	Glutamine Metabolism	6.1.1.17	FALSE	glutamyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C00025 + C01641 --> C00020 + C02987 + C00013
R_PEPCKm	0	Glycolysis/Gluconeogenesis	4.1.1.32	FALSE	Phosphoenolpyruvatecarboxykinase(GTP)	[m] : C00044 + C00036 --> C00011 + C00035 + C00074
R_mobdt	0	Transport Database	.	FALSE	mobdtransport	C06232[e] --> C06232[c]

R_inst	0	Transport Database	.	FALSE	instransport	C00294[e] --> C00294[c]
R_GCCa	0	.	1.4.4.2	FALSE	glycine-cleavagecomplex	[c] : C00037 + C00080 + C02051 --> C01242 + C00011
R_GCCb	0	.	2.1.2.10	FALSE	glycinecleavagecomplex	[c] : C01242 + C00101 --> C02972 + C00143 + C01342
R_GCCc	0	Glycine and Serine Metabolism	1.8.1.4	FALSE	glycine-cleavagecomplex	[c] : C02972 + C00003 --> C00080 + C02051 + C00004
R_AMID3	0	Tyrosine, Tryptophan and Phenyla	3.5.1.4	FALSE	amidase	[c] : C00001 + C02693 --> C00954 + C01342
R_GCCcm	0	Glycine, Serine, and Threonine Me	1.8.1.4	TRUE	glycine-cleavagecomplex(lipoylprotein),mitocho	[m] : C02972 + C00003 <==> C00080 + C02051 + C00004
R_DOLPMT_U	0	N-Glycan Biosynthesis	2.4.1.83	FALSE	Dolichyl-phosphateD-mannosyltransferase(uter	[c] : 0.1 dolp_u + C00096 --> 0.1 dolmanp_u + C00035
R_AIRCr	0	IMP Biosynthesis	4.1.1.21	TRUE	phosphoribosylaminoimidazolecarboxylase	[c] : C03373 + C00011 <==> C04751 + C00080
R_AMID4	0	Others	3.5.1.4	FALSE	amidase	[c] : C06244 + C00001 --> C00033 + C01342
R_BETALDHy	0	Glycine, Serine, and Threonine Me	1.2.1.8	FALSE	betaine-aldehydedehydrogenase	[c] : C00576 + C00001 + C00006 --> C00719 + 2 C00080 + C00005
R_PPCOACm	0	Valine, Leucine and Isoleucine Met	6.4.1.3	FALSE	Propionyl-CoAcarboxylase,mitochondrial	[m] : C00002 + C01353 + C00100 --> C00008 + C00080 + C00683 + C00009
R_nadt	0.0076	Transport Database	.	FALSE	nadtransport	C00003[e] --> C00003[c]
R_FAOXC140	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : 6 C00010 + 6 C00016 + 6 C00001 + 6 C00003 + C02593 --> 7 C00024 + 6
R_thymdt	0	Transport Database	.	FALSE	thymdtransport	C00214[e] --> C00214[c]
R_ACACT1m	1000	Fatty Acid Biosynthesis	2.3.1.9	FALSE	acetyl-CoAC-acetyltransferase,mitochondrial	[m] : 2 C00024 --> C00332 + C00010
R_SRC_C00185_e	0.2	SourceFlux	.	FALSE	. source flux	C00185[b] --> C00185[e]
R_FTHFD	0	Folate Metabolism	3.5.1.10	FALSE	formyltetrahydrofolatedeformylase	[c] : C00234 + C00001 --> C00058 + C00080 + C00101
R_NACHEX18ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg31 --> C00140 + ksi_deg32
R_mal_Lt	0	Transport Database	.	TRUE	mal-Ltransport	C00711[c] <==> C00711[e]
R_ESC_C00011_e	0	EscapeFlux	.	FALSE	. escape flux	C00011[e] --> C00011[b]
R_VALTRS	0	Valine, Leucine and Isoleucine Met	6.1.1.9	FALSE	Valyl-tRNAsynthetase	[c] : C00002 + C01653 + C00183 --> C00020 + C00013 + C02554
R_AMPTASECG	0	Glutathione Metabolism	3.4.11.2	FALSE	alanylaminopeptidase(cys-gly)	[c] : C01419 + C00001 --> C00097 + C00037
R_METS	0	Methionine Metabolism	2.1.1.13	FALSE	methioninesynthase	[c] : C00440 + C05330 --> C00080 + C00073 + C00101
R_ACACT1r	-1000	Tryptophan Metabolism	2.3.1.9	TRUE	acetyl-CoAC-acetyltransferase	[c] : 2 C00024 <==> C00332 + C00010
R_SRC_C00183_e	0.2005	SourceFlux	.	FALSE	. source flux	C00183[b] --> C00183[e]
R_cu2t	0.0038	Transport Database	.	FALSE	cu2transport	C00070[e] --> C00070[c]
R_METTRS	0	Methionine Metabolism	6.1.1.10	FALSE	Methionyl-tRNAsynthetase	[c] : C00002 + C00073 + C01647 --> C00020 + C02430 + C00013
R_so4t	0.0038	Transport Database	.	FALSE	so4transport	C00059[e] --> C00059[c]
R_PDHam1m	0	Pyruvate Metabolism	1.2.4.2	TRUE	pyruvatedehydrogenase(lipoamide)	[m] : C00022 + C00068 <==> 2ahethmpp + C00011
R_SUCOAS	-500.02	Citric Acid Cycle	6.2.1.5	TRUE	succinyl-CoAsynthetase(ADP-forming)	[c] : C00002 + C00010 + C00042 <==> C00008 + C00009 + C00091
R_ASPCTn	0	Purine and Pyrimidine Biosynthes	2.1.3.2	FALSE	aspartatecarbamoyltransferase,nuclear	[n] : C00049 + C00169 --> C00438 + C00080 + C00009
R_BG_CELLB_	0.2	.	.	FALSE	.	[c] : C00185 + C00001 --> 2 C00267
R_ALAR	-1000	Alanine and Aspartate Metabolism	5.1.1.1	TRUE	alanineracemase	[c] : C00041 <==> C00133
R_UAAGDS	0	Cell Envelope Biosynthesis	6.3.2.13	FALSE	UDP-N-acetylmuramoyl-L-alanyl-D-glutamyl-me	[c] : C00680 + C00002 + C00692 --> C00008 + C00080 + C00009 + C04877
R_PSP_L	0.1022	Glycine, Serine, and Threonine Me	3.1.3.3	FALSE	phosphoserinephosphatase(L-serine)	[c] : C00001 + C01005 --> C00009 + C00716
R_GLYCK2	0	Glyoxylate and Dicarboxylate Meta	2.7.1.31	FALSE	glyceratekinase	[c] : C00002 + C00258 --> C00631 + C00008 + C00080
R_ICDHyr	-1000	Citric Acid Cycle	1.1.1.42	TRUE	isocitratedehydrogenase(NADP)	[c] : C00311 + C00006 <==> C00026 + C00011 + C00005
R_ICDHyp	0	Citric Acid Cycle	1.1.1.42	FALSE	Isocitratedehydrogenase(NADP+)	[x] : C00311 + C00006 --> C00026 + C00011 + C00005
R_PYLALDOX	0	Limonene and pinene Degradation	1.2.1.3	FALSE	Perillylaldehyde:NAD+oxidoreductase	[c] : C00001 + C00003 + pylald --> 2 C00080 + C00004 + peracd
R_ICDHym	1000	Citric Acid Cycle	1.1.1.42	FALSE	Isocitratedehydrogenase(NADP+)	[m] : C00311 + C00006 --> C00026 + C00011 + C00005
R_ASPCTr	0	Pyrimidine Biosynthesis	2.1.3.2	TRUE	aspartatecarbamoyltransferase(reversible)	[c] : C00049 + C00169 <==> C00438 + C00080 + C00009
R_NADKm	0	NAD Biosynthesis	2.7.1.23	FALSE	NADkinase,mitochondrial	[m] : C00002 + C00003 --> C00008 + C00080 + C00006
R_NADH2_DASH_	1000	Oxidative Phosphorylation	1.6.99.3	FALSE	NADHdehydrogenase,cytosolic/mitochondrial	C00080[c] + C00004[c] + C17568[m] --> C00003[c] + C00390[m]
R_PFK	0	Glycolysis/Gluconeogenesis	2.7.1.11	FALSE	phosphofructokinase	[c] : C00002 + C05345 --> C00008 + C00354 + C00080
R_vitd2t	0	Transport Database	.	FALSE	vitd2transport	vitd2[e] --> vitd2[c]
R_FAOXC80	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationofmed/longchainfattyacid	[m] : 3 C00010 + 3 C00016 + 3 C00001 + 3 C00003 + C01944 --> 4 C00024 + 3
R_SRC_C00079_e	0.088	SourceFlux	.	FALSE	. source flux	C00079[b] --> C00079[e]
R_PSD_HP	0	Glycerolipid Synthesis	4.1.1.65	FALSE	PhosphatidylserinedecarboxylaseHpspecific	[c] : C00080 + ps_hp --> C00011 + pe_hp
R_DHORTSn	0	Purine and Pyrimidine Biosynthes	3.5.2.3	TRUE	dihydroorotase,nuclear	[n] : C00337 + C00001 <==> C00438 + C00080
R_CYRDAAT	0	Vitamins and Cofactor Biosynthesi	2.5.1.17	FALSE	cob(I)yrinicacida,c-diamideadenosyltransferase	[c] : C00002 + C06505 + C00080 --> C06506 + C00536
R_co2t	500.33	Transport Database	.	TRUE	co2transport	C00011[c] <==> C00011[e]
R_LFORKYNHYD	0	Tryptophan Metabolism	3.7.1.3	FALSE	L-Formylkynureninehydrolase	[c] : C02700 + C00001 --> C00041 + C00080 + nformanth
R_ACACT7p	0	Fatty Acid Metabolism	2.3.1.16	FALSE	acetyl-CoAacyltransferase(tetradecanoyl-CoA),p	[x] : C05259 + C00010 --> C00024 + C02593
R_SRC_C00711_c	0.34	SourceFlux	.	FALSE	. source flux	C00711[b] --> C00711[c]
R_EXCH_nh4_e	499.3	ExchangeFlux	.	TRUE	. exchange flux	C01342[e] <==> C01342[b]
R_FAOXC245225	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : C00010 + C00001 + C00003 + C00007 + tetpent3coa --> C00024 + clpndc

R_R04640	-1000	Histidine Metabolism	5.3.1.16	TRUE	N-(5'-Phospho-D-ribosylformimino)-5-amino-1-	[c] : C04896 <==> C04916
R_GALASE19ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : f1a + C00001 --> core6 + C00124
R_BAMPPALDOX	0	beta-Alanine Metabolism	1.2.1.3	FALSE	beta-Aminopropionaldehyde:NAD+oxidoreducta	[m] : bamppald + C00001 + C00003 --> C00099 + 2 C00080 + C00004
R_TYRTRSm	0	Tyrosine, Tryptophan and Phenyla	6.1.1.1	FALSE	tyrosyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C00787 + C00082 --> C00020 + C00013 + C02839
R_EXCH_C00007_	-500	ExchangeFlux	.	TRUE	. exchange flux	C00007[e] <==> C00007[b]
R_GNK	0	Alternate Carbon Metabolism	2.7.1.12	FALSE	gluconokinase	[c] : C00002 + C00257 --> C00345 + C00008 + C00080
R_G5SDym	0	Urea cycle/amino group Metabolis	1.2.1.41	FALSE	glutamate-5-semialdehydedehydrogenase(m)	[m] : C03287 + C00080 + C00005 --> C01165 + C00006 + C00009
R_RNDR2n	0	Nucleotide Salvage Pathway	1.17.4.1	FALSE	ribonucleoside-diphosphatereductase(GDP),nuc	[n] : C00035 + C00342 --> C00361 + C00001 + C00343
R_EXCH_C00266_	0	ExchangeFlux	.	TRUE	. exchange flux	C00266[c] <==> C00266[b]
R_SRC_C00229_c	0.0038	SourceFlux	.	FALSE	. source flux	C00229[b] --> C00229[c]
R_NACHEX22ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg41 --> C00140 + m2mn
R_UAGCVT	0	Cell Envelope Biosynthesis	2.5.1.7	FALSE	UDP-N-acetylglucosamine1-carboxyvinyltransfer	[c] : C00074 + C00043 --> C00009 + C04631
R_AGPRim	0	Urea cycle/amino group Metabolis	1.2.1.38	FALSE	N-acetyl-g-glutamyl-phosphatereductase,irrever	[m] : C04133 + C00080 + C00005 --> C01250 + C00006 + C00009
R_UDCPDP	0	Cell Envelope Biosynthesis	3.6.1.27	FALSE	undecaprenyl-diphosphatase	[c] : C00001 + C04574 --> C00080 + C00009 + C17556
R_a_D_glucoset	0	Transport Database	.	FALSE	a-D-glucosetransport	C00267[e] --> C00267[c]
R_CHTNASEe	0	Aminosugar Metabolism	3.2.1.14	FALSE	chitinase,extracellular	[e] : chtn + 2 C00001 --> 3 C00140
R_NACHEX7ly	0	Chondroitin Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : cs_d_deg5 + C00001 --> C01132 + cs_d_deg6
R_FAOXC205184	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : C00010 + C00001 + C00003 + tmndnccoa --> C00024 + C00080 + C00004
R_UDPGALM	0	Cell Envelope Biosynthesis	5.4.99.9	FALSE	UDPgalactopyranosemutase	[c] : C00052 --> C03733
R_NDPK3m	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:CDP),mitoch	[m] : C00002 + C00112 <==> C00008 + C00063
R_ncamt	0	Transport Database	.	FALSE	ncamtransport	C00153[e] --> C00153[c]
R_NDPK3n	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:CDP),nuclea	[n] : C00002 + C00112 <==> C00008 + C00063
R_pit	0.6031	Transport Database	.	FALSE	pitransport	C00009[e] --> C00009[c]
R_ribflvt	0.0038	Transport Database	.	FALSE	ribflvtransport	C00255[e] --> C00255[c]
R_PGCD	0.1022	Glycine, Serine, and Threonine Me	1.1.1.95	FALSE	phosphoglyceratedehydrogenase	[c] : C00197 + C00003 --> C03232 + C00080 + C00004
R_NACHEX26ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : 2 C00001 + ksii_core4_deg4 --> 2 C00140 + ksii_core2_deg5
R_ACYP_2	0	Carbohydrate Metabolism	3.6.1.7	FALSE	acylphosphatase(2)	[c] : C00227 + C00001 --> C00033 + C00080 + C00009
R_SRC_C00148_e	0.1049	SourceFlux	.	FALSE	. source flux	C00148[b] --> C00148[e]
R_R08165	0	Ubiquinone and other terpenoid-q	2.2.1.9	TRUE	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexe	[c] : C00885 + C00026 <==> C16519 + C00011
R_thr_Lt	0	Transport Database	.	FALSE	thr-Ltransport	C00188[e] --> C00188[c]
R_T2M26DCOAH	0	Limonene and pinene Degradation	4.2.1.17	TRUE	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA	[m] : C00001 + t2m26dcoa <==> 3h26dm5coa
R_GLYKr	-1000	Glycerolipid Metabolism	2.7.1.30	TRUE	glycerolkinase(reversible)	[c] : C00002 + C00116 <==> C00008 + C00623 + C00080
R_FBA5	0	Galactose Metabolism	4.1.2.13	TRUE	D-Tagatose1-phosphateD-glyceraldehyde-3-phos	[c] : tag1p-D <==> C00111 + C00577
R_MDHm	0	Citric Acid Cycle	1.1.1.37	TRUE	malatedehydrogenase,mitochondrial	[m] : C00711 + C00003 <==> C00080 + C00004 + C00036
R_ECOAH8p	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxyoctad	[x] : C16217 <==> C00001 + C16218
R_pydxt	0	Transport Database	.	FALSE	pydxtransport	C00250[e] --> C00250[c]
R_RNDR3n	0	Nucleotide Salvage Pathway	1.17.4.1	FALSE	ribonucleoside-diphosphatereductase(CDP),nucl	[n] : C00112 + C00342 --> C00705 + C00001 + C00343
R_GCC2cm	-1000	Glycine, Serine, and Threonine Me	1.8.1.4	TRUE	glycine-cleavagecomplex(lipoamide),mitochondri	[m] : C00579 + C00003 <==> C00080 + C15972 + C00004
R_MDHg	-1000	Glycolysis/Gluconeogenesis	1.1.1.37	TRUE	malatedehydrogenase,peroxisomal	[x] : C00711 + C00003 <==> C00080 + C00004 + C00036
R_PMPK	0	Cofactor and Prosthetic Group Bio	2.7.4.7	FALSE	phosphomethylpyrimidinekinase	[c] : C04556 + C00002 --> C04752 + C00008
R_OMPDC	0	Pyrimidine Biosynthesis	4.1.1.23	FALSE	orotidine-5'-phosphatedecarboxylase	[c] : C00080 + C01103 --> C00011 + C00105
R_T2M26DCOAH	0	Limonene and pinene Degradation	4.2.1.17	TRUE	trans-2-Methyl-5-isopropylhexa-2,5-dienoyl-CoA	[x] : C00001 + t2m26dcoa <==> 3h26dm5coa
R_MDHp	1000	Oxidative Phosphorylation	1.1.1.37	TRUE	malatedehydrogenase,peroxisomal	[x] : C00711 + C00003 <==> C00080 + C00004 + C00036
R_phemet	0	Transport Database	.	FALSE	phemetransport	C00032[e] --> C00032[c]
R_clt	0.0038	Transport Database	.	FALSE	cltransport	C00698[e] --> C00698[c]
R_PROD2m	0	Arginine and Proline Metabolism	1.5.99.8	FALSE	Prolinedehydrogenase(m)	[m] : C00016 + C00148 --> C03912 + C01352 + C00080
R_G1SATi	0	Cofactor and Prosthetic Group Bio	5.4.3.8	FALSE	glutamate-1-semialdehydeaminotransferase	[c] : C03741 --> C00430
R_ACOAD5	0	.	1.3.99.3	TRUE	acyl-CoAdehydrogenase(dodecanoyl-CoA)	[c] : ddcacoa + C00003 <==> dd2coa + C00080 + C00004
R_NACHEX14ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg19 --> C00140 + ksi_deg20
R_B_MANNASEly	0	N-Glycan Degradation	3.2.1.25	FALSE	beta-mannosidase,lysosomal	[l] : C00001 + mn --> C00140 + C00936
R_ECOAH1x	0	Tryptophan Metabolism	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxybutan	[x] : 3hbcoa <==> b2coa + C00001
R_ACOAD4	0	.	1.3.99.3	TRUE	acyl-CoAdehydrogenase(decanoyl-CoA)	[c] : dcacoa + C00003 <==> C05275 + C00080 + C00004
R_SRC_C00407_e	0.1376	SourceFlux	.	FALSE	. source flux	C00407[b] --> C00407[e]
R_ACOAD7	0	.	1.3.99.3	FALSE	acyl-CoAdehydrogenase(hexadecanoyl-CoA)	[c] : C00003 + C00154 --> C00080 + C05272 + C00004
R_SHK3D	1000	Tyrosine, Tryptophan and Phenyla	1.1.1.25	FALSE	shikimatedehydrogenase	[c] : C02637 + C00080 + C00005 --> C00006 + C00493
R_ECOAH1m	0	Tryptophan Metabolism	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxybutan	[m] : 3hbcoa <==> b2coa + C00001

R_FAOXC161802	0	Fatty Acid Activation	1.3.99.3	FALSE	Betaoxidationfattyacid	[m] : 4 C00010 + 3 C00016 + 4 C00001 + C05272 + 4 C00003 --> 4 C00024 + 3
R_ACOAD6	0	Fatty Acid Degradation	1.3.99.3	TRUE	acyl-CoAdehydrogenase(tetradecanoyl-CoA)	[c] : C00003 + C02593 <==> C00080 + C00004 + C05273
R_HACD5p	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxodecano	[x] : C05263 + C00080 + C00004 <==> C05262 + C00003
R_ME1	0.4964	Anaplerotic reactions	1.1.1.38	FALSE	malicenzyme(NAD)	[c] : C00711 + C00003 --> C00011 + C00004 + C00022
R_adnt	0	Transport Database	.	FALSE	adntransport	C00212[e] --> C00212[c]
R_BAMPPALDOX	0	beta-Alanine Metabolism	1.2.1.3	FALSE	beta-Aminopropionaldehyde:NAD+oxidoreducta	[c] : bamppald + C00001 + C00003 --> C00099 + 2 C00080 + C00004
R_SRC_C00059_e	0	SourceFlux	.	FALSE	. source flux	C00059[b] --> C00059[e]
R_malttrt	0	Transport Database	.	FALSE	malttrtransport	C01835[e] --> C01835[c]
R_PRMICIi	1000	Histidine Metabolism	5.3.1.16	FALSE	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamir	[c] : C04896 --> C04916
R_GLPASE2	0	Starch and Sucrose Metabolism	2.4.1.1	FALSE	glycogenphosphorylase(amyls->glc-D)	[c] : glygn3 + 7 C00001 --> tyr-ggn + 7 C00267
R_ACACT4r	0	Fatty Acid Degradation	2.3.1.16	TRUE	acetyl-CoAC-acyltransferase(octanoyl-CoA)(r)	[c] : C00024 + C01944 <==> C05265 + C00010
R_GLPASE1	0	Starch and Sucrose Metabolism	2.4.1.1	FALSE	glycogenphosphorylase(glygn2->dxtrn)	[c] : glygn2 + 3 C00009 --> dxtrn + 3 C00103
R_FAOXC170m	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid(oddchain)	[m] : 7 C00010 + 7 C00016 + 7 C00001 + hpdcacoa + 7 C00003 --> 7 C00024 +
R_IPPMIa	0	Valine, Leucine and Isoleucine Met	4.2.1.33	TRUE	3-isopropylmalatedehydratase	[c] : C04411 <==> C02631 + C00001
R_IPPMIb	0	Valine, Leucine and Isoleucine Met	4.2.1.33	TRUE	2-isopropylmalatehydratase	[c] : C02631 + C00001 <==> C02504
R_NDPK10	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dIDP)	[c] : C00002 + C01344 <==> C00008 + C01345
R_ECOAH12m	0	Valine, Leucine and Isoleucine Met	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxyisobu	[m] : C03460 + C00001 <==> C04047
R_GHMT2r	0	Glycine, Serine, and Threonine Me	2.1.2.1	TRUE	glycinehydroxymethyltransferase,reversible	[c] : C00716 + C00101 <==> C00037 + C00001 + C00143
R_HACDp	0	Fatty Acid Biosynthesis	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase	[x] : C00640 + C00003 <==> C00264 + C00080 + C00004
R_DAPE	0	Threonine and Lysine Metabolism	5.1.1.7	TRUE	diaminopimelateepimerase	[c] : C00666 <==> C00680
R_CDGGGS	0	Lipid and Cell Wall Metabolism	2.7.7.41	FALSE	CDP-2,3-di-O-geranylgeranyl-sn-glycerolsynthas	[c] : C00063 + dgggp + C00080 --> cdgggp + C00013
R_EXCH_co2_e	0	ExchangeFlux	.	TRUE	. exchange flux	C00011[e] <==> C00011[b]
R_HSERTA	0	Methionine Metabolism	2.3.1.31	TRUE	homoserineO-trans-acetylase	[c] : C00024 + C00263 <==> C01077 + C00010
R_NACHEX16ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg25 --> C00140 + ksi_deg26
R_TKT1	-0.2	Pentose Phosphate Pathway	2.2.1.1	TRUE	transketolase	[c] : C03736 + C00231 <==> C00118 + C05382
R_TKT2	-0.2	Pentose Phosphate Pathway	2.2.1.1	TRUE	transketolase	[c] : C00279 + C00231 <==> C05345 + C00118
R_AKGDbm	0	Citric Acid Cycle	2.3.1.61	FALSE	oxoglutaratedehydrogenase(dihydrolipoamideS-	[m] : C00010 + C16254 --> C00579 + C00091
R_sucrt	0	Transport Database	.	FALSE	sucrtransport	C00089[e] --> C00089[c]
R_SRC_C00001_e	0	SourceFlux	.	FALSE	. source flux	C00001[b] --> C00001[e]
R_DHAD1	0	Valine, Leucine and Isoleucine Met	4.2.1.9	FALSE	dihydroxy-aciddehydratase(2,3-dihydroxy-3-me	[c] : C04039 --> C00141 + C00001
R_HACD5	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxododeca	[c] : C05263 + C00080 + C00004 <==> C05262 + C00003
R_UPPDC2	0	Heme Biosynthesis	4.1.1.37	FALSE	uroporphyrinogendecarboxylase(uroporphyrino	[c] : 4 C00080 + C05766 --> 4 C00011 + C05768
R_UPPDC1	0	Heme Biosynthesis	4.1.1.37	FALSE	uroporphyrinogendecarboxylase(uroporphyrino	[c] : 4 C00080 + C01051 --> 4 C00011 + C03263
R_PPCOAOm	0	Propanoate Metabolism	1.3.99.3	FALSE	Propanoyl-CoA:FAD2,3-oxidoreductase,mitochor	[m] : C00016 + C00100 --> C01352 + prpncoa
R_EXCH_so4_e	-0.0038	ExchangeFlux	.	TRUE	. exchange flux	C00059[e] <==> C00059[b]
R_SADT	0	Nucleotides	2.7.7.4	FALSE	sulfateadenylyltransferase	[c] : C00002 + C00080 + C00059 --> C00224 + C00013
R_ADKd	0	Nucleotides	2.7.4.3	TRUE	adenylatekinase(dform)	[c] : C00360 + C00131 <==> 2 C00206
R_CYSTGL	0	Cysteine Metabolism	4.4.1.1	FALSE	cystathionineg-lyase	[c] : cyst-L + C00001 --> C00109 + C00097 + C01342
R_acact	0	Transport Database	.	FALSE	acactransport	C00164[c] --> C00164[e]
R_chsterolt	0	Transport Database	.	FALSE	chsteroltransport	C00187[e] --> C00187[c]
R_HSDyi	0	Glycine and Serine Metabolism	1.1.1.3	FALSE	homoserinedehydrogenase(NADP),irreversible	[c] : C00441 + C00080 + C00005 --> C00263 + C00006
R_EXCH_C00009_	0	ExchangeFlux	.	TRUE	. exchange flux	C00009[e] <==> C00009[b]
R_arg_Lt	0.1404	Transport Database	.	FALSE	arg-Ltransport	C00062[e] --> C00062[c]
R_EXCH_ac_c	0	ExchangeFlux	.	TRUE	. exchange flux	C00033[c] <==> C00033[b]
R_FAOXC240200	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : 2 C00010 + 2 C00001 + lgnccoa + 2 C00003 + 2 C00007 --> 2 C00024 + ar
R_spmdt	0	Transport Database	.	FALSE	spmdtransport	C00315[e] --> C00315[c]
R_HISTRSm	0	Histidine Metabolism	6.1.1.21	FALSE	histidyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C00135 + C01643 --> C00020 + C02988 + C00013
R_ATPSm	0	Oxidative Phosphorylation	3.6.3.14	FALSE	ATPsynthase,mitochondrial	C00008[m] + 3 C00080[c] + C00009[m] --> C00002[m] + C00001[m] + 2 C00
R_HXPRT	0.2	Salvage Pathway	2.4.2.8	FALSE	hypoxanthinephosphoribosyltransferase(Hypox	[c] : C00262 + C00119 --> C00130 + C00013
R_ACGSm	0	Urea cycle/amino group Metabolis	2.3.1.1	FALSE	N-acteylglutamatesynthase,mitochondrial	[m] : C00024 + C00025 --> C00624 + C00010 + C00080
R_ACOAD1	0	Fatty Acid Degradation	1.3.99.2	TRUE	acyl-CoAdehydrogenase(butanoyl-CoA)	[c] : b2coa + C00080 + C00004 <==> C00136 + C00003
R_ACOAD3	0	Fatty Acid Degradation	1.3.99.3	TRUE	acyl-CoAdehydrogenase(octanoyl-CoA)	[c] : C00003 + C01944 <==> C00080 + C00004 + C05276
R_MI1PP	0	Inositol Phosphate Metabolism	3.1.3.25	FALSE	myo-inositol1-phosphatase	[c] : C00001 + C01177 --> C00137 + C00009
R_NACHEX3ly	0	Chondroitin Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : cs_b_deg1 + C00001 --> C01132 + cs_b_deg2
R_HACD2	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxohexano	[c] : C05269 + C00080 + C00004 <==> C05268 + C00003
R_HACD3	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxooctanoy	[c] : C05267 + C00080 + C00004 <==> C05266 + C00003

R_HACD4	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxodecano	[c] : C05265 + C00080 + C00004 <==> 3hdcoa + C00003
R_NPHS	1000	Cofactor and Prosthetic Group Bio	4.1.3.36	FALSE	naphthoatesynthase	[c] : C03160 --> C00010 + C03657
R_HACD6	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxotetrade	[c] : C05261 + C00080 + C00004 <==> C05260 + C00003
R_CBPS	0	Pyrimidine Biosynthesis	6.3.5.5	FALSE	carbamoyl-phosphatesynthase(glutamine-hydro	[c] : 2 C00002 + C00064 + C00001 + C01353 --> 2 C00008 + C00169 + C00025
R_acetonet	0	Transport Database	.	FALSE	acetonetransport	C00207[c] --> C00207[e]
R_NTPP10	0	Nucleotides	3.6.1.19	FALSE	Nucleosidetriphosphatepyrophosphorylase(ditp	[c] : C01345 + C00001 --> C06196 + C00080 + C00013
R_strch2t	0	Transport Database	.	FALSE	strch2transport	C00369[e] --> C00369[c]
R_FAOXC260240	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : C00010 + C00001 + hexccoa + C00003 + C00007 --> C00024 + C00080 + C
R_ADK1	-1000	Nucleotides	2.7.4.3	TRUE	adenylatekinase	[c] : C00020 + C00002 <==> 2 C00008
R_RNDR2	0.0057	Nucleotides	1.17.4.1	FALSE	ribonucleoside-diphosphatereductase(GDP)	[c] : C00035 + C00342 --> C00361 + C00001 + C00343
R_PTPATim	0	Pantothenate and CoA Biosynthesi	2.7.7.3	FALSE	pantetheine-phosphateadenylyltransferase	[m] : C00002 + C00080 + C01134 --> C00882 + C00013
R_ADK2	999.93	Nucleotide Metabolism	2.7.4.3	TRUE	adenylatekinase(Inorganictriphosphate)	[c] : C00020 + C00536 <==> C00008 + C00013
R_PYLALDOXm	0	Limonene and pinene Degradation	1.2.1.3	FALSE	Perillylaldehyde:NAD+oxidoreductase(m)	[m] : C00001 + C00003 + pylald --> 2 C00080 + C00004 + peracd
R_trp_Lt	0.0269	Transport Database	.	FALSE	trp-Ltransport	C00078[e] --> C00078[c]
R_EXCH_o2_e	0	ExchangeFlux	.	TRUE	. exchange flux	C00007[e] <==> C00007[b]
R_RNDR1	0.0057	Nucleotides	1.17.4.1	FALSE	ribonucleoside-diphosphatereductase(ADP)	[c] : C00008 + C00342 --> C00206 + C00001 + C00343
R_SRC_C00041_e	0.2436	SourceFlux	.	FALSE	. source flux	C00041[b] --> C00041[e]
R_RPE	-0.4	Pentose Phosphate Pathway	5.1.3.1	TRUE	ribulose5-phosphate3-epimerase	[c] : C00199 <==> C00231
R_NNAT	1000	NAD Metabolism	2.7.7.18	FALSE	nicotinate-nucleotideadenylyltransferase	[c] : C00002 + C00080 + C01185 --> C00857 + C00013
R_GALASE18ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksii_core2_deg8 --> C00124 + ksii_core2_deg9
R_CELBpts	0	.	.	FALSE	.	[c] : C00074 + C00185 --> C04534 + C00022
R_GLB1	0	Sphingolipid Metabolism	3.2.1.23	FALSE	Beta-galactosidase	[l] : galgluside_hs + C00001 --> C00124 + gluside_hs
R_BETALDHx	0	Glycine, Serine, and Threonine Me	1.2.1.8	FALSE	betaine-aldehydedehydrogenase	[c] : C00576 + C00001 + C00003 --> C00719 + 2 C00080 + C00004
R_ACS	0	Glycolysis/Gluconeogenesis	6.2.1.1	FALSE	acetyl-CoAsynthetase	[c] : C00033 + C00002 + C00010 --> C00024 + C00020 + C00013
R_SELCYSTS	0	Selenoamino Acid Metabolism	4.2.1.22	FALSE	selanocystathioninebeta-synthase	[c] : selhcys + C00716 --> C00001 + selcyst
R_SRC_C00025_e	500.27	SourceFlux	.	FALSE	. source flux	C00025[b] --> C00025[e]
R_AMID2	0	Tyrosine, Tryptophan and Phenyla	3.5.1.4	FALSE	amidase	[c] : C00001 + C02505 --> C01342 + C07086
R_EXCH_C00185_	0	ExchangeFlux	.	TRUE	. exchange flux	C00185[e] <==> C00185[b]
R_NACHEX15ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg22 --> C00140 + ksi_deg23
R_NACHEX1ly	0	Chondroitin Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : cs_a_deg1 + C00001 --> C01132 + cs_a_deg2
R_EXCH_C00711_	-0.0983	ExchangeFlux	.	TRUE	. exchange flux	C00711[c] <==> C00711[b]
R_ALAD_L	0	Amino Acid Degradation	1.4.1.1	FALSE	L-alaninedehydrogenase	[c] : C00041 + C00001 + C00003 --> C00080 + C00004 + C01342 + C00022
R_GALASE15ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg40 --> C00124 + ksi_deg41
R_FAOXC200180	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : arachcoa + C00010 + C00016 + C00001 + C00003 --> C00024 + C01352 +
R_NAPRTr	-1000	NAD Biosynthesis	2.4.2.11	TRUE	NAPRTase(rev)	[c] : C00080 + C11486 + C00119 <==> C01185 + C00013
R_NDPK7n	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dCDP),nucle	[n] : C00002 + C00705 <==> C00008 + C00458
R_GALASE10ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg26 --> C00124 + ksi_deg27
R_ECOAH4p	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxydecan	[x] : 3hdcoa <==> C05275 + C00001
R_MMEm	0	Valine, Leucine and Isoleucine Met	5.1.99.1	TRUE	methylmalonyl-CoAepimerase/racemase	[m] : C01213 <==> C00683
R_AHC	-1000	Methionine Metabolism	3.3.1.1	TRUE	adenosylhomocysteinase	[c] : C00021 + C00001 <==> C00212 + C05330
R_AMID5	0	Others	3.5.1.4	FALSE	amidase	[c] : C01659 + C00001 --> C00511 + C01342
R_DASYN_SC	0	Phospholipid Biosynthesis	2.7.7.41	TRUE	CDP-Diacylglycerolsynthetase,yeast-specific	[c] : C00063 + C00080 + 0.01 C00416 <==> 0.01 cdpdag_sc + C00013
R_PFK_2	0	Alternate Carbon Metabolism	2.7.1.11	FALSE	Phosphofructokinase	[c] : C00002 + C01097 --> C00008 + C00080 + C03785
R_DASYN_SA	0	Lipid and Cell Wall Metabolism	2.7.7.41	TRUE	CDP-Diacylglycerolsynthetase(Saureus)	[c] : C00063 + C00080 + 0.02 pa_sa <==> 0.02 cdpdag_sa + C00013
R_HACD8p	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxooctaded	[x] : C16216 + C00080 + C00004 <==> C16217 + C00003
R_ptrct	0	Transport Database	.	FALSE	ptrctransport	C00134[e] --> C00134[c]
R_glu_Lt	500.27	Transport Database	.	FALSE	glu-Ltransport	C00025[e] --> C00025[c]
R_UDPG4E	-0.1373	Galactose Metabolism	5.1.3.2	TRUE	UDPglucose4-epimerase	[c] : C00029 <==> C00052
R_FAOXC181160	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationfattyacid	[m] : 5 C00010 + 4 C00016 + 5 C00001 + 5 C00003 + vacccoa --> 5 C00024 + 4
R_MALTAT	0	.	2.3.1.79	FALSE	maltoseO-acetyltransferase	[c] : C00024 + C00208 --> C02130 + C00010
R_DCTPD	0	Nucleotide Salvage Pathway	3.5.4.13	FALSE	dCTPdeaminase	[c] : C00458 + C00080 + C00001 --> C00460 + C01342
R_ACKr	0	Pyruvate Metabolism	2.7.2.1	TRUE	acetatekinase	[c] : C00033 + C00002 <==> C00227 + C00008
R_CYSTRS	0	Cysteine Metabolism	6.1.1.16	FALSE	Cysteinyl-tRNAsynthetase	[c] : C00002 + C00097 + C01639 --> C00020 + C03125 + C00013
R_NACHEX9ly	0	Chondroitin Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : cs_e_deg6 + C00001 --> C01132 + cs_e_deg7
R_val_Lt	0.2005	Transport Database	.	FALSE	val-Ltransport	C00183[e] --> C00183[c]
R_ADPT	0	Salvage Pathway	2.4.2.7	FALSE	adeninephosphoribosyltransferase	[c] : C00147 + C00119 --> C00020 + C00013

R_dribt	0	Transport Database	.	FALSE	dribtransport	C01801[e] --> C01801[c]
R_DHORD4	-1000	Purine and Pyrimidine Biosynthes	1.3.3.1	TRUE	dihydooroticacid(ubiquinone-6)	C00337[c] + C17568[m] <==> C00295[c] + C00390[m]
R_FBA	0	Glycolysis/Gluconeogenesis	4.1.2.13	TRUE	fructose-bisphosphatealdolase	[c] : C00354 <==> C00111 + C00118
R_DHORD2	0	Purine and Pyrimidine Biosynthes	1.3.3.1	FALSE	dihydooroticaciddehydrogenase(quinone8)	[c] : C00337 + C17569 --> C00295 + C00390
R_DPCOAKm	0	Pantothenate and CoA Biosynthesi	2.7.1.24	FALSE	dephospho-CoAkinase,mitochondrial	[m] : C00002 + C00882 --> C00008 + C00010 + C00080
R_GLYK	1000	Glycerophospholipid Metabolism	2.7.1.30	FALSE	glycerolkinase	[c] : C00002 + C00116 --> C00008 + C00623 + C00080
R_HISTP	0	Histidine Metabolism	3.1.3.15	FALSE	histidinol-phosphatase	[c] : C00001 + C01100 --> C00860 + C00009
R_FAOXC226	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[m] : c226coa + 10 C00010 + 4 C00016 + 10 C00001 + 10 C00003 --> 11 C000
R_NACHEX12ly	0	Keratan Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : C00001 + ksi_deg13 --> C00140 + ksi_deg14
R_EXCH_h_c	999.53	ExchangeFlux	.	TRUE	. exchange flux	C00080[c] <==> C00080[b]
R_PNTK	0	CoA Biosynthesis	2.7.1.33	FALSE	pantothenatekinase	[c] : C00002 + C00864 --> C03492 + C00008 + C00080
R_TRPO2	0	Tryptophan Metabolism	1.13.11.11	FALSE	L-Tryptophan:oxygen2,3-oxidoreductase(decycli	[c] : C00007 + C00078 --> C02700
R_ca2t	0.0038	Transport Database	.	FALSE	ca2transport	C00076[e] --> C00076[c]
R_HACD1x	0	Tryptophan Metabolism	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(acetoacetyl-C	[x] : C00332 + C00080 + C00004 <==> 3hbcoa + C00003
R_cys_Lt	0.0433	Transport Database	.	FALSE	cys-Ltransport	C00097[e] --> C00097[c]
R_SRC_C00698_e	0.0038	SourceFlux	.	FALSE	. source flux	C00698[b] --> C00698[e]
R_ME1m	0	Pyruvate Metabolism	1.1.1.38	FALSE	malicenzyme(NAD),mitochondrial	[m] : C00711 + C00003 --> C00011 + C00004 + C00022
R_HISTD	0	Histidine Metabolism	1.1.1.23	FALSE	histidinoldehydrogenase	[c] : C00001 + C00860 + 2 C00003 --> 3 C00080 + C00135 + 2 C00004
R_LEUTRSm	0	Valine, Leucine and Isoleucine Met	6.1.1.4	FALSE	leucyl-tRNAsynthetase,mitochondrial	[m] : C00002 + C00123 + C01645 --> C00020 + C02047 + C00013
R_DHPS	0	Folate Biosynthesis	2.5.1.15	FALSE	dihydropteroatesynthase	[c] : 2ahhmp + C00568 --> C00921 + C00001
R_ACACT4p	0	Fatty Acid Metabolism	2.3.1.16	FALSE	acetyl-CoAC-acetyltransferase(octanoyl-CoA),pe	[x] : C05265 + C00010 --> C00024 + C01944
R_EXCH_C00059_	0	ExchangeFlux	.	TRUE	. exchange flux	C00059[e] <==> C00059[b]
R_HACD1m	0	Tryptophan Metabolism	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(acetoacetyl-C	[m] : C00332 + C00080 + C00004 <==> 3hbcoa + C00003
R_PMANM	0	Fructose and Mannose Metabolism	5.4.2.8	TRUE	phosphomannomutase	[c] : C00636 <==> C00275
R_TYRTRS	0	Tyrosine, Tryptophan and Phenyla	6.1.1.1	FALSE	tyrosyl-tRNAsynthetase	[c] : C00002 + C00787 + C00082 --> C00020 + C00013 + C02839
R_acaldt	0	Transport Database	.	FALSE	acaldtransport	C00084[c] --> C00084[e]
R_glyt	0.2903	Transport Database	.	FALSE	glytransport	C00037[e] --> C00037[c]
R_PGLer	0	Pentose Phosphate Pathway	3.1.1.31	FALSE	6-phosphogluconolactonase,endoplasmicreticulu	[r] : C01236 + C00001 --> C00345 + C00080
R_FAOXC182806	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationoffattyacid	[m] : 5 C00010 + 3 C00016 + 5 C00001 + lnlccoa + 5 C00003 --> 5 C00024 + 3
R_CAT2p	0	Glycolysis/Gluconeogenesis	1.11.1.6	FALSE	catalaseA,peroxisomal(ethanol)	[x] : C00469 + C00027 --> C00084 + 2 C00001
R_PRAGSr	-1000	IMP Biosynthesis	6.3.4.13	TRUE	phosphoribosylglycinamidesynthase	[c] : C00002 + C00037 + C03090 <==> C00008 + C03838 + C00080 + C00009
R_ACYP	0	Glycolysis/Gluconeogenesis	3.6.1.7	FALSE	acylphosphatase	[c] : C00236 + C00001 --> C00197 + C00080 + C00009
R_PSD_SA	0	Lipid and Cell Wall Metabolism	4.1.1.65	FALSE	Phosphatidylserinedecarboxylase(Saureus)	[c] : C00080 + 0.02 ps_sa --> C00011 + 0.02 pe_sa
R_P5CRx	0	Urea cycle/amino group Metabolis	1.5.1.2	FALSE	pyrroline-5-carboxylatereductase	[c] : C03912 + 2 C00080 + C00004 --> C00003 + C00148
R_ACACT10m	0	Valine, Leucine and Isoleucine Met	2.3.1.9	TRUE	acetyl-CoAC-acetyltransferase,mitochondrial	[m] : C03344 + C00010 <==> C00024 + C00100
R_LYSTRS	0	Threonine and Lysine Metabolism	6.1.1.6	FALSE	Lysyl-tRNAsynthetase	[c] : C00002 + C00047 + C01646 --> C00020 + C01646 + C00013
R_ureat	0	Transport Database	.	FALSE	ureatransport	C00086[c] --> C00086[e]
R_PRAGS	1000	Purine and Pyrimidine Biosynthes	6.3.4.13	FALSE	phosphoribosylglycinamidesynthetase	[c] : C00002 + C00037 + C03090 --> C00008 + C03838 + C00080 + C00009
R_o2t	500	Transport Database	.	FALSE	o2transport	C00007[e] --> C00007[c]
R_ACACT9p	0	Fatty Acid Metabolism	2.3.1.16	FALSE	acetyl-CoAacyltransferase(tetracosanoyl-CoA),pe	[x] : 3ohxccoa + C00010 --> C00024 + C16529
R_FAOXC200180	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : arachcoa + C00010 + C00001 + C00003 + C00007 --> C00024 + C00080 +
R_AMALT2	0	Alternate Carbon Metabolism	2.4.1.25	FALSE	Amylomaltase(maltotetraose)	[c] : C00208 + C02052 --> C00267 + C06218
R_adet	0	Transport Database	.	FALSE	adetransport	C00147[e] --> C00147[c]
R_AMALT4	0	Alternate Carbon Metabolism	2.4.1.25	FALSE	Amylomaltase(maltohexaose)	[c] : C00208 + C01936 --> C00267 + C06216
R_CYSLYSL	0	Cysteine Metabolism	4.4.1.1	FALSE	L-CystineLysteine-lyase(deaminating)	[c] : lcystin + C00001 --> C01342 + C00022 + thcys
R_GALASE14ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg38 --> C00124 + ksi_deg39
R_hxant	0.2	Transport Database	.	FALSE	hxantransport	C00262[e] --> C00262[c]
R_PPAer	0	Miscellaneous	3.6.1.1	FALSE	inorganicdiphosphatase,endoplasmicreticulum	[r] : C00001 + C00013 --> C00080 + 2 C00009
R_strch1t	0	Transport Database	.	FALSE	strch1transport	C00369[e] --> C00369[c]
R_DHORD5	0	Purine and Pyrimidine Biosynthes	1.3.3.1	FALSE	dihydrooroticacid(menaquinone-8)	[c] : C00337 + C00828 --> C05819 + C00295
R_HSDy	999.88	Threonine and Lysine Metabolism	1.1.1.3	TRUE	homoserinedehydrogenase(NADPH)	[c] : C00263 + C00006 <==> C00441 + C00080 + C00005
R_fmnt	0	Transport Database	.	FALSE	fmntransport	C00061[e] --> C00061[c]
R_ascb_Lt	0	Transport Database	.	FALSE	ascb-Ltransport	C00072[e] --> C00072[c]
R_CBIAT	0	Vitamins and Cofactor Biosynthesi	2.5.1.17	TRUE	Cobinamideadenyltransferase	[c] : C00002 + C05774 + C00080 <==> C06508 + C00536
R_PSERDm_SC	0	Phospholipid Biosynthesis	4.1.1.65	FALSE	phosphatidylserinedecarboxylase,yeast-specific,	[m] : C00080 + 0.01 ps_sc --> C00011 + 0.01 pe_sc
R_SRC_C00073_e	0.0766	SourceFlux	.	FALSE	. source flux	C00073[b] --> C00073[e]

R_tyr_Lt	0.0654	Transport Database	.	FALSE	tyr-Ltransport	C00082[e] --> C00082[c]
R_NDPK9m	-1000	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:IDP),mitoch	[m] : C00002 + C00104 <==> C00008 + C00081
R_PEPCK	999.81	Glycolysis/Gluconeogenesis	4.1.1.32	FALSE	Phosphoenolpyruvatecarboxykinase(GTP)	[c] : C00044 + C00036 --> C00011 + C00035 + C00074
R_PTPAT	-1000	CoA Biosynthesis	2.7.7.3	TRUE	pantetheine-phosphateadenylyltransferase	[c] : C00002 + C00080 + C01134 <==> C00882 + C00013
R_HSDxi	1000	Glycine and Serine Metabolism	1.1.1.3	FALSE	homoserinedehydrogenase(NADH),irreversible	[c] : C00441 + C00080 + C00004 --> C00263 + C00003
R_PRASCS	0	IMP Biosynthesis	6.3.2.6	TRUE	phosphoribosylaminoimidazolesuccinocarboxan	[c] : C04751 + C00049 + C00002 <==> C04823 + C00008 + C00080 + C00009
R_CDS	0	Glycerophospholipid Metabolism	2.7.7.41	FALSE	phosphatidatecytidylyltransferase	[c] : C00063 + C00080 + pa_hs --> cdpdag_hs + C00013
R_XYLI2i	0	Alternate Carbon Metabolism	5.3.1.5	FALSE	xyloseisomerase	[c] : C10906 --> C00267
R_PRFGS	0	IMP Biosynthesis	6.3.5.3	FALSE	phosphoribosylformylglycinamidinesynthase	[c] : C00002 + C04376 + C00064 + C00001 --> C00008 + C04640 + C00025 + C
R_ECOAH2	0	Fatty Acid Degradation	4.2.1.17	TRUE	3-hydroxyacyl-CoAdehydratase(3-hydroxyhexan	[c] : C05268 <==> C00001 + C05271
R_FAOXC181160	0	Fatty Acid Oxidation	1.3.99.3	FALSE	Betaoxidationfattyacid	[m] : 5 C00010 + 4 C00016 + 5 C00001 + 5 C00003 + C16218 --> 5 C00024 + 4
R_GAPDg	0	Glycolysis/Gluconeogenesis	1.2.1.12	TRUE	glyceraldehyde-3-phosphatedehydrogenase,glyc	[x] : C00118 + C00003 + C00009 <==> C00236 + C00080 + C00004
R_FAOXC180x	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : C00010 + C00001 + C00003 + C00007 + C00412 --> C00024 + C00080 + C
R_etoht	0	Transport Database	.	FALSE	etohtransport	C00469[c] --> C00469[e]
R_NABTNOm	0	Arginine and Proline Metabolism	1.2.1.3	FALSE	N4-Acetylaminobutanal:NAD+oxidoreductase(m	[m] : C00001 + C05936 + C00003 --> C02946 + 2 C00080 + C00004
R_ALAALAr	0	Cell Envelope Biosynthesis	6.3.2.4	TRUE	D-alanine-D-alanineligase(reversible)	[c] : 2 C00133 + C00002 <==> C00008 + C00993 + C00080 + C00009
R_CPC4MT	0	Vitamins and Cofactor Biosynthesi	2.1.1.133	FALSE	precorrin-4C11-methyltransferase	[c] : C00019 + C11540 --> C00021 + C11541 + C00080
R_ESC_C00033_c	0	EscapeFlux	.	FALSE	. escape flux	C00033[c] --> C00033[b]
R_CHTNASE	0	Aminosugar Metabolism	3.2.1.14	FALSE	chitinase	[c] : chtn + 2 C00001 --> 3 C00140
R_ACACT1x	0	Cholesterol Metabolism	2.3.1.9	FALSE	acetyl-CoAC-acetyltransferase,mitochondrial	[x] : 2 C00024 --> C00332 + C00010
R_SRC_C17556_c	0.0451	SourceFlux	.	FALSE	. source flux	C17556[b] --> C17556[c]
R_ornt	0	Transport Database	.	FALSE	orntransport	C00077[e] --> C00077[c]
R_GLNS	0.2323	Glutamate Metabolism	6.3.1.2	FALSE	glutaminesynthetase	[c] : C00002 + C00025 + C01342 --> C00008 + C00064 + C00080 + C00009
R_GALASE5ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : C00001 + ksi_deg11 --> C00124 + ksi_deg12
R_PNP	0	NAD Metabolism	2.4.2.1	TRUE	purine-nucleosidephosphorylase	[c] : C00009 + C03150 <==> C00080 + C00153 + C00620
R_sprmt	0	Transport Database	.	FALSE	sprmtransport	C00750[e] --> C00750[c]
R_NACHEX5ly	0	Chondroitin Sulfate Degradation	3.2.1.52	FALSE	beta-N-acetylhexosaminidase,lysosomal	[l] : cs_c_deg4 + C00001 --> C01132 + cs_c_deg5
R_ARGTRSm	0	Arginine and Proline Metabolism	6.1.1.19	FALSE	Arginyl-tRNAsynthetase,mitochondrial	[m] : C00062 + C00002 + C01636 --> C00020 + C02163 + C00013
R_maltt	0	Transport Database	.	FALSE	malttransport	C00208[e] --> C00208[c]
R_PSP_D	0	Glycine and Serine Biosynthesis	3.1.3.3	FALSE	phosphoserinephosphatase(D-serine)	[c] : C00001 + C02532 --> C00009 + C00740
R_DOLPMTcer	0	Glycoprotein Metabolism	2.4.1.83	FALSE	Dolichyl-phosphateD-mannosyltransferase	C00110[c] + C00096[c] --> C03862[r] + C00035[c]
R_ITCOALm	0	C5-Branched dibasic Acid Metabol	6.2.1.5	TRUE	Itaconate--CoAligase(ADP-forming),mitochondri	[m] : C00002 + C00010 + C00490 <==> C00008 + C00531 + C00009
R_ARGSS	0	Alanine and Aspartate Metabolism	6.3.4.5	FALSE	argininosuccinatesynthase	[c] : C00049 + C00002 + C00327 --> C00020 + C03406 + C00080 + C00013
R_NBAH	0	.	3.5.1.32	TRUE	N-Benzoylglycineamidohydrolase	[c] : C01586 + C00001 <==> C00180 + C00037
R_b_D_glucoset	0	Transport Database	.	FALSE	b-D-glucosetransport	C00221[e] --> C00221[c]
R_ARGSL	-1000	Alanine and Aspartate Metabolism	4.3.2.1	TRUE	argininosuccinatelyase	[c] : C03406 <==> C00062 + C00122
R_LYSAM	0	Threonine and Lysine Metabolism	5.4.3.2	TRUE	lysine2,3-aminomutase	[c] : C00047 <==> C01142
R_ILETA	0	Valine, Leucine and Isoleucine Met	2.6.1.42	TRUE	isoleucinetransaminase	[c] : C00026 + C00407 <==> C03465 + C00025
R_AMALT3	0	Alternate Carbon Metabolism	2.4.1.25	FALSE	Amylomaltase(maltopentaose)	[c] : C00208 + C06218 --> C00267 + C01936
R_NADS1m	0	NAD Biosynthesis	6.3.1.5	FALSE	NADsynthase(nh3),mitochondrial	[m] : C00002 + C00857 + C01342 --> C00020 + C00080 + C00003 + C00013
R_PGM	0.3022	Glycolysis/Gluconeogenesis	5.4.2.1	TRUE	phosphoglyceratemutase	[c] : C00631 <==> C00197
R_R02110	-0.1373	Starch and Sucrose Metabolism	2.4.1.18	TRUE	1,4-alpha-D-Glucan:1,4-alpha-D-glucan 6-alpha-I	[c] : C00718 <==> strch2_strch1
R_FAOXC241181	0	Fatty Acid Oxidation, peroxisome	1.3.99.3	FALSE	Betaoxidationoflongchainfattyacid	[x] : 3 C00010 + 3 C00001 + 3 C00003 + nrvnccoa + 3 C00007 --> 3 C00024 + 3
R_GCC2am	0	Glycine, Serine, and Threonine Me	1.4.4.2	TRUE	glycine-cleavagecomplex(lipoamide),mitochondri	[m] : C00037 + C00080 + C15972 <==> alpam + C00011
R_celluloset	0	Transport Database	.	FALSE	cellulosetransport	C00760[e] --> C00760[c]
R_CYSTS	0	Methionine Metabolism	4.2.1.22	FALSE	cystathioninebeta-synthase	[c] : C05330 + C00716 --> cyst-L + C00001
R_HACD4p	0	Fatty Acid Degradation	1.1.1.35	TRUE	3-hydroxyacyl-CoAdehydrogenase(3-oxodecanoy	[x] : C05265 + C00080 + C00004 <==> 3hdcoa + C00003
R_PROD2	0	Arginine and Proline Metabolism	1.5.99.8	FALSE	Prolinedehydrogenase	[c] : C00016 + C00148 --> C03912 + C01352 + C00080
R_ACOAD1fm	0	Butanoate Metabolism	1.3.99.2	FALSE	acyl-CoAdehydrogenase(butanoyl-CoA),mitocho	[m] : C00136 + C00016 --> b2coa + C01352
R_GALASE20ly	0	Keratan Sulfate Degradation	3.2.1.23	FALSE	beta-galactosidase,lysosomal	[l] : 2 C00001 + ksii_core4_deg2 --> 2 C00124 + ksii_core4_deg3
R_HISTRS	0	Histidine Metabolism	6.1.1.21	FALSE	Histidyl-tRNAsynthetase	[c] : C00002 + C00135 + C01643 --> C00020 + C02988 + C00013
R_GTPCIn	0	Tetrahydrobiopterin	3.5.4.16	FALSE	GTPcyclohydrolaseI,nuclear	[n] : C00044 + C00001 --> C04895 + C00058 + C00080
R_ESC_C00001_e	0	EscapeFlux	.	FALSE	. escape flux	C00001[e] --> C00001[b]
R_ADA	0	Purine Catabolism	3.5.4.4	FALSE	Adenosinedeaminase	[c] : C00212 + C00080 + C00001 --> C00294 + C01342
R_THRTRS	0	Threonine and Lysine Metabolism	6.1.1.3	FALSE	Threonyl-tRNAsynthetase	[c] : C00002 + C00188 + C01651 --> C00020 + C00013 + C02992
R_gln_Lt	0	Transport Database	.	FALSE	gln-Ltransport	C00064[e] --> C00064[c]

R_SRC_C00037_e	0.2903	SourceFlux	.	FALSE	. source flux	C00037[b] --> C00037[e]
R_FOLD3m	0	Folate Metabolism	2.5.1.15	FALSE	dihydropteroatesynthase,mitochondrial	[m] : 2ahhmd + C00568 --> C00921 + C00013
R_LACZly	0	Galactose Metabolism	3.2.1.23	FALSE	b-galactosidase,lysosomal	[l] : C00001 + C00243 --> C00124 + C00267
R_PPA	0	Oxidative Phosphorylation	3.6.1.1	FALSE	inorganicdiphosphatase	[c] : C00001 + C00013 --> C00080 + 2 C00009
R_G6PDH2r	999.6	Pentose Phosphate Pathway	1.1.1.49	TRUE	glucose6-phosphatedehydrogenase	[c] : C00668 + C00006 <==> C01236 + C00080 + C00005
R_GLYCLm	0	Glycine and Serine Metabolism	2.1.2.10	FALSE	glycinecleavagesystem,mitochondrial	[m] : C00037 + C00003 + C00101 --> C00011 + C00143 + C00004 + C01342
R_HPPKm	0	Folate Metabolism	2.7.6.3	FALSE	2-amino-4-hydroxy-6-hydroxymethyldihydropte	[m] : 2ahhmp + C00002 --> 2ahhmd + C00020 + C00080
R_coat	0.0038	Transport Database	.	FALSE	coatransport	C00010[e] --> C00010[c]
R_MCOATA	0	Fatty Acid Metabolism	2.3.1.39	TRUE	Malonyl-CoA-ACPtransacylase	[c] : C00229 + C00083 <==> C00010 + C01209
R_KARA2im	0	Valine, Leucine and Isoleucine Met	1.1.1.86	FALSE	ketol-acidreductoisomerase(2-Aceto-2-hydroxyb	[m] : C00659 + C00080 + C00005 --> C04104 + C00006
R_EXCH_C00469_	0	ExchangeFlux	.	TRUE	. exchange flux	C00469[c] <==> C00469[b]
R_XYLI1	0	Alternate Carbon Metabolism	5.3.1.5	TRUE	xyloseisomerase	[c] : C01394 <==> C00310
R_ni2t	0	Transport Database	.	FALSE	ni2transport	C00291[e] --> C00291[c]
R_DASYN_HP	0	Glycerolipid Synthesis	2.7.7.41	TRUE	CDP-DiacylglycerolsynthetaseHpspecific	[c] : C00063 + C00080 + pa_hp <==> cdpdag_hp + C00013
R_R03508	0	Phenylalanine, tyrosine and tryptc	4.1.1.48	TRUE	1-(2-Carboxyphenylamino)-1-deoxy-D-ribulose-	[c] : C01302 <==> C03506 + C00011 + C00001
R_PPDK	999.53	Central Metabolism	2.7.9.1	FALSE	Pyruvate,phosphatedikinase.	[c] : C00002 + C00009 + C00022 --> C00020 + C00080 + C00074 + C00013
R_CYOOm3	0	Oxidative Phosphorylation	1.9.3.1	FALSE	cytochromecoxidase,mitochondrialComplexIV	4 C01071[m] + 7.92 C00080[m] + C00007[m] --> 4 C01070[m] + 4 C00080[c]
R_SRC_C00042_c	499.98	SourceFlux	.	FALSE	. source flux	C00042[b] --> C00042[c]
R_GARFT	-1000	IMP Biosynthesis	2.1.2.2	TRUE	phosphoribosylglycinamideformyltransferase	[c] : C00234 + C03838 <==> C04376 + C00080 + C00101
R_NDPK7m	0	Nucleotides	2.7.4.6	TRUE	nucleoside-diphosphatekinase(ATP:dCDP),mitoc	[m] : C00002 + C00705 <==> C00008 + C00458
R_PHETRS	0	Tyrosine, Tryptophan and Phenyla	6.1.1.20	FALSE	Phenylalanyl-tRNAsynthetase	[c] : C00002 + C00079 + C01648 --> C00020 + C03511 + C00013
R_PRATPP	0	Histidine Metabolism	3.6.1.31	FALSE	phosphoribosyl-ATPpyrophosphatase	[c] : C00001 + C02739 --> C00080 + C00013 + C02741
R_act	0	Transport Database	.	TRUE	actransport	C00033[c] <==> C00033[e]
R_PRAIS	0	IMP Biosynthesis	6.3.3.1	FALSE	phosphoribosylaminoimidazolesynthase	[c] : C00002 + C04640 --> C00008 + C03373 + 2 C00080 + C00009
R_AGDC	1000	Aminosugar Metabolism	3.5.1.25	FALSE	N-acetylglucosamine-6-phosphatedeacetylase	[c] : C00357 + C00001 --> C00033 + C00352
R_SUCD2_u6m	0	Citric Acid Cycle	1.3.5.1	TRUE	succinatedehydrogenase(ubiquinone-6),mitocho	[m] : C17568 + C00042 <==> C00122 + C00390
R_SRC_C00364_c	0.0057	SourceFlux	.	FALSE	. source flux	C00364[b] --> C00364[c]
R_TRPS1	0	Tyrosine, Tryptophan and Phenyla	4.2.1.20	FALSE	tryptophansynthase(indoleglycerolphosphate)	[c] : C03506 + C00716 --> C00118 + C00001 + C00078

Appendix - B - Tfu_v2+MILP Vs Tfu_v3 Flux Comparison

Rxn ID	Description	Reversible	Pathway	EC Number	yaml Flux	MILP Flux	Tfu_v3 Flux	Reaction
R_R05449	.	TRUE	1,4-Dichlorobenzene degradation	1.14.13.-	0	0		[c] : C07098 + 2 C00004 + C00007 <==> C07097 + 2 C00003 + C01328 + C00698
R_R05448	.	TRUE	1,4-Dichlorobenzene degradation	1.14.13.-	0	0		[c] : C07096 + C00007 + C00004 + C00080 <==> C07097 + C00003 + C00001
R_R06917	alcohol:NAD+ oxidoreductase	TRUE	1- and 2-Methylnaphthalene degrada	1.1.1.1	0	0		[c] : C14089 + C00003 <==> C14090 + C00004 + C00080
R_R06927	alcohol:NAD+ oxidoreductase	TRUE	1- and 2-Methylnaphthalene degrada	1.1.1.1	0	0		[c] : C02909 + C00003 <==> C14099 + C00004 + C00080
R_R06926	.	TRUE	1- and 2-Methylnaphthalene degrada	1.14.13.-	0	0		[c] : C14098 + C00007 + C00004 + C00080 <==> C02909 + C00003 + C00001
R_R06916	.	TRUE	1- and 2-Methylnaphthalene degrada	1.14.13.-	0	0		[c] : C14082 + C00007 + C00004 + C00080 <==> C14089 + C00003 + C00001
R_R06905	.	TRUE	1- and 2-Methylnaphthalene degrada	1.3.99.-	0	0		[c] : C14116 <==> C14117 + 2 C00080
R_R05234	.	TRUE	3-Chloroacrylic acid degradation	1.1.1.1	0	0		[c] : C06612 <==> C16348 + 2 C00080
R_R05233	.	TRUE	3-Chloroacrylic acid degradation	1.1.1.1	0	0		[c] : C06611 <==> C06613 + 2 C00080
R_R05238	.	TRUE	3-Chloroacrylic acid degradation	1.2.1.3	0	0		[c] : C16348 + C00001 <==> C06615 + 2 C00080
R_R05237	.	TRUE	3-Chloroacrylic acid degradation	1.2.1.3	0	0		[c] : C06613 + C00001 <==> C06614 + 2 C00080
R_R00357	L-Aspartic acid:oxygen oxidoredu	TRUE	Alanine and aspartate metabolism	1.4.3.16	-33.09127	-0.1		[c] : C00049 + C00001 + C00007 <==> C00036 + C01342 + C00027
R_R00357	L-Aspartic acid:oxygen oxidoredu	TRUE	Alanine and aspartate metabolism	1.4.3.2	-33.09127	-0.1		[c] : C00049 + C00001 + C00007 <==> C00036 + C01342 + C00027
R_ASPCTn	carbamoyl-phosphate:L-aspartate	FALSE	Alanine and aspartate metabolism	2.1.3.2	6.1034255	1.50E-11	0	[c] : C00049 + C00169 --> C00438 + C00080 + C00009
R_APAT2rm	3-Aminopropanoate:2-oxoglutara	TRUE	Alanine and aspartate metabolism	2.6.1.19	0	0.1	0	[c] : C00026 + C00099 <==> C00025 + C00222
R_APAT2rm	3-Aminopropanoate:2-oxoglutara	TRUE	Alanine and aspartate metabolism	2.6.1.55	0	0.1	0	[c] : C00026 + C00099 <==> C00025 + C00222
R_ASP1DC	L-Aspartate 1-carboxy-lyase	FALSE	Alanine and aspartate metabolism	4.1.1.11	0.0011356	0.1	0	[c] : C00049 + C00080 --> C00099 + C00011
R_ASP1DC	L-Aspartate 1-carboxy-lyase	FALSE	Alanine and aspartate metabolism	4.1.1.15	0.0011356	0.1	0	[c] : C00049 + C00080 --> C00099 + C00011
R_ARGSL	2-(Nomega-L-arginino)succinate	TRUE	Alanine and aspartate metabolism	4.3.2.1	0	0.1	-936.20413	[c] : C03406 <==> C00062 + C00122
R_ADSL1	N6-(1,2-dicarboxyethyl)AMP AMI	FALSE	Alanine and aspartate metabolism	4.3.2.2	5.7646479	1.10E-10	1000	[c] : C03794 --> C00020 + C00122
R_ALAR	L-Alanine racemase	TRUE	Alanine and aspartate metabolism	5.1.1.1	0	4.50E-11	-1000	[c] : C00041 <==> C00133
R_ASPTRS	L-Aspartate:tRNA(Asp) ligase (AM	FALSE	Alanine and aspartate metabolism	6.1.1.12	0	0	0	[c] : C00049 + C00002 + C01638 --> C00020 + C02984 + C00013
R_ASPTRS	L-Aspartate:tRNA(Asp) ligase (AM	FALSE	Alanine and aspartate metabolism	6.1.1.23	0	0	0	[c] : C00049 + C00002 + C01638 --> C00020 + C02984 + C00013
R_ALATRS	L-Alanine:tRNA(Ala) ligase (AMP-	FALSE	Alanine and aspartate metabolism	6.1.1.7	0	0	0	[c] : C00041 + C00002 + C01635 --> C00886 + C00020 + C00013
R_ADSS	IMP:L-aspartate ligase (GDP-form	FALSE	Alanine and aspartate metabolism	6.3.4.4	5.7646479	1.10E-10	7.4870413	[c] : C00049 + C00044 + C00130 --> C03794 + C00035 + 2 C00080 + C00009
R_ARGSS	L-Citrulline:L-aspartate ligase (AM	FALSE	Alanine and aspartate metabolism	6.3.4.5	0	0.1	0	[c] : C00049 + C00002 + C00327 --> C00020 + C03406 + C00080 + C00013
R_ASNS1	L-aspartate:L-glutamine amido-li	FALSE	Alanine and aspartate metabolism	6.3.5.4	4.4077087	0		[c] : C00049 + C00002 + C00064 + C00001 --> C00020 + C00152 + C00025 + C00080 + C0
R_R04212	Asp-tRNA(Asn):L-glutamine amid	TRUE	Alanine and aspartate metabolism	6.3.5.6	0	0		[c] : C03402 + C00025 + C00009 + C00008 <==> C06113 + C00064 + C00002 + C00001
R_UAPGR	UDP-N-acetylmuramate:NADP+ o	FALSE	Aminosugars metabolism	1.1.1.158	0	1000	0.05000695	[c] : C00080 + C00005 + C04631 --> C00006 + C01050
R_R03191	UDP-N-acetylmuramate:NADP+ o	TRUE	Aminosugars metabolism	1.1.1.158	-0.038495	1000		[c] : C01050 + C00003 <==> C04631 + C00004 + C00080
R_R05332	Acetyl-CoA:D-glucosamine-1-pho	TRUE	Aminosugars metabolism	2.3.1.157	0.0384953	1.50E-11		[c] : C00024 + C06156 <==> C00010 + C04501
R_UAGCVT	Phosphoenolpyruvate:UDP-N-ace	FALSE	Aminosugars metabolism	2.5.1.7	0.0384953	1.50E-11	0.05000695	[c] : C00074 + C00043 --> C00009 + C04631
R_GF6PTA	L-Glutamine:D-fructose-6-phosph	FALSE	Aminosugars metabolism	2.6.1.16	0.0384953	5.00E-12	0.05000695	[c] : C05345 + C00064 --> C00352 + C00025
R_R08559	Protein-N(pai)-phosphohistidine-	TRUE	Aminosugars metabolism	2.7.1.69	0	0		[c] : C02713 + C04261 <==> C16698 + C00615
R_R00416	UTP:N-acetyl-alpha-D-glucosamir	TRUE	Aminosugars metabolism	2.7.7.23	0.0384953	1.50E-11		[c] : C00075 + C04501 <==> C00013 + C00043
R_R00022	.	TRUE	Aminosugars metabolism	3.2.1.52	0	0		[c] : C01674 + C00001 <==> 2 C00140
R_AGDC_r	N-Acetyl-D-glucosamine-6-phosp	TRUE	Aminosugars metabolism	3.5.1.25	0	1.00E-11	-1000	[c] : C00357 + C00001 <==> C00033 + C00352
R_R08555	N-acetylmuramic acid 6-phospha	TRUE	Aminosugars metabolism	4.2.-.-	0	1.00E-11		[c] : C16698 + C00001 <==> C00357 + C00256
R_PGAMT	D-Glucosamine 1-phosphate 1,6-p	TRUE	Aminosugars metabolism	5.4.2.10	-0.038495	-1.50E-11	-0.050007	[c] : C06156 <==> C00352
R_R03089	.	TRUE	Androgen and estrogen metabolism	1.14.13.-	0	0		[c] : C00951 + C00080 + C00007 + C00005 <==> C05141 + C00006 + C00001
R_R02356	.	TRUE	Androgen and estrogen metabolism	1.14.13.-	0	0		[c] : C00468 + C00080 + C00007 + C00005 <==> C05300 + C00006 + C00001
R_R03090	.	TRUE	Androgen and estrogen metabolism	1.14.13.-	-1000	-1000		[c] : C00951 + C00080 + C00007 + C00005 <==> C05301 + C00006 + C00001
R_R02354	.	TRUE	Androgen and estrogen metabolism	1.14.13.-	1000	1000		[c] : C00468 + C00080 + C00007 + C00004 <==> C05298 + C00003 + C00001
R_R02355	.	TRUE	Androgen and estrogen metabolism	1.14.13.-	-1000	-1000		[c] : C00468 + C00080 + C00007 + C00005 <==> C05298 + C00006 + C00001
R_R03088	.	TRUE	Androgen and estrogen metabolism	1.14.13.-	1000	1000		[c] : C00951 + C00080 + C00007 + C00004 <==> C05301 + C00003 + C00001
R_R04764	.	TRUE	Androgen and estrogen metabolism	2.1.1.-	0	0		[c] : C05301 + C00019 <==> C05302 + C00021
R_R07035	Glutathione: 15-HPETE oxidoredu	TRUE	Arachidonic acid metabolism	1.11.1.9	0	0		[c] : 2 C00051 + 15HPET <==> C00127 + C04742 + C00001
R_R07034	Glutathione: 5-HPETE oxidoreduc	TRUE	Arachidonic acid metabolism	1.11.1.9	0	0		[c] : 2 C00051 + 5HPET <==> C00127 + C04805 + C00001
R_4HGLSDn	L-erythro-4-Hydroxyglutamate:N	TRUE	Arginine and proline metabolism	1.5.1.12	0	0		[c] : C05938 + C00001 + C00003 <==> e4hglu + 2 C00080 + C00004
R_PUTA3	L-Glutamate 5-semialdehyde:NAD	FALSE	Arginine and proline metabolism	1.5.1.12	0	0.2		[c] : C01165 + C00001 + C00003 --> C00025 + 2 C00080 + C00004
R_R00708	L-1-Pyrroline-5-carboxylate:NAD	TRUE	Arginine and proline metabolism	1.5.1.12	-4.042004	-1000		[c] : C03912 + C00006 + 2 C00001 <==> C00025 + C00005 + C00080
R_P5CD	L-1-Pyrroline-5-carboxylate:NAD	FALSE	Arginine and proline metabolism	1.5.1.12	0	1000	-5.2507303	[c] : C03912 + 2 C00001 + C00003 --> C00025 + C00080 + C00004
R_PHCDm	L-1-Pyrroline-3-hydroxy-5-carbo	FALSE	Arginine and proline metabolism	1.5.1.12	293.86814	0.1		[c] : C04281 + 2 C00001 + C00003 --> e4hglu + C00080 + C00004
R_R04445	L-1-Pyrroline-3-hydroxy-5-carbo	TRUE	Arginine and proline metabolism	1.5.1.12	-293.8681	-0.1		[c] : C04281 + C00006 + 2 C00001 <==> e4hglu + C00005 + C00080

R_P5CR	L-Proline:NADP+ 5-oxidoreducta	FALSE	Arginine and proline metabolism	1.5.1.2	364.29867	1000	0	[c] : C03912 + 2 C00080 + C00005 --> C00006 + C00148
R_HPROxm	trans-4-Hydroxy-L-proline:NAD+	FALSE	Arginine and proline metabolism	1.5.1.2	0	0		[c] : C01157 + C00003 --> C04281 + 2 C00080 + C00004
R_PRO1x	L-Proline:NAD+ 5-oxidoreductase	FALSE	Arginine and proline metabolism	1.5.1.2	0	613.28501	994.131684	[c] : C00003 + C00148 --> C03912 + 2 C00080 + C00004
R_HPROym	trans-4-Hydroxy-L-proline:NADP	FALSE	Arginine and proline metabolism	1.5.1.2	0	0		[c] : C01157 + C00006 --> C04281 + 2 C00080 + C00005
R_4HGLSDn	L-erythro-4-Hydroxyglutamate:N	TRUE	Arginine and proline metabolism	1.5.99.8	0	0		[c] : C05938 + C00001 + C00003 <==> e4hglu + 2 C00080 + C00004
R_R01253	L-proline:(acceptor) oxidoreducta	TRUE	Arginine and proline metabolism	1.5.99.8	360.25666	386.71499		[c] : C00148 + C00028 <==> C03912 + C00030
R_OCBT	Carbamoyl-phosphate:L-ornithin	TRUE	Arginine and proline metabolism	2.1.3.3	5.4085858	0	7.02597717	[c] : C00169 + C00077 <==> C00327 + C00080 + C00009
R_ORNTArn	L-Ornithine:2-oxo-acid aminotrar	TRUE	Arginine and proline metabolism	2.6.1.13	0	0.1		[c] : C00026 + C00077 <==> C00025 + C01165
R_ARGN	L-Arginine amidinohydrolase	FALSE	Arginine and proline metabolism	3.5.3.1	0	0		[c] : C00062 + C00001 --> C00077 + C00086
R_ARGDr	L-Arginine iminohydrolase	TRUE	Arginine and proline metabolism	3.5.3.6	-5.408586	0.1	-943.2301	[c] : C00062 + C00001 <==> C00327 + C01342
R_R00471	D-4-Hydroxy-2-oxoglutarate glyo	TRUE	Arginine and proline metabolism	4.1.1.3	0	0		[c] : C05946 <==> C00022 + C00048
R_R00471	D-4-Hydroxy-2-oxoglutarate glyo	TRUE	Arginine and proline metabolism	4.1.2.14	0	0		[c] : C05946 <==> C00022 + C00048
R_R00471	D-4-Hydroxy-2-oxoglutarate glyo	TRUE	Arginine and proline metabolism	4.1.3.16	0	0		[c] : C05946 <==> C00022 + C00048
R_ARGSL	2-(Nomega-L-arginino)succinate	TRUE	Arginine and proline metabolism	4.3.2.1	0	0.1	-936.20413	[c] : C03406 <==> C00062 + C00122
R_PROTRS	L-Proline:tRNA(Pro) ligase (AMP-	FALSE	Arginine and proline metabolism	6.1.1.15	0	0	0	[c] : C00002 + C00148 + C01649 --> C00020 + C00013 + C02702
R_ARGTRS	L-Arginine:tRNA(Arg) ligase (AM	FALSE	Arginine and proline metabolism	6.1.1.19	0	0	0	[c] : C00062 + C00002 + C01636 --> C00020 + C02163 + C00013
R_ARGSS	L-Citrulline:L-aspartate ligase (A	FALSE	Arginine and proline metabolism	6.3.4.5	0	0.1	0	[c] : C00049 + C00002 + C00327 --> C00020 + C03406 + C00080 + C00013
R_UDPGDr	UDPglucose:NAD+ oxidoreductas	TRUE	Ascorbate and aldarate metabolism	1.1.1.22	0	0	-1000	[c] : C00001 + 2 C00003 + C00029 <==> 3 C00080 + 2 C00004 + C00167
R_GLACO	D-Glucuronolactone:NAD+ oxidor	FALSE	Ascorbate and aldarate metabolism	1.2.1.3	0	0	0	[c] : glac + 2 C00001 + C00003 --> C00818 + 3 C00080 + C00004
R_R02279	5-Dehydro-4-deoxy-D-glucarate l	TRUE	Ascorbate and aldarate metabolism	4.2.1.41	0	0		[c] : 5dh4dglc <==> C00433 + C00001 + C00011
R_R00412	Succinate:(acceptor) oxidoreduct	TRUE	Benzoate degradation via CoA ligatior	1.3.99.1	-350.8638	-96.510791		[c] : C00042 + C00028 <==> C00122 + C00030
R_R05579	Glutaryl-CoA:(acceptor) 2,3-oxid	TRUE	Benzoate degradation via CoA ligatior	1.3.99.7	0	0		[c] : C00527 + C00028 <==> C02411 + C00030
R_ACACT1n	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Benzoate degradation via CoA ligatior	2.3.1.16	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_ACACT1m	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Benzoate degradation via CoA ligatior	2.3.1.9	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_R05590	Acylamide aminohydrolase	TRUE	Benzoate degradation via CoA ligatior	3.5.1.4	0	0		[c] : C09815 + C00001 <==> C00180 + C01342
R_R01421	Benzoyl phosphate phosphohydr	TRUE	Benzoate degradation via CoA ligatior	3.6.1.7	0	0		[c] : C06206 + C00001 <==> C00180 + C00009
R_ECOAH1	(S)-3-Hydroxybutanoyl-CoA hydr	TRUE	Benzoate degradation via CoA ligatior	4.2.1.17	0	0	-0.0132768	[c] : 3hbcoa <==> b2coa + C00001
R_R00829	Succinyl-CoA:acetyl-CoA C-acyltra	TRUE	Benzoate degradation via hydroxylati	2.3.1.16	0	0		[c] : C00091 + C00024 <==> C00010 + C02232
R_R00829	Succinyl-CoA:acetyl-CoA C-acyltra	TRUE	Benzoate degradation via hydroxylati	2.3.1.174	0	0		[c] : C00091 + C00024 <==> C00010 + C02232
R_R02991	4-Carboxymethylbut-3-en-4-olide	TRUE	Benzoate degradation via hydroxylati	3.1.1.24	0	0		[c] : C03586 + C00001 <==> C00846
R_R04161	(S)-4-Hydroxymandelate racemas	TRUE	Benzoate degradation via hydroxylati	5.1.2.2	0	0		[c] : C03198 <==> C05343
R_R07839	.	TRUE	Benzoate degradation via hydroxylati	5.3.3.10	0	0		[c] : C04434 <==> C04451
R_R04805	.	TRUE	Bile acid biosynthesis	1.1.1.1	0	0		[c] : xol7ah3 + C00003 <==> xol7ah2al + C00004 + C00080
R_P4508B1	7alpha-hydroxycholest-4-en-3-or	FALSE	Bile acid biosynthesis	1.14.13.-	0	0		[c] : C00080 + C00005 + C00007 + xol7aone --> C00001 + C00006 + xoldiolone
R_P4508B1	7alpha-hydroxycholest-4-en-3-or	FALSE	Bile acid biosynthesis	1.14.13.95	0	0		[c] : C00080 + C00005 + C00007 + xol7aone --> C00001 + C00006 + xoldiolone
R_R04506	3alpha,7alpha-Dihydroxy-5beta-c	TRUE	Bile acid biosynthesis	1.2.1.3	0	0		[c] : xol7ah2al + C00003 + C00001 <==> dhcholestanate + C00004 + C00080
R_R04592	.	TRUE	Bile acid biosynthesis	1.3.99.-	0	0		[c] : cholcoar + C00016 <==> cholcoads + C01352
R_R04547	.	TRUE	Bile acid biosynthesis	1.3.99.-	0	0		[c] : dhcholestancoa + C00016 <==> dhcholoylcoa + C01352
R_R04546	Propanoyl-CoA:acetyl-CoA C-acyl	TRUE	Bile acid biosynthesis	2.3.1.16	0	0		[c] : C00100 + dcholcoa <==> C00010 + dhcholestancoa
R_SCPx	Propanoyl-CoA:acetyl-CoA C-acyl	FALSE	Bile acid biosynthesis	2.3.1.16	0	0		[c] : cholcoaone + C00010 --> cholcoa + C00100
R_SCP2x	Propanoyl-CoA:acetyl-CoA C-acyl	FALSE	Bile acid biosynthesis	2.3.1.16	0	0		[c] : C00010 + dhocholoylcoa --> dgcholcoa + C00100
R_biomass_	BiomassRxn	FALSE	BiomassObjective	.	19.247636	19.2476365	25.0034775	[c] : 0.05 C00440 + 0.00005 C00024 + 0.488 C00041 + 0.001 C00020 + 0.281 C00062 + 0.2
R_DHBD	2,3-dihydro-2,3-dihydroxybenzoa	TRUE	Biosynthesis of siderophore group no	1.3.1.28	0	0		[c] : C04171 + C00003 <==> C00196 + C00080 + C00004
R_ICHORT	Isochorismate pyruvate-hydrolas	FALSE	Biosynthesis of siderophore group no	3.3.2.1	0	0		[c] : C00001 + C00885 --> C04171 + C00022
R_ICHORSi	Chorismate hydroxymutase	FALSE	Biosynthesis of siderophore group no	5.4.4.2	0	0		[c] : C00251 --> C00885
R_DXPRIi	1-Deoxy-D-xylulose-5-phosphate	FALSE	Biosynthesis of steroids	1.1.1.267	0	0		[c] : C11437 + C00080 + C00005 --> C11434 + C00006
R_R05884	isopentenyl-diphosphate:NAD(P)	TRUE	Biosynthesis of steroids	1.17.1.2	0	0		[c] : C11811 + C00005 + C00080 <==> C00129 + C00006 + C00001
R_DXPS	1-Deoxy-D-xylulose-5-phosphate	FALSE	Biosynthesis of steroids	2.2.1.7	0	0.1		[c] : C00118 + C00080 + C00022 --> C00011 + C11437
R_HEXTT	.	FALSE	Biosynthesis of steroids	2.5.1.30	0	0	0	[c] : C01230 + C00129 --> C04216 + C00013
R_CDPMEK	ATP: 4-(Cytidine 5'-diphospho)-2	FALSE	Biosynthesis of steroids	2.7.1.148	0	0		[c] : C11435 + C00002 --> C11436 + C00008 + C00080
R_MECDPS	2-Phospho-4-(cytidine 5'-diphosp	FALSE	Biosynthesis of steroids	4.6.1.12	0	0		[c] : C11436 --> C11453 + C00055
R_R06637	.	TRUE	Biosynthesis of type II polyketide bac	.	0	0		[c] : C00136 + 7 C00083 <==> C12350 + 7 C00011 + 7 C00010
R_R06635	.	TRUE	Biosynthesis of type II polyketide bac	.	0	0		[c] : C00024 + 7 C00083 <==> C12348 + 7 C00011 + 7 C00010
R_R06636	.	TRUE	Biosynthesis of type II polyketide bac	.	0	0		[c] : C00100 + 7 C00083 <==> C12349 + 7 C00011 + 7 C00010
R_R07759	.	TRUE	Biosynthesis of unsaturated fatty acid	1.1.1.-	0	0		[c] : C16216 + C00005 + C00080 <==> C16217 + C00006
R_R07763	.	TRUE	Biosynthesis of unsaturated fatty acid	1.1.1.100	0	0		[c] : C16219 + C00005 + C00080 <==> C16220 + C00006
R_R07950	.	TRUE	Biosynthesis of unsaturated fatty acid	1.3.3.6	0	0		[c] : C16172 + C00016 <==> C16387 + C01352
R_R07934	.	TRUE	Biosynthesis of unsaturated fatty acid	1.3.3.6	0	0		[c] : C16168 + C00016 <==> C16374 + C01352
R_R08176	Oleoyl-CoA hydrolase	TRUE	Biosynthesis of unsaturated fatty acid	3.1.2.2	0	0		[c] : C00510 + C00001 <==> C00010 + C00712

R_PTE2x	Palmitoyl-CoA hydrolase	FALSE	Biosynthesis of unsaturated fatty acid	3.1.2.2	0	0		[c] : C00001 + C00154 --> C00010 + C00080 + C00249
R_R08174	Stearoyl-CoA hydrolase	TRUE	Biosynthesis of unsaturated fatty acid	3.1.2.2	0	0		[c] : C00412 + C00001 <==> C00010 + C01530
R_PTE2x	Palmitoyl-CoA hydrolase	FALSE	Biosynthesis of unsaturated fatty acid	3.1.2.22	0	0		[c] : C00001 + C00154 --> C00010 + C00080 + C00249
R_BACCLm	biotin:CoA ligase (AMP-forming);	FALSE	Biotin metabolism	6.2.1.11	0	0		[c] : C00002 + C00120 + C00080 --> C05921 + C00013
R_BACCLm	biotin:CoA ligase (AMP-forming);	FALSE	Biotin metabolism	6.3.4.10	0	0		[c] : C00002 + C00120 + C00080 --> C05921 + C00013
R_R05145	Biotinyl-5'-AMP:apo-[carboxylase	TRUE	Biotin metabolism	6.3.4.10	0	0		[c] : C05921 + C06249 <==> C00020 + C06250
R_BACCLm	biotin:CoA ligase (AMP-forming);	FALSE	Biotin metabolism	6.3.4.11	0	0		[c] : C00002 + C00120 + C00080 --> C05921 + C00013
R_R05145	Biotinyl-5'-AMP:apo-[carboxylase	TRUE	Biotin metabolism	6.3.4.11	0	0		[c] : C05921 + C06249 <==> C00020 + C06250
R_R05145	Biotinyl-5'-AMP:apo-[carboxylase	TRUE	Biotin metabolism	6.3.4.15	0	0		[c] : C05921 + C06249 <==> C00020 + C06250
R_BACCLm	biotin:CoA ligase (AMP-forming);	FALSE	Biotin metabolism	6.3.4.15	0	0		[c] : C00002 + C00120 + C00080 --> C05921 + C00013
R_R05145	Biotinyl-5'-AMP:apo-[carboxylase	TRUE	Biotin metabolism	6.3.4.9	0	0		[c] : C05921 + C06249 <==> C00020 + C06250
R_BACCLm	biotin:CoA ligase (AMP-forming);	FALSE	Biotin metabolism	6.3.4.9	0	0		[c] : C00002 + C00120 + C00080 --> C05921 + C00013
R_R06890	.	TRUE	Bisphenol A degradation	1.14.13.-	0	0		[c] : C13637 + C00005 + C00080 + C00007 <==> C13638 + C00006 + C00001
R_R06884	.	TRUE	Bisphenol A degradation	1.14.13.-	0	0		[c] : C13624 + C00004 + C00080 + C00007 <==> C13631 + C00003 + C00001
R_R06888	.	TRUE	Bisphenol A degradation	1.14.13.-	0	0		[c] : C13631 + C00004 + C00080 + C00007 <==> C13634 + C00003 + C00001
R_R06883	.	TRUE	Bisphenol A degradation	1.14.13.-	0	0		[c] : C13624 + C00004 + C00080 + C00007 <==> C13629 + C00003 + C00001
R_BDHm	(R)-3-Hydroxybutanoate:NAD+ o	TRUE	Butanoate metabolism	1.1.1.30	0	-5.00E-12		[c] : C01089 + C00003 <==> C00164 + C00080 + C00004
R_HACD1	(S)-3-Hydroxybutanoyl-CoA:NAD	TRUE	Butanoate metabolism	1.1.1.35	0	0	-0.0132768	[c] : C00332 + C00080 + C00004 <==> 3hbcoa + C00003
R_SSALy	Succinate-semialdehyde:NADP+ (	FALSE	Butanoate metabolism	1.2.1.16	0	0.1	0	[c] : C00001 + C00006 + C00232 --> 2 C00080 + C00005 + C00042
R_SSALx	Succinate-semialdehyde:NAD+ ox	FALSE	Butanoate metabolism	1.2.1.16	0	0.1		[c] : C00001 + C00003 + C00232 --> 2 C00080 + C00004 + C00042
R_SSALx	Succinate-semialdehyde:NAD+ ox	FALSE	Butanoate metabolism	1.2.1.24	0	0.1		[c] : C00001 + C00003 + C00232 --> 2 C00080 + C00004 + C00042
R_R05119	3-Butyn-1-al:NAD+ oxidoreductas	TRUE	Butanoate metabolism	1.2.1.3	0	0		[c] : C06145 + C00003 + C00001 <==> C06144 + C00004 + C00080
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Butanoate metabolism	1.2.4.1	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_ACOAD1	Butanoyl-CoA:(acceptor) 2,3-oxid	TRUE	Butanoate metabolism	1.3.1.44	0	0	-0.0132768	[c] : b2coa + C00080 + C00004 <==> C00136 + C00003
R_SUCD1i	Succinate:(acceptor) oxidoreduct	FALSE	Butanoate metabolism	1.3.99.1	0	0		[c] : C00016 + C00042 --> C01352 + C00122
R_ACOAD1	Butanoyl-CoA:(acceptor) 2,3-oxid	TRUE	Butanoate metabolism	1.3.99.2	0	0	-0.0132768	[c] : b2coa + C00080 + C00004 <==> C00136 + C00003
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Butanoate metabolism	2.2.1.6	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_R03050	2-Acetolactate pyruvate-lyase (ca	TRUE	Butanoate metabolism	2.2.1.6	-1000	0.1		[c] : C00900 + C00068 <==> C05125 + C00022
R_ACACT1n	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Butanoate metabolism	2.3.1.16	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_ACACT1n	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Butanoate metabolism	2.3.1.9	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_ABTArm	4-Aminobutanoate:2-oxoglutarat	TRUE	Butanoate metabolism	2.6.1.19	0	0.2	0	[c] : C00334 + C00026 <==> C00025 + C00232
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Butanoate metabolism	4.1.1.1	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_ECOAH1	(S)-3-Hydroxybutanoyl-CoA hydr	TRUE	Butanoate metabolism	4.2.1.17	0	0	-0.0132768	[c] : 3hbcoa <==> b2coa + C00001
R_AACOAT	Acetoacetate:CoA ligase (AMP-for	TRUE	Butanoate metabolism	6.2.1.16	0	-9.00E-11	-3.2754556	[c] : C00164 + C00002 + C00010 <==> C00332 + C00020 + C00013
R_ACLS	(S)-2-Acetolactate pyruvate-lyase	FALSE	C5-Branched dibasic acid metabolism	2.2.1.6	0	96.810791	20.7528863	[c] : C00080 + 2 C00022 --> C06010 + C00011
R_ITCOALm	Itaconate:CoA ligase (ADP-formin	TRUE	C5-Branched dibasic acid metabolism	6.2.1.5	0	0	0	[c] : C00002 + C00010 + C00490 <==> C00008 + C00531 + C00009
R_R07963	.	TRUE	Caffeine metabolism	1.13.12.-	1000	-1000		[c] : C07480 + C00004 + C00080 + C00007 <==> C16357 + C00003 + C00067 + C00001
R_R07964	.	TRUE	Caffeine metabolism	1.13.12.-	1000	-1000		[c] : C07480 + C00005 + C00080 + C00007 <==> C16357 + C00006 + C00067 + C00001
R_R07971	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	1000		[c] : C07481 + C00004 + C00080 + C00007 <==> C07130 + C00003 + C00067 + C00001
R_R07954	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	1000		[c] : C07481 + C00004 + C00080 + C00007 <==> C13747 + C00003 + C00067 + C00001
R_R07967	.	TRUE	Caffeine metabolism	1.13.12.-	1000	-1000		[c] : C16357 + C00004 + C00080 + C00007 <==> C00385 + C00003 + C00067 + C00001
R_R07974	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	1000		[c] : C07130 + C00005 + C00080 + C00007 <==> C16357 + C00006 + C00067 + C00001
R_R07962	.	TRUE	Caffeine metabolism	1.13.12.-	1000	1000		[c] : C07480 + C00005 + C00080 + C00007 <==> C16353 + C00006 + C00067 + C00001
R_R07966	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	-451.894604		[c] : C16353 + C00005 + C00080 + C00007 <==> C00385 + C00006 + C00067 + C00001
R_R07970	.	TRUE	Caffeine metabolism	1.13.12.-	1000	451.894604		[c] : C16358 + C00005 + C00080 + C00007 <==> C00385 + C00006 + C00067 + C00001
R_R07959	.	TRUE	Caffeine metabolism	1.13.12.-	1000	-1000		[c] : C13747 + C00004 + C00080 + C00007 <==> C16358 + C00003 + C00067 + C00001
R_R07968	.	TRUE	Caffeine metabolism	1.13.12.-	1000	-1000		[c] : C16357 + C00005 + C00080 + C00007 <==> C00385 + C00006 + C00067 + C00001
R_R07955	.	TRUE	Caffeine metabolism	1.13.12.-	1000	-451.894604		[c] : C07481 + C00004 + C00080 + C00007 <==> C07480 + C00003 + C00067 + C00001
R_R07957	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	-1000		[c] : C13747 + C00004 + C00080 + C00007 <==> C16353 + C00003 + C00067 + C00001
R_R07961	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	-451.894604		[c] : C07480 + C00004 + C00080 + C00007 <==> C16353 + C00003 + C00067 + C00001
R_R07973	.	TRUE	Caffeine metabolism	1.13.12.-	1000	-1000		[c] : C07130 + C00004 + C00080 + C00007 <==> C16357 + C00003 + C00067 + C00001
R_R07975	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	1000		[c] : C07130 + C00004 + C00080 + C00007 <==> C16358 + C00003 + C00067 + C00001
R_R07956	.	TRUE	Caffeine metabolism	1.13.12.-	1000	-1000		[c] : C07481 + C00005 + C00080 + C00007 <==> C07480 + C00006 + C00067 + C00001
R_R07960	.	TRUE	Caffeine metabolism	1.13.12.-	1000	1000		[c] : C13747 + C00005 + C00080 + C00007 <==> C16358 + C00006 + C00067 + C00001
R_R07939	.	TRUE	Caffeine metabolism	1.13.12.-	1000	-1000		[c] : C07481 + C00005 + C00007 + C00080 <==> C13747 + C00006 + C00067 + C00001
R_R07958	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	1000		[c] : C13747 + C00005 + C00080 + C00007 <==> C16353 + C00006 + C00067 + C00001
R_R07976	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	451.894604		[c] : C07130 + C00005 + C00080 + C00007 <==> C16358 + C00006 + C00067 + C00001
R_R07969	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	1000		[c] : C16358 + C00004 + C00080 + C00007 <==> C00385 + C00003 + C00067 + C00001
R_R07972	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	451.894604		[c] : C07481 + C00005 + C00080 + C00007 <==> C07130 + C00006 + C00067 + C00001

R_R07965	.	TRUE	Caffeine metabolism	1.13.12.-	-1000	1000		[c] : C16353 + C00004 + C00080 + C00007 <==> C00385 + C00003 + C00067 + C00001
R_R07939	.	TRUE	Caffeine metabolism	1.14.14.1	1000	-1000		[c] : C07481 + C00005 + C00007 + C00080 <==> C13747 + C00006 + C00067 + C00001
R_R06941	(S)-3-hydroxyacyl-CoA:NAD+ oxi	TRUE	Caprolactam degradation	1.1.1.35	0	0		[c] : C14145 + C00003 <==> C02232 + C00004 + C00080
R_R06942	(3S)-3-hydroxyacyl-CoA hydro-ly	TRUE	Caprolactam degradation	4.2.1.17	0	0		[c] : C14144 + C00001 <==> C14145
R_MDHm	(S)-malate:NAD+ oxidoreductase	TRUE	Carbon fixation in photosynthetic org	1.1.1.37	-308.7728	-96.210791	0	[c] : C00711 + C00003 <==> C00080 + C00004 + C00036
R_TKT2	D-Fructose 6-phosphate:D-glycer	TRUE	Carbon fixation in photosynthetic org	2.2.1.1	-999.9615	-193.921582	-9.5396601	[c] : C00279 + C00231 <==> C05345 + C00118
R_R01641	Sedoheptulose-7-phosphate:D-gly	TRUE	Carbon fixation in photosynthetic org	2.2.1.1	-329.0234	-64.6405273		[c] : C05382 + C00118 <==> C03736 + C00231
R_R02320	NTP:pyruvate O2-phosphotransfe	TRUE	Carbon fixation in photosynthetic org	2.7.1.40	0	0		[c] : C00201 + C00022 <==> C00454 + C00074
R_PYK	ATP:pyruvate 2-O-phosphotransf	FALSE	Carbon fixation in photosynthetic org	2.7.1.40	0	1000	944.841429	[c] : C00008 + C00080 + C00074 --> C00002 + C00022
R_PGK	ATP:3-phospho-D-glycerate 1-ph	TRUE	Carbon fixation in photosynthetic org	2.7.2.3	-673.4434	0.2	-558.84991	[c] : C00197 + C00002 <==> C00236 + C00008
R_PPDK	ATP:pyruvate,orthophosphate ph	FALSE	Carbon fixation in photosynthetic org	2.7.9.1	628.79312	0.1	588.40369	[c] : C00002 + C00009 + C00022 --> C00020 + C00080 + C00074 + C00013
R_FBP	D-Fructose-1,6-bisphosphate 1-p	FALSE	Carbon fixation in photosynthetic org	3.1.3.11	0	0.1		[c] : C00354 + C00001 --> C05345 + C00009
R_PPC	Orthophosphate:oxaloacetate car	FALSE	Carbon fixation in photosynthetic org	4.1.1.31	0	0.1	0	[c] : C00011 + C00001 + C00074 --> C00080 + C00036 + C00009
R_FBA	D-fructose-1,6-bisphosphate D-gl	TRUE	Carbon fixation in photosynthetic org	4.1.2.13	0	-0.1	80.6300907	[c] : C00354 <==> C00111 + C00118
R_FBA3	Sedoheptulose 1,7-bisphosphate	TRUE	Carbon fixation in photosynthetic org	4.1.2.13	0	0	0	[c] : C00447 <==> C00111 + C00279
R_R00761	D-fructose-6-phosphate D-erythr	TRUE	Carbon fixation in photosynthetic org	4.1.2.22	-1000	-193.821582		[c] : C05345 + C00009 <==> C00227 + C00279 + C00001
R_RPE	D-Ribulose-5-phosphate 3-epime	TRUE	Carbon fixation in photosynthetic org	5.1.3.1	-346.3031	-64.5405273	-13.32852	[c] : C00199 <==> C00231
R_TPI	D-glyceraldehyde-3-phosphate al	TRUE	Carbon fixation in photosynthetic org	5.3.1.1	674.35873	160.401318	486.409291	[c] : C00111 <==> C00118
R_R01056	D-ribose-5-phosphate aldose-ket	TRUE	Carbon fixation in photosynthetic org	5.3.1.6	-346.3028	-64.6405273	-13.32802	[c] : C03736 <==> C00199
R_R06962	.	TRUE	Carotenoid biosynthesis	.	0	0		[c] : C08586 <==> C05433
R_R04801	.	TRUE	Carotenoid biosynthesis	.	0	0		[c] : C05431 <==> C05434
R_R07857	.	TRUE	Carotenoid biosynthesis	.	0	0		[c] : caro <==> C16340
R_R07541	.	TRUE	Carotenoid biosynthesis	.	0	0		[c] : C05435 <==> C15908
R_R07856	.	TRUE	Carotenoid biosynthesis	.	0	0		[c] : C05434 <==> C16291
R_R05341	.	TRUE	Carotenoid biosynthesis	.	0	0		[c] : C05432 <==> C05435
R_R03824	.	TRUE	Carotenoid biosynthesis	.	0	0		[c] : C05435 <==> caro
R_R07858	.	TRUE	Carotenoid biosynthesis	.	0	0		[c] : C16340 <==> C15943
R_R07916	.	TRUE	Carotenoid biosynthesis	2.5.1.32	0	0		[c] : C00353 <==> C05413
R_MDHm	(S)-malate:NAD+ oxidoreductase	TRUE	Citrate cycle (TCA cycle)	1.1.1.37	-308.7728	-96.210791	0	[c] : C00711 + C00003 <==> C00080 + C00004 + C00036
R_R00268	Oxalosuccinate:NADP+ oxidoredu	TRUE	Citrate cycle (TCA cycle)	1.1.1.42	-1000	-0.1		[c] : C05379 <==> C00026 + C00011
R_R01899	Isocitrate:NADP+ oxidoreductase	TRUE	Citrate cycle (TCA cycle)	1.1.1.42	-1000	-0.1		[c] : C00311 + C00006 <==> C05379 + C00005 + C00080
R_R03270	.	TRUE	Citrate cycle (TCA cycle)	1.2.4.1	696.14778	96.910791		[c] : C05125 + C15972 <==> C16255 + C00068
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Citrate cycle (TCA cycle)	1.2.4.1	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_R03316	.	TRUE	Citrate cycle (TCA cycle)	1.2.4.2	-350.8638	-96.910791		[c] : C05381 + C15972 <==> C16254 + C00068
R_R00621	.	TRUE	Citrate cycle (TCA cycle)	1.2.4.2	-350.8638	-96.910791		[c] : C00026 + C00068 <==> C05381 + C00011
R_OOR	2-oxoglutarate:ferredoxin oxidor	FALSE	Citrate cycle (TCA cycle)	1.2.7.3	0	0		[c] : C00026 + C00010 + C00139 + C00080 --> C00011 + C00138 + C00091
R_R00412	Succinate:(acceptor) oxidoreduct	TRUE	Citrate cycle (TCA cycle)	1.3.99.1	-350.8638	-96.510791		[c] : C00042 + C00028 <==> C00122 + C00030
R_R07618	enzyme N6-(dihydrolipoyl)lysine	TRUE	Citrate cycle (TCA cycle)	1.8.1.4	-654.716	-0.1	0	[c] : C15973 + C00003 <==> C15972 + C00004 + C00080
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Citrate cycle (TCA cycle)	2.2.1.6	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_R02569	acetyl-CoA:enzyme N6-(dihydroli	TRUE	Citrate cycle (TCA cycle)	2.3.1.12	-696.1478	-96.910791		[c] : C00024 + C15973 <==> C00010 + C16255
R_R02570	succinyl-CoA:enzyme N6-(dihydr	TRUE	Citrate cycle (TCA cycle)	2.3.1.61	350.86376	96.910791		[c] : C00091 + C15973 <==> C00010 + C16254
R_CS	Citrate oxaloacetate-lyase ((pro-3	FALSE	Citrate cycle (TCA cycle)	2.3.3.1	0	0.1	26.0286951	[c] : C00024 + C00001 + C00036 --> C00158 + C00010 + C00080
R_CS	Citrate oxaloacetate-lyase ((pro-3	FALSE	Citrate cycle (TCA cycle)	2.3.3.3	0	0.1	26.0286951	[c] : C00024 + C00001 + C00036 --> C00158 + C00010 + C00080
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Citrate cycle (TCA cycle)	4.1.1.1	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_PEPCK	GTP:oxaloacetate carboxy-lyase (	FALSE	Citrate cycle (TCA cycle)	4.1.1.32	988.96292	0.5	0	[c] : C00044 + C00036 --> C00011 + C00035 + C00074
R_R00726	ITP:oxaloacetate carboxy-lyase (t	TRUE	Citrate cycle (TCA cycle)	4.1.1.32	-1000	0.1		[c] : C00081 + C00036 <==> C00104 + C00074 + C00011
R_CITL	Citrate oxaloacetate-lyase ((pro-3	FALSE	Citrate cycle (TCA cycle)	4.1.3.6	330.82697	96.910791		[c] : C00158 --> C00033 + C00036
R_FUMm	(S)-malate hydro-lyase (fumarate	TRUE	Citrate cycle (TCA cycle)	4.2.1.2	-335.7081	-96.410791	0	[c] : C00122 + C00001 <==> C00711
R_R01900	isocitrate hydro-lyase (cis-aconit	TRUE	Citrate cycle (TCA cycle)	4.2.1.3	330.82697	96.810791		[c] : C00311 <==> C00417 + C00001
R_R01325	citrate hydro-lyase (cis-aconitate	TRUE	Citrate cycle (TCA cycle)	4.2.1.3	-330.827	-96.810791		[c] : C00158 <==> C00417 + C00001
R_R01325	citrate hydro-lyase (cis-aconitate	TRUE	Citrate cycle (TCA cycle)	4.2.1.4	-330.827	-96.810791		[c] : C00158 <==> C00417 + C00001
R_SUCOAS	Succinate:CoA ligase (ADP-formir	TRUE	Citrate cycle (TCA cycle)	6.2.1.5	350.86382	96.810791	0	[c] : C00002 + C00010 + C00042 <==> C00008 + C00009 + C00091
R_PMDPHT	pyrimidinephosphatase	TRUE	Cofactor and Prosthetic Group Biosyn	.	0.0001925	0	0.00025003	[c] : C04454 + C00001 <==> C04732 + C00009
R_ADCL	_4-aminobenzoatesynthase	TRUE	Cofactor and Prosthetic Group Biosyn	.	0.9623818	0	1.25017387	[c] : C11355 <==> C00568 + C00080 + C00022
R_DPR	2-dehydropantoate2-reductase	TRUE	Cofactor and Prosthetic Group Biosyn	1.1.1.169	0.0011356	0		[c] : C00966 + C00080 + C00005 <==> C00006 + C00522
R_GHMT2r	5,10-Methylenetetrahydrofolate:g	TRUE	Cyanoamino acid metabolism	2.1.2.1	20.791836	96.210791	179.709014	[c] : C00716 + C00101 <==> C00037 + C00001 + C00143
R_R04949	Cyanoglycoside glucohydrolase	TRUE	Cyanoamino acid metabolism	3.2.1.21	0	0	0	[c] : C05713 + C00001 <==> C05712 + C00267
R_R03909	Monocarboxylic acid amide amid	TRUE	Cyanoamino acid metabolism	3.5.1.4	0	0		[c] : C03620 + C00001 <==> C00060 + C01342
R_R03132	O3-Acetyl-L-serine acetate-lyase (	TRUE	Cysteine metabolism	2.5.1.47	0	0		[c] : C00979 + C05529 <==> C05824 + C00033

R_CYSSr	O3-Acetyl-L-serine acetate-lyase (	TRUE	Cysteine metabolism	2.5.1.47	-1000	-1000		[c] : C00979 + C00297 <==> C00033 + C00097 + C00080
R_R04859	O3-Acetyl-L-serine acetate-lyase (	TRUE	Cysteine metabolism	2.5.1.47	990.60715	709.795801		[c] : C00979 + C05529 + C00342 + C00080 <==> C00097 + C00094 + C00343 + C00033
R_R03132	O3-Acetyl-L-serine acetate-lyase (	TRUE	Cysteine metabolism	2.5.1.48	0	0		[c] : C00979 + C05529 <==> C05824 + C00033
R_R04859	O3-Acetyl-L-serine acetate-lyase (	TRUE	Cysteine metabolism	2.5.1.49	990.60715	709.795801		[c] : C00979 + C05529 + C00342 + C00080 <==> C00097 + C00094 + C00343 + C00033
R_CYSSr	O3-Acetyl-L-serine acetate-lyase (	TRUE	Cysteine metabolism	2.5.1.65	-1000	-1000		[c] : C00979 + C00297 <==> C00033 + C00097 + C00080
R_R03105	3-Mercaptopyruvate:cyanide sulf	TRUE	Cysteine metabolism	2.8.1.2	0	0		[c] : C00957 + C00094 <==> C05529 + C00022
R_CYSTRS	L-Cysteine:tRNA(Cys) ligase (AMI	FALSE	Cysteine metabolism	6.1.1.16	0	0	0	[c] : C00002 + C00097 + C01639 --> C00020 + C03125 + C00013
R_ALAR	L-Alanine racemase	TRUE	D-Alanine metabolism	5.1.1.1	0	4.50E-11	-1000	[c] : C00041 <==> C00133
R_ALAALAr	D-alanine:D-alanine ligase (ADP-f	TRUE	D-Alanine metabolism	6.3.2.4	0	2.25E-11	0	[c] : 2 C00133 + C00002 <==> C00008 + C00993 + C00080 + C00009
R_GLUR	L-Glutamate racemase	TRUE	D-Glutamine and D-glutamate metabo	5.1.1.3	0	-1.50E-11		[c] : C00217 <==> C00025
R_UAMAS	UDP-N-acetylmuramate:L-alanine	FALSE	D-Glutamine and D-glutamate metabo	6.3.2.8	0	1.50E-11	0	[c] : C00041 + C00002 + C01050 --> C00008 + C00080 + C00009 + C01212
R_UAMAGS	UDP-N-acetylmuramoyl-L-alanine	FALSE	D-Glutamine and D-glutamate metabo	6.3.2.9	0	1.50E-11	0	[c] : C00002 + C00217 + C01212 --> C00008 + C00080 + C00009 + C00692
R_R08281	alcophosphamide:NAD+ oxidored	TRUE	Drug metabolism - cytochrome P450	1.1.1.1	0	0		[c] : C07645 + C00004 + C00080 <==> C16551 + C00003
R_R08310	4-hydroxy-5-phenyltetrahydro-1,	TRUE	Drug metabolism - cytochrome P450	1.1.1.1	0	0		[c] : C16595 + C00003 <==> C16596 + C00004 + C00080
R_R08306	2-phenyl-1,3-propanediol monoc	TRUE	Drug metabolism - cytochrome P450	1.1.1.1	0	0		[c] : C16586 + C00003 <==> C16587 + C00004 + C00080
R_R08240	6-thioinosine 5'-monophosphate:	TRUE	Drug metabolism - other enzymes	1.1.1.205	0	0		[c] : C04646 + C00003 + C00001 <==> C16618 + C00004 + C00080
R_R08231	5-fluorouridine monophosphate:(	TRUE	Drug metabolism - other enzymes	2.4.2.10	0	0		[c] : C07649 + C00119 <==> C16634 + C00013
R_R08238	6-methylthiopurine 5'-monophos	TRUE	Drug metabolism - other enzymes	2.4.2.8	0	0		[c] : C16614 + C00119 <==> C16615 + C00013
R_R08237	6-thioinosine 5'-monophosphate:	TRUE	Drug metabolism - other enzymes	2.4.2.8	0	0		[c] : C02380 + C00119 <==> C04646 + C00013
R_R08245	6-thioguanosine monophosphate	TRUE	Drug metabolism - other enzymes	2.4.2.8	0	0		[c] : C07648 + C00119 <==> C16619 + C00013
R_R08255	.	TRUE	Drug metabolism - other enzymes	3.1.1.1	0	0		[c] : C16641 + C00001 <==> C11173 + C16836
R_R08258	.	TRUE	Drug metabolism - other enzymes	3.1.1.1	0	0		[c] : C16543 + C00001 <==> C11173 + C16837
R_R08244	6-thioxanthine 5'-monophosphat	TRUE	Drug metabolism - other enzymes	6.3.5.2	0	0		[c] : C16618 + C00002 + C00064 + C00001 <==> C16619 + C00020 + C00013 + C00025
R_ESC_C000	. escape flux	FALSE	EscapeFlux	.	77.530134	77.5301341		C00009[c] --> C00009[b]
R_ESC_C000	. escape flux	FALSE	EscapeFlux	.	1000	1000		C00001[c] --> C00001[b]
R_ESC_C001	. escape flux	FALSE	EscapeFlux	.	0	0		C00185[c] --> C00185[b]
R_ESC_C000	. escape flux	FALSE	EscapeFlux	.	0	0		C00007[c] --> C00007[b]
R_ESC_C013	. escape flux	FALSE	EscapeFlux	.	837.01767	837.017674		C01342[c] --> C01342[b]
R_ESC_C000	. escape flux	FALSE	EscapeFlux	.	0	0		C00059[c] --> C00059[b]
R_R07763	.	TRUE	Fatty acid biosynthesis	1.1.1.100	0	0		[c] : C16219 + C00005 + C00080 <==> C16220 + C00006
R_R04964	(3R)-3-Hydroxydodecanoyl-[acyl	TRUE	Fatty acid biosynthesis	1.1.1.100	0	0		[c] : C05757 + C00006 <==> C05756 + C00005 + C00080
R_R04534	(3R)-3-Hydroxydecanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	1.1.1.100	0	0		[c] : C04619 + C00006 <==> C05753 + C00005
R_R04536	(3R)-3-Hydroxyoctanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	1.1.1.100	0	0		[c] : C04620 + C00006 <==> C05750 + C00005 + C00080
R_R04533	(3R)-3-Hydroxybutanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	1.1.1.100	0	0		[c] : C04618 + C00006 <==> C05744 + C00005 + C00080
R_R04566	(3R)-3-Hydroxytetradecanoyl-[ac	TRUE	Fatty acid biosynthesis	1.1.1.100	0	0		[c] : 3hmrsACP + C00006 <==> C05759 + C00005 + C00080
R_R04543	(3R)-3-Hydroxypalmitoyl-[acyl-c	TRUE	Fatty acid biosynthesis	1.1.1.100	0	0		[c] : C04633 + C00006 <==> C05762 + C00005 + C00080
R_R04953	(3R)-3-Hydroxyhexanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	1.1.1.100	0	0		[c] : C05747 + C00006 <==> C05746 + C00005 + C00080
R_R07765	.	TRUE	Fatty acid biosynthesis	1.3.1.-	0	0		[c] : C16221 + C00004 + C00080 <==> C04088 + C00003
R_R04955	Hexanoyl-[acyl-carrier protein]:n	TRUE	Fatty acid biosynthesis	1.3.1.9	0	0		[c] : C05749 + C00003 <==> C05748 + C00004 + C00080
R_R04958	Octanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	1.3.1.9	0	0		[c] : C05752 + C00003 <==> C05751 + C00004 + C00080
R_R04429	Butyryl-[acyl-carrier protein]:ma	TRUE	Fatty acid biosynthesis	1.3.1.9	0	0		[c] : C05745 + C00003 <==> C04246 + C00004 + C00080
R_R04969	Hexadecanoyl-[acyl-carrier prote	TRUE	Fatty acid biosynthesis	1.3.1.9	0	0		[c] : palmACP + C00003 <==> C05763 + C00004 + C00080
R_R04724	Dodecanoyl-[acyl-carrier protein	TRUE	Fatty acid biosynthesis	1.3.1.9	0	0		[c] : C05223 + C00003 <==> C05758 + C00004 + C00080
R_R04966	Tetradecanoyl-[acyl-carrier prote	TRUE	Fatty acid biosynthesis	1.3.1.9	0	0		[c] : C05761 + C00003 <==> C05760 + C00004 + C00080
R_R04961	Decanoyl-[acyl-carrier protein]:n	TRUE	Fatty acid biosynthesis	1.3.1.9	0	0		[c] : dcaACP + C00003 <==> C05754 + C00004 + C00080
R_R07762	.	TRUE	Fatty acid biosynthesis	2.3.1.-	0	0		[c] : palmACP + C01209 <==> C16219 + apoACP_ACP + C00011
R_R04963	Decanoyl-[acyl-carrier protein]:n	TRUE	Fatty acid biosynthesis	2.3.1.179	0	0		[c] : dcaACP + C01209 <==> C05756 + C00011 + apoACP_ACP
R_R04968	Tetradecanoyl-[acyl-carrier prote	TRUE	Fatty acid biosynthesis	2.3.1.179	0	0		[c] : C05761 + C01209 <==> C05762 + C00011 + apoACP_ACP
R_R07762	.	TRUE	Fatty acid biosynthesis	2.3.1.179	0	0		[c] : palmACP + C01209 <==> C16219 + apoACP_ACP + C00011
R_R04726	dodecanoyl-[acyl-carrier-protein]	TRUE	Fatty acid biosynthesis	2.3.1.179	0	0		[c] : C05223 + C01209 <==> C05759 + C00011 + apoACP_ACP
R_R04957	hexanoyl-[acyl-carrier protein]:n	TRUE	Fatty acid biosynthesis	2.3.1.179	0	0		[c] : C05749 + C01209 <==> C05750 + C00011 + apoACP_ACP
R_KAS14	Acyl-[acyl-carrier-protein]:malon	FALSE	Fatty acid biosynthesis	2.3.1.179	0	0		[c] : C03939 + C00080 + C01209 --> C00229 + C05744 + C00011
R_R04960	Octanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.179	0	0		[c] : C05752 + C01209 <==> C05753 + C00011 + apoACP_ACP
R_R04952	butyryl-[acyl-carrier protein]:ma	TRUE	Fatty acid biosynthesis	2.3.1.179	0	0		[c] : C05745 + C01209 <==> C05746 + C00011 + apoACP_ACP
R_R04963	Decanoyl-[acyl-carrier protein]:n	TRUE	Fatty acid biosynthesis	2.3.1.180	0	0		[c] : dcaACP + C01209 <==> C05756 + C00011 + apoACP_ACP
R_R04957	hexanoyl-[acyl-carrier protein]:n	TRUE	Fatty acid biosynthesis	2.3.1.180	0	0		[c] : C05749 + C01209 <==> C05750 + C00011 + apoACP_ACP
R_R04726	dodecanoyl-[acyl-carrier-protein]	TRUE	Fatty acid biosynthesis	2.3.1.180	0	0		[c] : C05223 + C01209 <==> C05759 + C00011 + apoACP_ACP
R_R04968	Tetradecanoyl-[acyl-carrier prote	TRUE	Fatty acid biosynthesis	2.3.1.180	0	0		[c] : C05761 + C01209 <==> C05762 + C00011 + apoACP_ACP
R_KAS14	Acyl-[acyl-carrier-protein]:malon	FALSE	Fatty acid biosynthesis	2.3.1.180	0	0		[c] : C03939 + C00080 + C01209 --> C00229 + C05744 + C00011

R_ACOATAr	acetyl-CoA:[acyl-carrier-protein]	TRUE	Fatty acid biosynthesis	2.3.1.180	0	0		[c] : C00229 + C00024 <==> C03939 + C00010
R_R04960	Octanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.180	0	0		[c] : C05752 + C01209 <==> C05753 + C00011 + apoACP_ACP
R_R04952	butyryl-[acyl-carrier protein]:ma	TRUE	Fatty acid biosynthesis	2.3.1.180	0	0		[c] : C05745 + C01209 <==> C05746 + C00011 + apoACP_ACP
R_ACOATAr	acetyl-CoA:[acyl-carrier-protein]	TRUE	Fatty acid biosynthesis	2.3.1.38	0	0		[c] : C00229 + C00024 <==> C03939 + C00010
R_MCOATA	Malonyl-CoA:[acyl-carrier-protei	TRUE	Fatty acid biosynthesis	2.3.1.39	0	0	0	[c] : C00229 + C00083 <==> C00010 + C01209
R_R04963	Decanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.41	0	0		[c] : dcaACP + C01209 <==> C05756 + C00011 + apoACP_ACP
R_R04960	Octanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.41	0	0		[c] : C05752 + C01209 <==> C05753 + C00011 + apoACP_ACP
R_R04726	dodecanoyl-[acyl-carrier-protein	TRUE	Fatty acid biosynthesis	2.3.1.41	0	0		[c] : C05223 + C01209 <==> C05759 + C00011 + apoACP_ACP
R_R04968	Tetradecanoyl-[acyl-carrier prote	TRUE	Fatty acid biosynthesis	2.3.1.41	0	0		[c] : C05761 + C01209 <==> C05762 + C00011 + apoACP_ACP
R_KAS14	Acyl-[acyl-carrier-protein]:malon	FALSE	Fatty acid biosynthesis	2.3.1.41	0	0		[c] : C03939 + C00080 + C01209 --> C00229 + C05744 + C00011
R_R04957	hexanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.41	0	0		[c] : C05749 + C01209 <==> C05750 + C00011 + apoACP_ACP
R_R07762	.	TRUE	Fatty acid biosynthesis	2.3.1.41	0	0		[c] : palmACP + C01209 <==> C16219 + apoACP_ACP + C00011
R_R04952	butyryl-[acyl-carrier protein]:ma	TRUE	Fatty acid biosynthesis	2.3.1.41	0	0		[c] : C05745 + C01209 <==> C05746 + C00011 + apoACP_ACP
R_ACOATAr	acetyl-CoA:[acyl-carrier-protein]	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C00229 + C00024 <==> C03939 + C00010
R_R04533	(3R)-3-Hydroxybutanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C04618 + C00006 <==> C05744 + C00005 + C00080
R_R04726	dodecanoyl-[acyl-carrier-protein	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C05223 + C01209 <==> C05759 + C00011 + apoACP_ACP
R_R04963	Decanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : dcaACP + C01209 <==> C05756 + C00011 + apoACP_ACP
R_KAS14	Acyl-[acyl-carrier-protein]:malon	FALSE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C03939 + C00080 + C01209 --> C00229 + C05744 + C00011
R_R04534	(3R)-3-Hydroxydecanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C04619 + C00006 <==> C05753 + C00005
R_MCOATA	Malonyl-CoA:[acyl-carrier-protei	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0	0	[c] : C00229 + C00083 <==> C00010 + C01209
R_R04566	(3R)-3-Hydroxytetradecanoyl-[ac	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : 3hmrsACP + C00006 <==> C05759 + C00005 + C00080
R_R04960	Octanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C05752 + C01209 <==> C05753 + C00011 + apoACP_ACP
R_R04953	(3R)-3-Hydroxyhexanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C05747 + C00006 <==> C05746 + C00005 + C00080
R_R04536	(3R)-3-Hydroxyoctanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C04620 + C00006 <==> C05750 + C00005 + C00080
R_R04952	butyryl-[acyl-carrier protein]:ma	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C05745 + C01209 <==> C05746 + C00011 + apoACP_ACP
R_R04543	(3R)-3-Hydroxypalmitoyl-[acyl-c	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C04633 + C00006 <==> C05762 + C00005 + C00080
R_R04968	Tetradecanoyl-[acyl-carrier prote	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C05761 + C01209 <==> C05762 + C00011 + apoACP_ACP
R_R04957	hexanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C05749 + C01209 <==> C05750 + C00011 + apoACP_ACP
R_R04964	(3R)-3-Hydroxydodecanoyl-[acyl	TRUE	Fatty acid biosynthesis	2.3.1.85	0	0		[c] : C05757 + C00006 <==> C05756 + C00005 + C00080
R_R04968	Tetradecanoyl-[acyl-carrier prote	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05761 + C01209 <==> C05762 + C00011 + apoACP_ACP
R_R04724	Dodecanoyl-[acyl-carrier protein	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05223 + C00003 <==> C05758 + C00004 + C00080
R_R04963	Decanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : dcaACP + C01209 <==> C05756 + C00011 + apoACP_ACP
R_KAS14	Acyl-[acyl-carrier-protein]:malon	FALSE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C03939 + C00080 + C01209 --> C00229 + C05744 + C00011
R_MCOATA	Malonyl-CoA:[acyl-carrier-protei	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0	0	[c] : C00229 + C00083 <==> C00010 + C01209
R_R04533	(3R)-3-Hydroxybutanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C04618 + C00006 <==> C05744 + C00005 + C00080
R_R04429	Butyryl-[acyl-carrier protein]:ma	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05745 + C00003 <==> C04246 + C00004 + C00080
R_R04960	Octanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05752 + C01209 <==> C05753 + C00011 + apoACP_ACP
R_R04543	(3R)-3-Hydroxypalmitoyl-[acyl-c	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C04633 + C00006 <==> C05762 + C00005 + C00080
R_R04536	(3R)-3-Hydroxyoctanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C04620 + C00006 <==> C05750 + C00005 + C00080
R_R04958	Octanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05752 + C00003 <==> C05751 + C00004 + C00080
R_R04952	butyryl-[acyl-carrier protein]:ma	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05745 + C01209 <==> C05746 + C00011 + apoACP_ACP
R_R04957	hexanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05749 + C01209 <==> C05750 + C00011 + apoACP_ACP
R_R04961	Decanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : dcaACP + C00003 <==> C05754 + C00004 + C00080
R_R04969	Hexadecanoyl-[acyl-carrier prote	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : palmACP + C00003 <==> C05763 + C00004 + C00080
R_R04966	Tetradecanoyl-[acyl-carrier prote	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05761 + C00003 <==> C05760 + C00004 + C00080
R_R04566	(3R)-3-Hydroxytetradecanoyl-[ac	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : 3hmrsACP + C00006 <==> C05759 + C00005 + C00080
R_R04964	(3R)-3-Hydroxydodecanoyl-[acyl	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05757 + C00006 <==> C05756 + C00005 + C00080
R_R04534	(3R)-3-Hydroxydecanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C04619 + C00006 <==> C05753 + C00005
R_R04726	dodecanoyl-[acyl-carrier-protein	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05223 + C01209 <==> C05759 + C00011 + apoACP_ACP
R_ACOATAr	acetyl-CoA:[acyl-carrier-protein]	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C00229 + C00024 <==> C03939 + C00010
R_R04955	Hexanoyl-[acyl-carrier protein]:m	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05749 + C00003 <==> C05748 + C00004 + C00080
R_R04953	(3R)-3-Hydroxyhexanoyl-[acyl-ca	TRUE	Fatty acid biosynthesis	2.3.1.86	0	0		[c] : C05747 + C00006 <==> C05746 + C00005 + C00080
R_R04385	biotin-carboxyl-carrier-protein:c	TRUE	Fatty acid biosynthesis	6.3.4.14	0	0		[c] : C00002 + C06250 + C01353 <==> C00008 + C00009 + C04419
R_R04386	Acetyl-CoA:carbon-dioxide ligase	TRUE	Fatty acid biosynthesis	6.4.1.2	0	0		[c] : C00024 + C04419 <==> C00083 + C06250
R_HACD2	(S)-hydroxyhexanoyl-CoA:NAD+	TRUE	Fatty acid elongation in mitochondria	1.1.1.211	0	0	-0.0132768	[c] : C05269 + C00080 + C00004 <==> C05268 + C00003
R_HACD4p	(S)-hydroxydecanoyl-CoA:NAD+	TRUE	Fatty acid elongation in mitochondria	1.1.1.211	0	0	0	[c] : C05265 + C00080 + C00004 <==> 3hdcoa + C00003
R_R04745	(S)-hydroxyoctanoyl-CoA:NAD+	TRUE	Fatty acid elongation in mitochondria	1.1.1.211	0	0		[c] : C05266 + C00003 <==> C05267 + C00004 + C00080
R_HACD4p	(S)-hydroxydecanoyl-CoA:NAD+	TRUE	Fatty acid elongation in mitochondria	1.1.1.35	0	0	0	[c] : C05265 + C00080 + C00004 <==> 3hdcoa + C00003
R_R04745	(S)-hydroxyoctanoyl-CoA:NAD+	TRUE	Fatty acid elongation in mitochondria	1.1.1.35	0	0		[c] : C05266 + C00003 <==> C05267 + C00004 + C00080

R_HACD2	(S)-hydroxyhexanoyl-CoA:NAD+ (	TRUE	Fatty acid elongation in mitochondria	1.1.1.35	0	0	-0.0132768	[c] : C05269 + C00080 + C00004 <==> C05268 + C00003
R_FOLD3m	2-Amino-4-hydroxy-6-hydroxym	FALSE	Folate biosynthesis	2.5.1.15	0	0	0	[c] : 2ahhmd + C00568 --> C00921 + C00013
R_DHPSm	2-Amino-4-hydroxy-6-hydroxym	FALSE	Folate biosynthesis	2.5.1.15	0.9623818	0	0	[c] : 2ahhmp + C00568 --> C00921 + C00001
R_ADCS	chorismate:L-glutamine aminotra	FALSE	Folate biosynthesis	2.6.1.85	0.9623818	0		[c] : C00251 + C00064 --> C11355 + C00025
R_HPPKm	ATP:2-amino-4-hydroxy-6-hydro	FALSE	Folate biosynthesis	2.7.6.3	0	0	0	[c] : 2ahhmp + C00002 --> 2ahhmd + C00020 + C00080
R_R05046	Formamidopyrimidine nucleosid	TRUE	Folate biosynthesis	3.5.4.16	0.9623818	0		[c] : C05922 + C00001 <==> C05923 + C00058
R_R04639	2-Amino-4-hydroxy-6-(erythro-1	TRUE	Folate biosynthesis	3.5.4.16	-0.962382	0		[c] : C04895 + C00001 <==> C06148
R_R05048	GTP 7,8-8,9-dihydrolase	TRUE	Folate biosynthesis	3.5.4.16	0.9623818	0		[c] : C05923 <==> C06148
R_R00428	GTP 7,8-8,9-dihydrolase	TRUE	Folate biosynthesis	3.5.4.16	0.9623818	0		[c] : C00044 + C00001 <==> C05922
R_DNMPPA	.	FALSE	Folate biosynthesis	3.6.1.-	0.9623818	0		[c] : C05925 + C00001 --> C04874 + C00009
R_DNTPPA	.	FALSE	Folate biosynthesis	3.6.1.-	0.9623818	0		[c] : C04895 + C00001 --> C05925 + C00080 + C00013
R_DHNPAm	2-Amino-4-hydroxy-6-(D-erythro	FALSE	Folate biosynthesis	4.1.2.25	0.9623818	0		[c] : C04874 --> 2ahhmp + C00266 + C00080
R_R05048	GTP 7,8-8,9-dihydrolase	TRUE	Folate biosynthesis	6.-.-.-	0.9623818	0		[c] : C05923 <==> C06148
R_DHFS	7,8-dihydropteroate:L-glutamate	FALSE	Folate biosynthesis	6.3.2.12	0.9623818	0	1.25017387	[c] : C00002 + C00921 + C00025 --> C00008 + C00415 + C00009
R_THFGLUS	Tetrahydrofolate:L-glutamate gar	TRUE	Folate biosynthesis	6.3.2.17	0	0		[c] : C00002 + C00025 + C00101 <==> C00008 + C00080 + C00009 + C03541
R_DHFS	7,8-dihydropteroate:L-glutamate	FALSE	Folate biosynthesis	6.3.2.17	0.9623818	0	1.25017387	[c] : C00002 + C00921 + C00025 --> C00008 + C00415 + C00009
R_R00867	ATP:D-fructose 6-phosphotransfe	TRUE	Fructose and mannose metabolism	2.7.1.1	20.752917	0.2		[c] : C00002 + C10906 <==> C00008 + f6p-B
R_R00867	ATP:D-fructose 6-phosphotransfe	TRUE	Fructose and mannose metabolism	2.7.1.4	20.752917	0.2		[c] : C00002 + C10906 <==> C00008 + f6p-B
R_R02071	ATP:D-fructose-1-phosphate 6-ph	TRUE	Fructose and mannose metabolism	2.7.1.56	0	-0.1		[c] : C00002 + C01094 <==> C00008 + C05378
R_R02073	diphosphate:beta-D-fructose-6-ph	TRUE	Fructose and mannose metabolism	2.7.1.90	-325.5887	-612.68501		[c] : C00013 + f6p-B <==> C00009 + C05378
R_MAN1PT	GTP:alpha-D-mannose-1-phospha	FALSE	Fructose and mannose metabolism	2.7.7.13	0	0		[c] : C00044 + C00080 + C00636 --> C00096 + C00013
R_R04780	beta-D-Fructose 1,6-bisphosphat	TRUE	Fructose and mannose metabolism	3.1.3.11	-1000	-581.564746		[c] : C05378 + C00001 <==> f6p-B + C00009
R_R01070	beta-D-fructose-1,6-bisphosphate	TRUE	Fructose and mannose metabolism	4.1.2.13	674.41127	-31.2202637		[c] : C05378 <==> C00111 + C00118
R_FBA2	D-Fructose 1-phosphate D-glycer	TRUE	Fructose and mannose metabolism	4.1.2.13	0	0.1	0	[c] : C01094 <==> C00111 + C00577
R_TPI	D-glyceraldehyde-3-phosphate al	TRUE	Fructose and mannose metabolism	5.3.1.1	674.35873	160.401318	486.409291	[c] : C00111 <==> C00118
R_R00878	alpha-D-Glucose ketol-isomerase	TRUE	Fructose and mannose metabolism	5.3.1.5	-0.057743	0.1		[c] : C00267 <==> C10906
R_R01819	D-mannose-6-phosphate aldose-k	TRUE	Fructose and mannose metabolism	5.3.1.8	0	0		[c] : C00275 <==> f6p-B
R_PMANM	D-Mannose 6-phosphate 1,6-phos	TRUE	Fructose and mannose metabolism	5.4.2.8	0	0	0	[c] : C00636 <==> C00275
R_R01786	ATP:alpha-D-glucose 6-phosphot	TRUE	Galactose metabolism	2.7.1.1	-1000	-1000		[c] : C00002 + C00267 <==> C00008 + C00668
R_R01786	ATP:alpha-D-glucose 6-phosphot	TRUE	Galactose metabolism	2.7.1.2	-1000	-1000		[c] : C00002 + C00267 <==> C00008 + C00668
R_GALK	ATP:D-galactose 1-phosphotrans	FALSE	Galactose metabolism	2.7.1.6	0	0		[c] : C00002 + C00124 --> C00008 + C00446 + C00080
R_GALUi	UTP:alpha-D-glucose-1-phosphat	FALSE	Galactose metabolism	2.7.7.9	0	0.1	0	[c] : C00103 + C00080 + C00075 --> C00013 + C00029
R_R01678	Lactose galactohydrolase	TRUE	Galactose metabolism	3.2.1.108	0	0		[c] : C00243 + C00001 <==> C00267 + C00124
R_GALS3	melibiose galactohydrolase	FALSE	Galactose metabolism	3.2.1.20	0	0		[c] : C00001 + C05402 --> C00124 + C00267
R_SUCR	alpha-D-Glucoside glucohydrolas	FALSE	Galactose metabolism	3.2.1.20	0	0.1		[c] : C00001 + C00089 --> C10906 + C00267
R_GALS3	melibiose galactohydrolase	FALSE	Galactose metabolism	3.2.1.22	0	0		[c] : C00001 + C05402 --> C00124 + C00267
R_R01678	Lactose galactohydrolase	TRUE	Galactose metabolism	3.2.1.23	0	0		[c] : C00243 + C00001 <==> C00267 + C00124
R_GALCTNL	D-Galactonate hydro-lyase	FALSE	Galactose metabolism	4.2.1.6	0	0	0	[c] : C00880 --> C01216 + C00001
R_UDPG4E	UDPglucose 4-epimerase	TRUE	Galactose metabolism	5.1.3.2	0	0	0	[c] : C00029 <==> C00052
R_R08094	3-hydroxy-5-methylhex-4-enoyl-(	TRUE	Geraniol degradation	1.1.1.35	0	0		[c] : C16469 + C00003 <==> C16471 + C00004 + C00080
R_R08092	.	TRUE	Geraniol degradation	1.3.99.-	0	0		[c] : C16470 + C00016 <==> C16468 + C01352
R_R08089	.	TRUE	Geraniol degradation	1.3.99.-	0	0		[c] : C16464 + C00028 <==> C01920 + C00030
R_R08091	7-methyl-3-oxo-6-octenoyl-CoA:a	TRUE	Geraniol degradation	2.3.1.16	0	0		[c] : C16466 + C00010 <==> C16470 + C00024
R_R08095	3-methylcrotonyl-CoA:acetyl-CoA	TRUE	Geraniol degradation	2.3.1.16	0	0		[c] : C16471 + C00010 <==> C03069 + C00024
R_R08093	3-hydroxy-5-methylhex-4-enoyl-(	TRUE	Geraniol degradation	4.2.1.17	0	0		[c] : C16468 + C00001 <==> C16469
R_SSALx	Succinate-semialdehyde:NAD+ ox	FALSE	Glutamate metabolism	1.2.1.16	0	0.1		[c] : C00001 + C00003 + C00232 --> 2 C00080 + C00004 + C00042
R_SSALy	Succinate-semialdehyde:NADP+ (	FALSE	Glutamate metabolism	1.2.1.16	0	0.1	0	[c] : C00001 + C00006 + C00232 --> 2 C00080 + C00005 + C00042
R_SSALx	Succinate-semialdehyde:NAD+ ox	FALSE	Glutamate metabolism	1.2.1.24	0	0.1		[c] : C00001 + C00003 + C00232 --> 2 C00080 + C00004 + C00042
R_GLUSy	L-Glutamate:NADP+ oxidoreducta	FALSE	Glutamate metabolism	1.4.1.13	0	0.1		[c] : C00026 + C00064 + C00080 + C00005 --> 2 C00025 + C00006
R_GLUSx	L-glutamate:NAD+ oxidoreductas	FALSE	Glutamate metabolism	1.4.1.14	0	0.1	0	[c] : C00026 + C00064 + C00080 + C00004 --> 2 C00025 + C00003
R_GLUDx	L-Glutamate:NAD+ oxidoreductas	TRUE	Glutamate metabolism	1.4.1.2	961.6972	0.1	431.73093	[c] : C00025 + C00001 + C00003 <==> C00026 + C00080 + C00004 + C01342
R_GLUDx	L-Glutamate:NAD+ oxidoreductas	TRUE	Glutamate metabolism	1.4.1.3	961.6972	0.1	431.73093	[c] : C00025 + C00001 + C00003 <==> C00026 + C00080 + C00004 + C01342
R_GLUDym	L-Glutamate:NADP+ oxidoreducta	TRUE	Glutamate metabolism	1.4.1.3	-1000	0.6		[c] : C00025 + C00001 + C00006 <==> C00026 + C00080 + C00005 + C01342
R_GLUDym	L-Glutamate:NADP+ oxidoreducta	TRUE	Glutamate metabolism	1.4.1.4	-1000	0.6		[c] : C00025 + C00001 + C00006 <==> C00026 + C00080 + C00005 + C01342
R_GLUDx	L-Glutamate:NAD+ oxidoreductas	TRUE	Glutamate metabolism	1.4.1.4	961.6972	0.1	431.73093	[c] : C00025 + C00001 + C00003 <==> C00026 + C00080 + C00004 + C01342
R_P5CD	L-1-Pyrroline-5-carboxylate:NAD	FALSE	Glutamate metabolism	1.5.1.12	0	1000	-5.2507303	[c] : C03912 + 2 C00001 + C00003 --> C00025 + C00080 + C00004
R_R00708	L-1-Pyrroline-5-carboxylate:NAD	TRUE	Glutamate metabolism	1.5.1.12	-4.042004	-1000		[c] : C03912 + C00006 + 2 C00001 <==> C00025 + C00005 + C00080
R_GLUPRT	5-phosphoribosylamine:diphosph	FALSE	Glutamate metabolism	2.4.2.14	9.3910951	6.00E-11	12.1979465	[c] : C00064 + C00001 + C00119 --> C00025 + C00013 + C03090
R_GF6PTA	L-Glutamine:D-fructose-6-phosph	FALSE	Glutamate metabolism	2.6.1.16	0.0384953	5.00E-12	0.05000695	[c] : C05345 + C00064 --> C00352 + C00025

R_ABTArm	4-Aminobutanoate:2-oxoglutarat	TRUE	Glutamate metabolism	2.6.1.19	0	0.2	0	[c] : C00334 + C00026 <==> C00025 + C00232
R_GLUR	L-Glutamate racemase	TRUE	Glutamate metabolism	5.1.1.3	0	-1.50E-11		[c] : C00217 <==> C00025
R_GLUTRS	L-Glutamate:tRNA(Glu) ligase (AM	FALSE	Glutamate metabolism	6.1.1.17	0	2.80E-10	0	[c] : C00002 + C00025 + C01641 --> C00020 + C02987 + C00013
R_GLUTRS	L-Glutamate:tRNA(Glu) ligase (AM	FALSE	Glutamate metabolism	6.1.1.24	0	2.80E-10	0	[c] : C00002 + C00025 + C01641 --> C00020 + C02987 + C00013
R_GLNS	L-Glutamate:ammonia ligase (AD	FALSE	Glutamate metabolism	6.3.1.2	42.29953	0.3	48.2844654	[c] : C00002 + C00025 + C01342 --> C00008 + C00064 + C00080 + C00009
R_NADS2	Deamido-NAD+:L-glutamine amid	FALSE	Glutamate metabolism	6.3.5.1	0.052546	0		[c] : C00002 + C00857 + C00064 + C00001 --> C00020 + C00025 + C00080 + C00003 + C0
R_GMPS2	Xanthosine-5'-phosphate:L-glutar	FALSE	Glutamate metabolism	6.3.5.2	0	0	6.96121817	[c] : C00002 + C00064 + C00001 + C00655 --> C00020 + C00025 + C00144 + 2 C00080 + C
R_CBPSn	hydrogen-carbonate:L-glutamine	FALSE	Glutamate metabolism	6.3.5.5	11.512011	1.50E-11	0	[c] : 2 C00002 + C00064 + C00001 + C01353 --> 2 C00008 + C00169 + C00025 + 2 C00080
R_GLNTRAT	Glu-tRNA(Gln):L-glutamine amid	FALSE	Glutamate metabolism	6.3.5.7	0	0		[c] : C00002 + C00064 + glutrna_LPAREN_gln_RPAREN_ + C00001 --> C00008 + C02282 +
R_ICDHyr	Isocitrate:NADP+ oxidoreductase	TRUE	Glutathione metabolism	1.1.1.42	669.17303	-96.810791	26.0286951	[c] : C00311 + C00006 <==> C00026 + C00011 + C00005
R_GND	6-phospho-D-gluconate:NADP+ 2	FALSE	Glutathione metabolism	1.1.1.44	0	0.1		[c] : C00345 + C00006 --> C00011 + C00005 + C00199
R_R02736	beta-D-Glucose-6-phosphate:NAD	TRUE	Glutathione metabolism	1.1.1.49	0	0.1	1000	[c] : C01172 + C00006 <==> C01236 + C00005 + C00080
R_GTHPe	glutathione:hydrogen-peroxide o	TRUE	Glutathione metabolism	1.11.1.9	0	0		[e] : 2 C00051 + C00027 <==> C00127 + 2 C00001
R_R08359	S-adenosylmethioninamine:cadav	TRUE	Glutathione metabolism	2.5.1.16	0	0		[c] : C01137 + C01672 <==> C00170 + C16565
R_SPMS	S-adenosylmethioninamine:putre	FALSE	Glutathione metabolism	2.5.1.16	0	5.00E-12		[c] : C01137 + C00134 --> C00170 + C00080 + C00315
R_R04951	.	TRUE	Glutathione metabolism	3.4.11.1	0	0		[c] : C05729 + C00001 <==> C05726 + C00037
R_AMPTASE	membrane alanyl aminopeptidase	FALSE	Glutathione metabolism	3.4.11.1	0	0	0	[c] : C01419 + C00001 --> C00097 + C00037
R_R04951	.	TRUE	Glutathione metabolism	3.4.11.2	0	0		[c] : C05729 + C00001 <==> C05726 + C00037
R_AMPTASE	membrane alanyl aminopeptidase	FALSE	Glutathione metabolism	3.4.11.2	0	0	0	[c] : C01419 + C00001 --> C00097 + C00037
R_R04951	.	TRUE	Glutathione metabolism	3.4.11.23	0	0		[c] : C05729 + C00001 <==> C05726 + C00037
R_AMPTASE	membrane alanyl aminopeptidase	FALSE	Glutathione metabolism	3.4.11.23	0	0	0	[c] : C01419 + C00001 --> C00097 + C00037
R_R04951	.	TRUE	Glutathione metabolism	3.4.13.3	0	0		[c] : C05729 + C00001 <==> C05726 + C00037
R_AMPTASE	membrane alanyl aminopeptidase	FALSE	Glutathione metabolism	3.4.13.3	0	0	0	[c] : C01419 + C00001 --> C00097 + C00037
R_GLYCDx	glycerol:NAD+ 2-oxidoreductase	FALSE	Glycerolipid metabolism	1.1.1.6	0	191.521582		[c] : C00116 + C00003 --> C01227 + C00080 + C00004
R_R01752	D-Glyceraldehyde:NAD+ oxidored	TRUE	Glycerolipid metabolism	1.2.1.3	0	0.1		[c] : C00577 + C00003 + C00001 <==> C00258 + C00004 + C00080
R_R02241	acyl-CoA:1-acyl-sn-glycerol-3-ph	TRUE	Glycerolipid metabolism	2.3.1.51	0	0		[c] : pa_Hp_pa_hs_pa_SC_pa_EC_pa_SA + C00010 <==> 1ag3p_SC + C00040
R_DHAK	ATP:glycerone phosphotransferas	FALSE	Glycerolipid metabolism	2.7.1.29	0	191.521582	0	[c] : C00002 + C01227 --> C00008 + C00111 + C00080
R_GLYKm	ATP:glycerol 3-phosphotransfera	FALSE	Glycerolipid metabolism	2.7.1.30	0	0.1	0	[c] : C00002 + C00116 --> C00008 + C00623 + C00080
R_GLYCK	ATP:(R)-glycerate 3-phosphotran	FALSE	Glycerolipid metabolism	2.7.1.31	0	0.1	0	[c] : C00002 + C00258 --> C00197 + C00008 + C00080
R_R02687	1,2-Diacyl-sn-glycerol acylhydrol	TRUE	Glycerolipid metabolism	3.1.1.3	0	0		[c] : 12dgr_SC_12dgr_EC + C00001 <==> mag_hs + C00162
R_R02250	Triacylglycerol acylhydrolase	TRUE	Glycerolipid metabolism	3.1.1.3	0	0		[c] : triglyc_SC_tag_hs + C00001 <==> 12dgr_SC_12dgr_EC + C00162
R_R03616	Galactosylglycerol galactohydrola	TRUE	Glycerolipid metabolism	3.2.1.23	0	0		[c] : C05401 + C00001 <==> C01582 + C00116
R_G3PD1	sn-Glycerol-3-phosphate:NAD+ 2	TRUE	Glycerophospholipid metabolism	1.1.1.8	998.5622	0.2	312.481575	[c] : C00623 + C00003 <==> C00111 + C00080 + C00004
R_G3PD2	sn-Glycerol-3-phosphate:NADP+	TRUE	Glycerophospholipid metabolism	1.1.1.94	-1000	-0.1	-320.41018	[c] : C00623 + C00006 <==> C00111 + C00080 + C00005
R_G3PD1	sn-Glycerol-3-phosphate:NAD+ 2	TRUE	Glycerophospholipid metabolism	1.1.1.94	998.5622	0.2	312.481575	[c] : C00623 + C00003 <==> C00111 + C00080 + C00004
R_G3PDm	sn-Glycerol-3-phosphate:(accepto	FALSE	Glycerophospholipid metabolism	1.1.5.3	1.4377984	0		[c] : C00016 + C00623 --> C00111 + C01352
R_R02056	S-Adenosyl-L-methionine:phosph	TRUE	Glycerophospholipid metabolism	2.1.1.17	0	0		[c] : C00019 + pe_EC_pe_SC_pe_HP_pe_hs_pe_SA <==> C00021 + C01241
R_PMETM_S	S-Adenosyl-L-methionine:phosph	FALSE	Glycerophospholipid metabolism	2.1.1.71	0	0		[c] : C00019 + 0.01 C04308 --> C00021 + C00080 + 0.01 C00157
R_R03424	S-Adenosyl-L-methionine:phosph	TRUE	Glycerophospholipid metabolism	2.1.1.71	-0.016926	-1.94365234		[c] : C00019 + C01241 <==> C00021 + C04308
R_R02241	acyl-CoA:1-acyl-sn-glycerol-3-ph	TRUE	Glycerophospholipid metabolism	2.3.1.51	0	0		[c] : pa_Hp_pa_hs_pa_SC_pa_EC_pa_SA + C00010 <==> 1ag3p_SC + C00040
R_DASYNm	CTP:phosphatidate cytidyltransfe	TRUE	Glycerophospholipid metabolism	2.7.7.41	0	0	0	[c] : C00063 + C00080 + 0.01 C00416 <==> 0.01 cdpdag_SC + C00013
R_CLPNS_E	.	TRUE	Glycerophospholipid metabolism	2.7.8.-	0	0		[c] : 0.04 pg_EC <==> 0.02 C05980 + C00116
R_CLS_hs	CDP-diacylglycerol:phosphatidylg	FALSE	Glycerophospholipid metabolism	2.7.8.-	0	0		[c] : cdpdag_hs + pglyc_hs --> clpn_hs + C00055 + C00080
R_PGPPT	CDP-diacylglycerol:sn-glycerol-3-	FALSE	Glycerophospholipid metabolism	2.7.8.5	0	0	-0.0800869	[c] : cdpdag_hs + C00623 --> C00055 + C00080 + pgp_hs
R_PSSA_HP	CDP-diacylglycerol:L-serine 3-ph	TRUE	Glycerophospholipid metabolism	2.7.8.8	0	0		[c] : cdpdag_HP + C00716 <==> C00055 + C00080 + ps_HP
R_GPDDA1	sn-Glycero-3-phosphocholine gly	FALSE	Glycerophospholipid metabolism	3.1.4.2	0	0		[c] : C00670 + C00001 --> C00114 + C00623 + C00080
R_GPDDA2	sn-Glycero-3-phosphoethanolami	FALSE	Glycerophospholipid metabolism	3.1.4.2	0	0		[c] : C01233 + C00001 --> C00189 + C00623 + C00080
R_GPDDA2	sn-Glycero-3-phosphoethanolami	FALSE	Glycerophospholipid metabolism	3.1.4.46	0	0		[c] : C01233 + C00001 --> C00189 + C00623 + C00080
R_GPDDA1	sn-Glycero-3-phosphocholine gly	FALSE	Glycerophospholipid metabolism	3.1.4.46	0	0		[c] : C00670 + C00001 --> C00114 + C00623 + C00080
R_PSD_SA	Phsophatidyl-L-serine carboxy-ly	FALSE	Glycerophospholipid metabolism	4.1.1.65	0	0	0	[c] : C00080 + 0.02 ps_SA --> C00011 + 0.02 pe_SA
R_HSDxi	L-Homoserine:NAD+ oxidoreduct	FALSE	Glycine, serine and threonine metabo	1.1.1.3	0	1000	1000	[c] : C00441 + C00080 + C00004 --> C00263 + C00003
R_HSDy	L-Homoserine:NADP+ oxidoredu	TRUE	Glycine, serine and threonine metabo	1.1.1.3	-2.963	1000	989.248505	[c] : C00263 + C00006 <==> C00441 + C00080 + C00005
R_PGCD	3-Phospho-D-glycerate:NAD+ 2-o	FALSE	Glycine, serine and threonine metabo	1.1.1.95	0	0.1	188.360217	[c] : C00197 + C00003 --> C03232 + C00080 + C00004
R_ASAD	L-Aspartate-4-semialdehyde:NAD	TRUE	Glycine, serine and threonine metabo	1.2.1.11	-2.963	8.00E-11	-320.02552	[c] : C00441 + C00006 + C00009 <==> C03082 + C00080 + C00005
R_BETALDH	p-Cumic alcohol:NADP+ oxidored	FALSE	Glycine, serine and threonine metabo	1.2.1.8	0	0	0	[c] : C00576 + C00001 + C00006 --> C00719 + 2 C00080 + C00005
R_BETALDH	p-cumic alcohol:NAD+ oxidoredu	FALSE	Glycine, serine and threonine metabo	1.2.1.8	0	0	0	[c] : C00576 + C00001 + C00003 --> C00719 + 2 C00080 + C00004
R_GCCa	glycine:lipoylprotein oxidoreduct	FALSE	Glycine, serine and threonine metabo	1.4.4.2	0.1986164	0.1	152.959044	[c] : C00037 + C00080 + C02051 --> C01242 + C00011
R_GCCcm	dihydrolipoylprotein:NAD+ oxidc	TRUE	Glycine, serine and threonine metabo	1.8.1.4	0.1986164	0.1	0	[c] : C02972 + C00003 <==> C00080 + C02051 + C00004
R_R02056	S-Adenosyl-L-methionine:phosph	TRUE	Glycine, serine and threonine metabo	2.1.1.17	0	0		[c] : C00019 + pe_EC_pe_SC_pe_HP_pe_hs_pe_SA <==> C00021 + C01241

R_R03424	S-Adenosyl-L-methionine:phosph	TRUE	Glycine, serine and threonine metabo	2.1.1.71	-0.016926	-1.94365234		[c] : C00019 + C01241 <==> C00021 + C04308
R_PMETM_S	S-Adenosyl-L-methionine:phosph	FALSE	Glycine, serine and threonine metabo	2.1.1.71	0	0		[c] : C00019 + 0.01 C04308 --> C00021 + C00080 + 0.01 C00157
R_GHMT2r	5,10-Methylenetetrahydrofolate:g	TRUE	Glycine, serine and threonine metabo	2.1.2.1	20.791836	96.210791	179.709014	[c] : C00716 + C00101 <==> C00037 + C00001 + C00143
R_GCCbim	S-aminomethyldihydrolipoylprot	FALSE	Glycine, serine and threonine metabo	2.1.2.10	0.1986164	0.1	0	[c] : C01242 + C00101 --> C02972 + C00143 + C01342
R_R06978	L-2,4-diaminobutyrate acetyltran	TRUE	Glycine, serine and threonine metabo	2.3.1.178	0	0		[c] : C03283 + C00024 <==> C06442 + C00010
R_PSERT	3-Phosphoserine:2-oxoglutarate a	FALSE	Glycine, serine and threonine metabo	2.6.1.52	0	0.1	188.360217	[c] : C03232 + C00025 --> C00026 + C01005
R_R06977	L-2,4-diaminobutyrate:2-oxoglut	TRUE	Glycine, serine and threonine metabo	2.6.1.76	0	0		[c] : C00025 + C00441 <==> C00026 + C03283
R_GLYCK	ATP:(R)-glycerate 3-phosphotran	FALSE	Glycine, serine and threonine metabo	2.7.1.31	0	0.1	0	[c] : C00002 + C00258 --> C00197 + C00008 + C00080
R_HSK	ATP:L-homoserine O-phosphotra	FALSE	Glycine, serine and threonine metabo	2.7.1.39	333.78997	709.695801	10.7514953	[c] : C00002 + C00263 --> C00008 + C00080 + C01102
R_ASPK	ATP:L-aspartate 4-phosphotransf	TRUE	Glycine, serine and threonine metabo	2.7.2.4	2.9630004	-8.00E-11	320.025524	[c] : C00049 + C00002 <==> C03082 + C00008
R_PSSA_HP	CDP-diacylglycerol:L-serine 3-ph	TRUE	Glycine, serine and threonine metabo	2.7.8.8	0	0		[c] : cdpdag_HP + C00716 <==> C00055 + C00080 + ps_HP
R_PSP_L	L-O-Phosphoserine phosphohydr	FALSE	Glycine, serine and threonine metabo	3.1.3.3	0	0.1	188.360217	[c] : C00001 + C01005 --> C00009 + C00716
R_PSD_SA	Phsophatidyl-L-serine carboxy-ly	FALSE	Glycine, serine and threonine metabo	4.1.1.65	0	0	0	[c] : C00080 + 0.02 ps_SA --> C00011 + 0.02 pe_SA
R_R06979	Ectoine hydro-lyase	TRUE	Glycine, serine and threonine metabo	4.2.1.108	0	0		[c] : C06442 <==> C00001 + C06231
R_R00891	L-Serine hydro-lyase (adding hon	TRUE	Glycine, serine and threonine metabo	4.2.1.22	11.068527	290.204199		[c] : C00716 + C00297 <==> C00097 + C00001
R_CYSTS	L-serine hydro-lyase (adding hon	FALSE	Glycine, serine and threonine metabo	4.2.1.22	0	0	2.17530254	[c] : C05330 + C00716 --> cyst-L + C00001
R_THRS	O-phospho-L-homoserine phosph	FALSE	Glycine, serine and threonine metabo	4.2.3.1	333.78997	709.695801	10.7514953	[c] : C00001 + C01102 --> C00009 + C00188
R_SERD_Lr	L-serine ammonia-lyase	TRUE	Glycine, serine and threonine metabo	4.3.1.17	-35.80613	-386.31499		[c] : C00716 <==> C01342 + C00022
R_SERD_Lr	L-serine ammonia-lyase	TRUE	Glycine, serine and threonine metabo	4.3.1.19	-35.80613	-386.31499		[c] : C00716 <==> C01342 + C00022
R_THRD_Lm	L-threonine ammonia-lyase (2-ox	FALSE	Glycine, serine and threonine metabo	4.3.1.19	329.15129	709.695801	0	[c] : C00188 --> C00109 + C01342
R_SERTRS	L-Serine:tRNA(Ser) ligase (AMP-f	FALSE	Glycine, serine and threonine metabo	6.1.1.11	0	0	0	[c] : C00002 + C00716 + C01650 --> C00020 + C00013 + C02553
R_GLYTRS	Glycine:tRNA(Gly) ligase (AMP-fo	FALSE	Glycine, serine and threonine metabo	6.1.1.14	0	0	0	[c] : C00002 + C00037 + C01642 --> C00020 + C02412 + C00013
R_THRTRSm	L-Threonine:tRNA(Thr) ligase (A	FALSE	Glycine, serine and threonine metabo	6.1.1.3	0	0	0	[c] : C00002 + C00188 + C01651 --> C00020 + C00013 + C02992
R_ALCD2if	Ethanol:NAD+ oxidoreductase	FALSE	Glycolysis / Gluconeogenesis	1.1.1.1	0	0.2		[c] : C00469 + C00003 --> C00084 + C00080 + C00004
R_ALCD2if	Ethanol:NAD+ oxidoreductase	FALSE	Glycolysis / Gluconeogenesis	1.1.1.71	0	0.2		[c] : C00469 + C00003 --> C00084 + C00080 + C00004
R_GAPD	D-glyceraldehyde-3-phosphate:N	TRUE	Glycolysis / Gluconeogenesis	1.2.1.12	-326.5566	-0.1	558.84991	[c] : C00118 + C00003 + C00009 <==> C00236 + C00080 + C00004
R_GAPD_LP	D-glyceraldehyde-3-phosphate:N	TRUE	Glycolysis / Gluconeogenesis	1.2.1.13	1000	-0.1		[c] : C00118 + C00006 + C00009 <==> C00236 + C00080 + C00005
R_ALDD2x	Acetaldehyde:NAD+ oxidoreducta	FALSE	Glycolysis / Gluconeogenesis	1.2.1.3	0	0.1	0	[c] : C00084 + C00001 + C00003 --> C00033 + 2 C00080 + C00004
R_ALDD2x	Acetaldehyde:NAD+ oxidoreducta	FALSE	Glycolysis / Gluconeogenesis	1.2.1.5	0	0.1	0	[c] : C00084 + C00001 + C00003 --> C00033 + 2 C00080 + C00004
R_GAPD_LP	D-glyceraldehyde-3-phosphate:N	TRUE	Glycolysis / Gluconeogenesis	1.2.1.59	1000	-0.1		[c] : C00118 + C00006 + C00009 <==> C00236 + C00080 + C00005
R_GAPD	D-glyceraldehyde-3-phosphate:N	TRUE	Glycolysis / Gluconeogenesis	1.2.1.59	-326.5566	-0.1	558.84991	[c] : C00118 + C00003 + C00009 <==> C00236 + C00080 + C00004
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Glycolysis / Gluconeogenesis	1.2.4.1	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_R03270	.	TRUE	Glycolysis / Gluconeogenesis	1.2.4.1	696.14778	96.910791		[c] : C05125 + C15972 <==> C16255 + C00068
R_R07618	enzyme N6-(dihydrolipoyl)lysine	TRUE	Glycolysis / Gluconeogenesis	1.8.1.4	-654.716	-0.1	0	[c] : C15973 + C00003 <==> C15972 + C00004 + C00080
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Glycolysis / Gluconeogenesis	2.2.1.6	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_R02569	acetyl-CoA:enzyme N6-(dihydroli	TRUE	Glycolysis / Gluconeogenesis	2.3.1.12	-696.1478	-96.910791		[c] : C00024 + C15973 <==> C00010 + C16255
R_R01600	ATP:beta-D-glucose 6-phosphotra	TRUE	Glycolysis / Gluconeogenesis	2.7.1.1	0	-160.501318		[c] : C00002 + C00221 <==> C00008 + C01172
R_R01786	ATP:alpha-D-glucose 6-phosphot	TRUE	Glycolysis / Gluconeogenesis	2.7.1.1	-1000	-1000		[c] : C00002 + C00267 <==> C00008 + C00668
R_R01786	ATP:alpha-D-glucose 6-phosphot	TRUE	Glycolysis / Gluconeogenesis	2.7.1.2	-1000	-1000		[c] : C00002 + C00267 <==> C00008 + C00668
R_R01600	ATP:beta-D-glucose 6-phosphotra	TRUE	Glycolysis / Gluconeogenesis	2.7.1.2	0	-160.501318		[c] : C00002 + C00221 <==> C00008 + C01172
R_PYK	ATP:pyruvate 2-O-phosphotransf	FALSE	Glycolysis / Gluconeogenesis	2.7.1.40	0	1000	944.841429	[c] : C00008 + C00080 + C00074 --> C00002 + C00022
R_R05132	Protein-N(pai)-phosphohistidine	TRUE	Glycolysis / Gluconeogenesis	2.7.1.69	0	0		[c] : C04261 + C06186 <==> C00615 + C06187
R_R02738	Protein-N(pai)-phosphohistidine	TRUE	Glycolysis / Gluconeogenesis	2.7.1.69	-0.057743	0.1		[c] : C04261 + C00267 <==> C00615 + C00668
R_R04394	Protein-N(pai)-phosphohistidine	TRUE	Glycolysis / Gluconeogenesis	2.7.1.69	0	0		[c] : C04261 + C01451 <==> C00615 + C06188
R_PGK	ATP:3-phospho-D-glycerate 1-ph	TRUE	Glycolysis / Gluconeogenesis	2.7.2.3	-673.4434	0.2	-558.84991	[c] : C00197 + C00002 <==> C00236 + C00008
R_R04780	beta-D-Fructose 1,6-bisphosphate	TRUE	Glycolysis / Gluconeogenesis	3.1.3.11	-1000	-581.564746		[c] : C05378 + C00001 <==> f6p-B + C00009
R_R05133	Arbutin 6-phosphate glucohydrol	TRUE	Glycolysis / Gluconeogenesis	3.2.1.86	0	0		[c] : C06187 + C00001 <==> C02389 + C01172
R_R05134	Salicin 6-phosphate glucohydrola	TRUE	Glycolysis / Gluconeogenesis	3.2.1.86	0	0		[c] : C06188 + C00001 <==> 2hymeph + C01172
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Glycolysis / Gluconeogenesis	4.1.1.1	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_PEPCK	GTP:oxaloacetate carboxy-lyase (	FALSE	Glycolysis / Gluconeogenesis	4.1.1.32	988.96292	0.5	0	[c] : C00044 + C00036 --> C00011 + C00035 + C00074
R_R00726	ITP:oxaloacetate carboxy-lyase (t	TRUE	Glycolysis / Gluconeogenesis	4.1.1.32	-1000	0.1		[c] : C00081 + C00036 <==> C00104 + C00074 + C00011
R_R01070	beta-D-fructose-1,6-bisphosphate	TRUE	Glycolysis / Gluconeogenesis	4.1.2.13	674.41127	-31.2202637		[c] : C05378 <==> C00111 + C00118
R_ENO	2-Phospho-D-glucerate hydro-lya	TRUE	Glycolysis / Gluconeogenesis	4.2.1.11	766.2444	-0.1	370.489693	[c] : C00631 <==> C00001 + C00074
R_R02739	alpha-D-Glucose 6-phosphate ket	TRUE	Glycolysis / Gluconeogenesis	5.1.3.15	1000	0.1		[c] : C00668 <==> C01172
R_TPI	D-glyceraldehyde-3-phosphate al	TRUE	Glycolysis / Gluconeogenesis	5.3.1.1	674.35873	160.401318	486.409291	[c] : C00111 <==> C00118
R_R02740	alpha-D-Glucose 6-phosphate ket	TRUE	Glycolysis / Gluconeogenesis	5.3.1.9	-1000	-0.1		[c] : C00668 <==> f6p-B
R_G6PI2	beta-D-Glucose 6-phosphate keto	TRUE	Glycolysis / Gluconeogenesis	5.3.1.9	1000	-160.501318	0	[c] : C01172 <==> f6p-B
R_R02739	alpha-D-Glucose 6-phosphate ket	TRUE	Glycolysis / Gluconeogenesis	5.3.1.9	1000	0.1		[c] : C00668 <==> C01172
R_PGM	2-Phospho-D-glycerate 2,3-phosp	TRUE	Glycolysis / Gluconeogenesis	5.4.2.1	-673.4434	0.2	-370.48969	[c] : C00631 <==> C00197

R_ACSm	Acetate:CoA ligase (AMP-forming	FALSE	Glycolysis / Gluconeogenesis	6.2.1.1	0	0.1	0	[c] : C00033 + C00002 + C00010 --> C00024 + C00020 + C00013
R_R07807	.	TRUE	Glycosaminoglycan degradation	3.2.1.23	0	0		[c] : G13032 + C00001 <==> G06780 + C00124
R_R07810	.	TRUE	Glycosaminoglycan degradation	3.2.1.52	0	0		[c] : G06780 + C00001 <==> G08421 + C01132
R_R07809	.	TRUE	Glycosaminoglycan degradation	3.2.1.52	0	0		[c] : G13033 + C00001 <==> G08421 + C01132
R_R06010	.	TRUE	Glycosphingolipid biosynthesis - gang	3.2.1.23	0	0		[c] : G00110 + C00001 <==> G00109 + C00124
R_R06004	.	TRUE	Glycosphingolipid biosynthesis - gang	3.2.1.52	0	0		[c] : G00109 + C00001 <==> G00108 + C01132
R_GCALDDr	Glycolaldehydedehydrogenase	TRUE	Glyoxylate and Dicarboxylate Metabo	1.2.1.21	26.935296	0.1		[c] : C00266 + C00001 + C00003 <==> C00160 + 2 C00080 + C00004
R_MDHm	(S)-malate:NAD+ oxidoreductase	TRUE	Glyoxylate and dicarboxylate metabol	1.1.1.37	-308.7728	-96.210791	0	[c] : C00711 + C00003 <==> C00080 + C00004 + C00036
R_R01747	(R)-Glycerate:NADP+ oxidoreduc	TRUE	Glyoxylate and dicarboxylate metabol	1.1.1.60	1000	1000		[c] : C00258 + C00006 <==> 2h3oppan + C00005 + C00080
R_TRSAR	(R)-Glycerate:NAD+ oxidoreducta	FALSE	Glyoxylate and dicarboxylate metabol	1.1.1.60	1000	1000		[c] : 2h3oppan + C00080 + C00004 --> C00258 + C00003
R_GLYCTO1	(S)-2-Hydroxy-acid:oxygen 2-oxid	FALSE	Glyoxylate and dicarboxylate metabol	1.1.3.15	26.935296	0.1		[c] : C00160 + C00007 --> C00048 + C00027
R_FDH	Formate:NAD+ oxidoreductase	FALSE	Glyoxylate and dicarboxylate metabol	1.2.1.2	0	0.1	0	[c] : C00058 + C00003 --> C00011 + C00004
R_MTHFD	5,10-methylenetetrahydrofolate:	TRUE	Glyoxylate and dicarboxylate metabol	1.5.1.5	19.551518	0.1		[c] : C00143 + C00006 <==> C00445 + C00005
R_CS	Citrate oxaloacetate-lyase ((pro-3	FALSE	Glyoxylate and dicarboxylate metabol	2.3.3.1	0	0.1	26.0286951	[c] : C00024 + C00001 + C00036 --> C00158 + C00010 + C00080
R_CS	Citrate oxaloacetate-lyase ((pro-3	FALSE	Glyoxylate and dicarboxylate metabol	2.3.3.3	0	0.1	26.0286951	[c] : C00024 + C00001 + C00036 --> C00158 + C00010 + C00080
R_MALS	L-Malate glyoxylate-lyase (CoA-ac	FALSE	Glyoxylate and dicarboxylate metabol	2.3.3.9	26.935296	0.2		[c] : C00024 + C00048 + C00001 --> C00010 + C00080 + C00711
R_GLYCK	ATP:(R)-glycerate 3-phosphotran	FALSE	Glyoxylate and dicarboxylate metabol	2.7.1.31	0	0.1	0	[c] : C00002 + C00258 --> C00197 + C00008 + C00080
R_FTHFD	10-Formyltetrahydrofolate amido	FALSE	Glyoxylate and dicarboxylate metabol	3.5.1.10	0	0.2	0	[c] : C00234 + C00001 --> C00058 + C00080 + C00101
R_MTHFCm	5,10-Methenyltetrahydrofolate 5-	TRUE	Glyoxylate and dicarboxylate metabol	3.5.4.9	19.551518	0.1		[c] : C00001 + C00445 <==> C00234 + C00080
R_ICL	Isocitrate glyoxylate-lyase	FALSE	Glyoxylate and dicarboxylate metabol	4.1.3.1	0	0.1	0	[c] : C00311 --> C00048 + C00042
R_R01325	citrate hydro-lyase (cis-aconitate-	TRUE	Glyoxylate and dicarboxylate metabol	4.2.1.3	-330.827	-96.810791		[c] : C00158 <==> C00417 + C00001
R_R01900	isocitrate hydro-lyase (cis-aconita	TRUE	Glyoxylate and dicarboxylate metabol	4.2.1.3	330.82697	96.810791		[c] : C00311 <==> C00417 + C00001
R_R01325	citrate hydro-lyase (cis-aconitate-	TRUE	Glyoxylate and dicarboxylate metabol	4.2.1.4	-330.827	-96.810791		[c] : C00158 <==> C00417 + C00001
R_FTHFLi	Formate:tetrahydrofolate ligase (	FALSE	Glyoxylate and dicarboxylate metabol	6.3.4.3	0.9629593	0.1		[c] : C00002 + C00058 + C00101 --> C00234 + C00008 + C00009
R_HISTP	histidinol-phosphatase	TRUE	Histidine Metabolism	3.1.3.15	1.7322873	3.50E-11	2.25031297	[c] : C00001 + C01100 <==> C00860 + C00009
R_R03012	L-Histidinol:NAD+ oxidoreductas	TRUE	Histidine metabolism	1.1.1.23	1.7322873	1.50E-11		[c] : C00860 + C00003 <==> C01929 + C00004 + C00080
R_R01163	L-Histidinal:NAD+ oxidoreductas	TRUE	Histidine metabolism	1.1.1.23	1.7322873	0		[c] : C01929 + C00001 + C00003 <==> C00135 + C00004 + C00080
R_R00069	.	TRUE	Histidine metabolism	1.14.13.-	0	0		[c] : 2 C05565 <==> C00007 + 2 C03680
R_IMACTD_	Imidazole acetaldehyde:NAD+ ox	FALSE	Histidine metabolism	1.2.1.3	0	0	0	[c] : C00001 + im4act + C00003 --> 2 C00080 + im4ac + C00004
R_R01159	S-adenosyl-L-methionine:L-histid	TRUE	Histidine metabolism	2.1.1.-	0	0		[c] : C00135 + C00019 <==> C01152 + C00021
R_R04558	.	TRUE	Histidine metabolism	2.4.2.-	1.7322873	4.50E-11		[c] : C04916 + C00064 <==> C04666 + C04677 + C00025
R_ATPPRT	1-(5-phospho-D-ribosyl)-ATP:dip	FALSE	Histidine metabolism	2.4.2.17	1.7322873	4.50E-11	2.25031297	[c] : C00002 + C00119 --> C00013 + C02739
R_HSTPT	5-Amino-2-oxopentanoate:2-oxog	FALSE	Histidine metabolism	2.6.1.9	1.7322873	4.50E-11	2.25031297	[c] : C00025 + C01267 --> C00026 + C01100
R_IZPN	4-imidazolone-5-propanoate ami	FALSE	Histidine metabolism	3.5.2.7	0	0	0	[c] : C03680 + C00001 --> C00439 + C00080
R_PRAMPC	1-(5-phospho-D-ribosyl)-AMP 1,6	FALSE	Histidine metabolism	3.5.4.19	1.7322873	4.50E-11	2.25031297	[c] : C00001 + C02741 --> C04896
R_PRATPP	Phosphoribosyl-ATP pyrophosph	FALSE	Histidine metabolism	3.6.1.31	1.7322873	4.50E-11	2.25031297	[c] : C00001 + C02739 --> C00080 + C00013 + C02741
R_R04558	.	TRUE	Histidine metabolism	4.1.3.-	1.7322873	4.50E-11		[c] : C04916 + C00064 <==> C04666 + C04677 + C00025
R_IGPDH	D-erythro-1-(Imidazol-4-yl)glyce	FALSE	Histidine metabolism	4.2.1.19	1.7322873	4.50E-11	2.25031297	[c] : C04666 --> C00001 + C01267
R_R04640	N-(5'-Phospho-D-ribosylformimi	TRUE	Histidine metabolism	5.3.1.16	1.7322873	4.50E-11	-997.74969	[c] : C04896 <==> C04916
R_HISTRS	L-Histidine:tRNA(His) ligase (AM	FALSE	Histidine metabolism	6.1.1.21	0	0	0	[c] : C00002 + C00135 + C01643 --> C00020 + C02988 + C00013
R_MMSAD3	3-Oxopropanoate:NAD+ oxidored	FALSE	Inositol phosphate metabolism	1.2.1.18	0	0.1	0	[c] : C00010 + C00222 + C00003 --> C00024 + C00011 + C00004
R_MMSAD3	3-Oxopropanoate:NAD+ oxidored	FALSE	Inositol phosphate metabolism	1.2.1.27	0	0.1	0	[c] : C00010 + C00222 + C00003 --> C00024 + C00011 + C00004
R_MI3PP	1D-myo-Inositol 3-phosphate pho	FALSE	Inositol phosphate metabolism	3.1.3.25	0	0	0	[c] : C00001 + C04006 --> C00137 + C00009
R_MI1PP	1D-myo-Inositol 1-phosphate pho	FALSE	Inositol phosphate metabolism	3.1.3.25	0	0	0	[c] : C00001 + C01177 --> C00137 + C00009
R_MI4PP	1D-myo-Inositol 4-phosphate pho	FALSE	Inositol phosphate metabolism	3.1.3.25	0	0	0	[c] : C00001 + C03546 --> C00137 + C00009
R_TPI	D-glyceraldehyde-3-phosphate al	TRUE	Inositol phosphate metabolism	5.3.1.1	674.35873	160.401318	486.409291	[c] : C00111 <==> C00118
R_R07324	1D-myo-inositol-3-phosphate lya	TRUE	Inositol phosphate metabolism	5.5.1.4	0	5.00E-12		[c] : C00668 <==> C04006
R_R06404	alpha-Pinene monooxygenase	TRUE	Limonene and pinene degradation	1.14.-.-	0	0		[c] : C09880 + C00007 + C00080 <==> C11941 + C00001
R_R06401	alpha-Pinene dehydrogenase	TRUE	Limonene and pinene degradation	1.14.-.-	0	0		[c] : C09880 + C00030 <==> C11938 + C00001 + C00028
R_R06400	(1S,4R)-1-hydroxy-2-oxolimonen	TRUE	Limonene and pinene degradation	1.14.13.-	0	0		[c] : C11937 + C00005 + C00007 <==> C11405 + C00006 + C01328
R_R06406	alpha-Pinene monooxygenase	TRUE	Limonene and pinene degradation	1.14.13.-	0	0		[c] : C09880 + C00004 + C00080 + C00007 <==> apnnox + C00003 + C00001
R_R06398	(+)-limonene,NADH:oxygen oxido	TRUE	Limonene and pinene degradation	1.14.13.-	0	0		[c] : C06099 + C00004 + C00007 <==> C07271 + C00003 + C01328
R_PYLALDQ	Aldehyde:NAD+ oxidoreductase	FALSE	Limonene and pinene degradation	1.2.1.3	0	0	0	[c] : C00001 + C00003 + pylald --> 2 C00080 + C00004 + peracd
R_C2M26D(	cis-2-Methyl-5-isopropylhexa-2,5	TRUE	Limonene and pinene degradation	4.2.1.17	0	0	0	[c] : c2m26dcoa + C00001 <==> 3h26dm5coa
R_T2M26D(	trans-2-Methyl-5-isopropylhexa-	TRUE	Limonene and pinene degradation	4.2.1.17	0	0	0	[c] : C00001 + t2m26dcoa <==> 3h26dm5coa
R_R07766	octanoyl-[acp]:protein N6-octano	TRUE	Lipoic acid metabolism	2.3.1.181	1000	0.1		[c] : C05752 + C03688 <==> C16236 + apoACP_ACP
R_R07769	lipoyl-[acp]:protein N6-lipoyltran	TRUE	Lipoic acid metabolism	2.3.1.181	-1000	-0.1		[c] : C16239 + C03688 <==> C16237 + apoACP_ACP
R_R07767	protein N6-(octanoyl)lysine:sulfu	TRUE	Lipoic acid metabolism	2.8.1.8	1000	0.1		[c] : C16236 + 2 C00087 + 2 C00019 <==> C16237 + 2 C00073 + 2 C05198
R_R07768	octanoyl-[acp]:sulfur sulfurtransf	TRUE	Lipoic acid metabolism	2.8.1.8	-1000	-0.1		[c] : C05752 + 2 C00087 + 2 C00019 <==> C16239 + 2 C00073 + 2 C05198

R_HSDy	L-Homoserine:NADP+ oxidoredu	TRUE	Lysine biosynthesis	1.1.1.3	-2.963	1000	989.248505	[c] : C00263 + C00006 <==> C00441 + C00080 + C00005
R_HSDxi	L-Homoserine:NAD+ oxidoreduct	FALSE	Lysine biosynthesis	1.1.1.3	0	1000	1000	[c] : C00441 + C00080 + C00004 --> C00263 + C00003
R_ASAD	L-Aspartate-4-semialdehyde:NAD	TRUE	Lysine biosynthesis	1.2.1.11	-2.963	8.00E-11	-320.02552	[c] : C00441 + C00006 + C00009 <==> C03082 + C00080 + C00005
R_DHDPRy	2,3,4,5-Tetrahydrodipicolinate:N	FALSE	Lysine biosynthesis	1.3.1.26	0	1000	309.274029	[c] : C03340 + C00080 + C00005 --> C00006 + C03972
R_R04198	2,3,4,5-Tetrahydrodipicolinate:N	TRUE	Lysine biosynthesis	1.3.1.26	0	1000		[c] : C03972 + C00003 <==> C03340 + C00004 + C00080
R_THDPS	Succinyl-CoA:2,3,4,5-tetrahydrop	FALSE	Lysine biosynthesis	2.3.1.117	0	0	0	[c] : C00001 + C00091 + C03972 --> C00010 + C04462
R_ASPK	ATP:L-aspartate 4-phosphotransf	TRUE	Lysine biosynthesis	2.7.2.4	2.9630004	-8.00E-11	320.025524	[c] : C00049 + C00002 <==> C03082 + C00008
R_SDPDS	N-Succinyl-LL-2,6-diaminoheptan	FALSE	Lysine biosynthesis	3.5.1.18	0	0		[c] : C00001 + C04421 --> C00666 + C00042
R_DAPDC	meso-2,6-Diaminoheptanedioate	FALSE	Lysine biosynthesis	4.1.1.20	0	1.50E-11	309.274029	[c] : C00680 + C00080 --> C00011 + C00047
R_DHDPS	L-Aspartate-4-semialdehyde hydr	FALSE	Lysine biosynthesis	4.2.1.52	0	0	309.274029	[c] : C00441 + C00022 --> C03340 + C00080 + 2 C00001
R_DAPE	LL-2,6-Diaminoheptanedioate 2-e	TRUE	Lysine biosynthesis	5.1.1.7	0	0	309.274029	[c] : C00666 <==> C00680
R_LYSTRS	L-Lysine:tRNALys ligase (AMP-fo	FALSE	Lysine biosynthesis	6.1.1.6	0	0.1	301.122895	[c] : C00002 + C00047 + C01646 --> C00020 + C01646 + C00013
R_UGMDDS	UDP-N-acetylmuramoyl-L-alanyl-	FALSE	Lysine biosynthesis	6.3.2.10	0	2.25E-11		[c] : C00993 + C00002 + C04877 --> C00008 + C00080 + C00009 + C04882
R_UAAGDS	UDP-N-acetylmuramoyl-L-alanyl-	FALSE	Lysine biosynthesis	6.3.2.13	0	1.50E-11	0	[c] : C00680 + C00002 + C00692 --> C00008 + C00080 + C00009 + C04877
R_HACD1	(S)-3-Hydroxybutanoyl-CoA:NAD	TRUE	Lysine degradation	1.1.1.35	0	0	-0.0132768	[c] : C00332 + C00080 + C00004 <==> 3hbcoa + C00003
R_TMABADI	4-Trimethylammoniobutanal:NAI	FALSE	Lysine degradation	1.2.1.3	0	0		[c] : 4tmeabut + C00001 + C00003 --> 4tmeabutn + 2 C00080 + C00004
R_TMABADI	4-Trimethylammoniobutanal:NAI	FALSE	Lysine degradation	1.2.1.47	0	0		[c] : 4tmeabut + C00001 + C00003 --> 4tmeabutn + 2 C00080 + C00004
R_R01940	2-Oxoadipate:lipoamde 2-oxidore	TRUE	Lysine degradation	1.2.4.2	-1000	-0.1		[c] : C00322 + C15972 <==> C06157 + C00011
R_R02488	Glutaryl-CoA:(acceptor) 2,3-oxid	TRUE	Lysine degradation	1.3.99.7	0	0		[c] : C00527 + C00028 <==> b2coa + C00030 + C00011
R_ACACT1m	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Lysine degradation	2.3.1.16	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_R02571	Glutaryl-CoA:dihydrolipoamide S	TRUE	Lysine degradation	2.3.1.61	1000	0.1		[c] : C00527 + C15973 <==> C00010 + C06157
R_ACACT1m	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Lysine degradation	2.3.1.9	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_ECOAH1	(S)-3-Hydroxybutanoyl-CoA hydr	TRUE	Lysine degradation	4.2.1.17	0	0	-0.0132768	[c] : 3hbcoa <==> b2coa + C00001
R_LYSAM	L-Lysine 2,3-aminomutase	TRUE	Lysine degradation	5.4.3.2	0	0	0	[c] : C00047 <==> C01142
R_R06983	S-(hydroxymethyl)glutathione de	TRUE	Methane metabolism	1.1.1.284	0	0		[c] : C14180 + C00003 <==> Sfglutth + C00004 + C00080
R_PRDX	Hydorogen-peroxide:hydrogen-p	FALSE	Methane metabolism	1.11.1.6	0	0		[c] : C00027 + C00132 --> C00067 + 2 C00001
R_PRDX	Hydorogen-peroxide:hydrogen-p	FALSE	Methane metabolism	1.11.1.7	0	0		[c] : C00027 + C00132 --> C00067 + 2 C00001
R_R05623	.	TRUE	Methane metabolism	1.14.13.-	0	0		[c] : C00565 + C00004 + C00080 + C00007 <==> C01104 + C00003 + C00001
R_FDH	Formate:NAD+ oxidoreductase	FALSE	Methane metabolism	1.2.1.2	0	0.1	0	[c] : C00058 + C00003 --> C00011 + C00004
R_R00296	Carbon-monoxide:(acceptor) oxid	TRUE	Methane metabolism	1.2.99.2	0	0		[c] : C00237 + C00001 + C00028 <==> C00011 + C00030
R_MTHFR2	5-methyltetrahydrofolate:NAD+ (	FALSE	Methane metabolism	1.5.1.20	0	192.321582	332.050472	[c] : C00080 + C00143 + C00004 --> C00440 + C00003
R_MTHFR3	5-methyltetrahydrofolate:NADP+	FALSE	Methane metabolism	1.5.1.20	0.9623818	0.1		[c] : 2 C00080 + C00143 + C00005 --> C00440 + C00006
R_GHMT2r	5,10-Methylenetetrahydrofolate:g	TRUE	Methane metabolism	2.1.2.1	20.791836	96.210791	179.709014	[c] : C00716 + C00101 <==> C00037 + C00001 + C00143
R_R02026	O-acetyl-L-homoserine acetate-ly	TRUE	Methionine metabolism	.	-990.6072	-709.795801		[c] : C01077 + C05529 + C00342 + C00080 <==> C05330 + C00094 + C00343 + C00033
R_METS	5-Methyltetrahydrofolate:L-homo	FALSE	Methionine metabolism	2.1.1.13	0	192.421582	330.800298	[c] : C00440 + C05330 --> C00080 + C00073 + C00101
R_FMETTRS	10-Formyltetrahydrofolate:L-met	FALSE	Methionine metabolism	2.1.2.9	0	0	0	[c] : C00234 + C02430 --> C03294 + C00080 + C00101
R_HSERTA	Acetyl-CoA:L-homoserine O-acety	TRUE	Methionine metabolism	2.3.1.31	-330.827	-709.695801	0	[c] : C00024 + C00263 <==> C01077 + C00010
R_SHSL2r	O4-succinyl-L-homoserine:hydro	TRUE	Methionine metabolism	2.5.1.-	329.15129	709.695801		[c] : C00297 + C01118 <==> C00080 + C05330 + C00042
R_SPMS	S-adenosylmethioninamine:putre	FALSE	Methionine metabolism	2.5.1.16	0	5.00E-12		[c] : C01137 + C00134 --> C00170 + C00080 + C00315
R_SHSL1	O-Succinyl-L-homoserine succina	FALSE	Methionine metabolism	2.5.1.48	0	0		[c] : C00097 + C01118 --> cyst-L + C00080 + C00042
R_SHSL4r	O-Succinyl-L-homoserine succina	TRUE	Methionine metabolism	2.5.1.48	-329.1513	-709.695801		[c] : C00001 + C01118 <==> C00109 + C00080 + C01342 + C00042
R_SHSL2r	O4-succinyl-L-homoserine:hydro	TRUE	Methionine metabolism	2.5.1.48	329.15129	709.695801		[c] : C00297 + C01118 <==> C00080 + C05330 + C00042
R_AHSERL2	O-acetyl-L-homoserine:hydrogen	FALSE	Methionine metabolism	2.5.1.49	659.78018	0.1		[c] : C01077 + C00297 --> C00033 + C00080 + C05330
R_METB1	O-Acetyl-L-homoserine succinate	FALSE	Methionine metabolism	2.5.1.49	0	0		[c] : C01077 + C00097 --> C00033 + cyst-L + C00080
R_METAT	ATP:L-methione S-adenosyltrans	FALSE	Methionine metabolism	2.5.1.6	1.67568	192.421582	0	[c] : C00002 + C00001 + C00073 --> C00019 + C00009 + C00013
R_AHCi	S-Adenosyl-L-homocysteine hydr	FALSE	Methionine metabolism	3.3.1.1	1.67568	192.421582	0	[c] : C00021 + C00001 --> C00212 + C05330
R_CYSTS	L-serine hydro-lyase (adding hon	FALSE	Methionine metabolism	4.2.1.22	0	0	2.17530254	[c] : C05330 + C00716 --> cyst-L + C00001
R_METTRS	L-Methionine:tRNAMet ligase (AM	FALSE	Methionine metabolism	6.1.1.10	0	0	0	[c] : C00002 + C00073 + C01647 --> C00020 + C02430 + C00013
R_R07706	nitrobenzene 1,2-dioxygenase	TRUE	Naphthalene and anthracene degrada	1.14.-.-	0	0		[c] : C06813 + C00007 <==> C00090 + C00088
R_R07700	aniline dioxygenase	TRUE	Naphthalene and anthracene degrada	1.14.-.-	0	0		[c] : C00292 + C00007 <==> C00090 + C01342
R_R07697	.	TRUE	Naphthalene and anthracene degrada	1.14.-.-	0	0		[c] : C16200 + C00007 <==> C00146 + C00001
R_R07687	.	TRUE	Naphthalene and anthracene degrada	1.14.-.-	0	0		[c] : C14315 + C00007 + 2 C00080 + 2 C05359 <==> C16205
R_R05654	phenanthrene 1,2-monooxygenas	TRUE	Naphthalene and anthracene degrada	1.14.13.-	0	0		[c] : C11422 + C00007 + C00004 + C00080 <==> C11431 + C00001 + C00003
R_R05655	.	TRUE	Naphthalene and anthracene degrada	1.14.13.-	0	0		[c] : C11422 + C00007 + C00004 + C00080 <==> C11432 + C00001 + C00003
R_R05653	phenanthrene 9,10-monooxygena	TRUE	Naphthalene and anthracene degrada	1.14.13.-	0	0		[c] : C11422 + C00007 + C00004 + C00080 <==> C11429 + C00001 + C00003
R_R07710	.	TRUE	Naphthalene and anthracene degrada	1.14.13.-	-1000	-1000		[c] : C00805 + C00005 + C00007 + C00080 <==> C00628 + C00006 + C00001
R_R07709	.	TRUE	Naphthalene and anthracene degrada	1.14.13.-	1000	1000		[c] : C00805 + C00004 + C00007 + C00080 <==> C00628 + C00003 + C00001
R_R05657	.	TRUE	Naphthalene and anthracene degrada	2.1.1.-	0	0		[c] : C11432 + C05694 <==> C11433 + C05693
R_QULNS	.	FALSE	Nicotinate and nicotinamide metaboli	.	0.052546	0	-414.95798	[c] : C00111 + C05840 --> C00080 + 2 C00001 + C00009 + C03722

R_ASPO6	.	FALSE	Nicotinate and nicotinamide metaboli	1.4.3.16	0.052546	0		[c] : C00049 + C00007 --> C00027 + C05840
R_PNP	N-Ribosylnicotinamide:orthopho	TRUE	Nicotinate and nicotinamide metaboli	2.4.2.1	-690.2974	-1000	0	[c] : C00009 + C03150 <==> C00080 + C00153 + C00620
R_NP1	Nicotinate D-ribonucleoside:orth	FALSE	Nicotinate and nicotinamide metaboli	2.4.2.1	0	0	0	[c] : C00080 + C11486 + C00620 --> nicrns + C00009
R_NAPRT	Nicotinate D-ribonucleotide:diph	FALSE	Nicotinate and nicotinamide metaboli	2.4.2.11	0	0	0	[c] : C00080 + C11486 + C00119 --> C01185 + C00013
R_NNDPR	Nicotinate-nucleotide:pyrophosp	FALSE	Nicotinate and nicotinamide metaboli	2.4.2.19	0.052546	0	-414.95798	[c] : 2 C00080 + C00119 + C03722 --> C00011 + C01185 + C00013
R_NADK	ATP:NAD+ 2'-phosphotransferase	FALSE	Nicotinate and nicotinamide metaboli	2.7.1.23	0.0102012	0	0.01325184	[c] : C00002 + C00003 --> C00008 + C00080 + C00006
R_NNATn	ATP:nicotinamide-nucleotide ade	FALSE	Nicotinate and nicotinamide metaboli	2.7.7.1	0.052546	0.1	0	[c] : C00002 + C00080 + C01185 --> C00857 + C00013
R_NMNATn	ATP:nicotinamide-nucleotide ade	FALSE	Nicotinate and nicotinamide metaboli	2.7.7.1	0	0		[c] : C00002 + C00080 + C00455 --> C00003 + C00013
R_NMNATn	ATP:nicotinamide-nucleotide ade	FALSE	Nicotinate and nicotinamide metaboli	2.7.7.18	0	0		[c] : C00002 + C00080 + C00455 --> C00003 + C00013
R_NNATn	ATP:nicotinamide-nucleotide ade	FALSE	Nicotinate and nicotinamide metaboli	2.7.7.18	0.052546	0.1	0	[c] : C00002 + C00080 + C01185 --> C00857 + C00013
R_R01273	N-ribosylnicotinamide ribohydro	TRUE	Nicotinate and nicotinamide metaboli	3.2.2.1	690.2974	1000		[c] : C03150 + C00001 <==> C00153 + C00121
R_NNAMrm	Nicotinamide amidohydrolase	TRUE	Nicotinate and nicotinamide metaboli	3.5.1.19	0	0		[c] : C00001 + C00153 <==> C11486 + C01342
R_NADDPe	NAD+ phosphohydrolase	FALSE	Nicotinate and nicotinamide metaboli	3.6.1.22	0	0		[e] : C00001 + C00003 --> C00020 + 2 C00080 + C00455
R_DNADDP	Deamino-NAD+ nucleotidohydrol	FALSE	Nicotinate and nicotinamide metaboli	3.6.1.22	0	0.1		[c] : C00857 + C00001 --> C00020 + 2 C00080 + C01185
R_NADDPe	NAD+ phosphohydrolase	FALSE	Nicotinate and nicotinamide metaboli	3.6.1.9	0	0		[e] : C00001 + C00003 --> C00020 + 2 C00080 + C00455
R_DNADDP	Deamino-NAD+ nucleotidohydrol	FALSE	Nicotinate and nicotinamide metaboli	3.6.1.9	0	0.1		[c] : C00857 + C00001 --> C00020 + 2 C00080 + C01185
R_NADS2	Deamido-NAD+:L-glutamine amid	FALSE	Nicotinate and nicotinamide metaboli	6.3.5.1	0.052546	0		[c] : C00002 + C00857 + C00064 + C00001 --> C00020 + C00025 + C00080 + C00003 + C0
R_GLUSy	L-Glutamate:NADP+ oxidoreducta	FALSE	Nitrogen metabolism	1.4.1.13	0	0.1		[c] : C00026 + C00064 + C00080 + C00005 --> 2 C00025 + C00006
R_GLUSx	L-glutamate:NAD+ oxidoreductas	FALSE	Nitrogen metabolism	1.4.1.14	0	0.1	0	[c] : C00026 + C00064 + C00080 + C00004 --> 2 C00025 + C00003
R_GLUDx	L-Glutamate:NAD+ oxidoreductas	TRUE	Nitrogen metabolism	1.4.1.2	961.6972	0.1	431.73093	[c] : C00025 + C00001 + C00003 <==> C00026 + C00080 + C00004 + C01342
R_GLUDym	L-Glutamate:NADP+ oxidoreducta	TRUE	Nitrogen metabolism	1.4.1.3	-1000	0.6		[c] : C00025 + C00001 + C00006 <==> C00026 + C00080 + C00005 + C01342
R_GLUDx	L-Glutamate:NAD+ oxidoreductas	TRUE	Nitrogen metabolism	1.4.1.3	961.6972	0.1	431.73093	[c] : C00025 + C00001 + C00003 <==> C00026 + C00080 + C00004 + C01342
R_GLUDx	L-Glutamate:NAD+ oxidoreductas	TRUE	Nitrogen metabolism	1.4.1.4	961.6972	0.1	431.73093	[c] : C00025 + C00001 + C00003 <==> C00026 + C00080 + C00004 + C01342
R_GLUDym	L-Glutamate:NADP+ oxidoreducta	TRUE	Nitrogen metabolism	1.4.1.4	-1000	0.6		[c] : C00025 + C00001 + C00006 <==> C00026 + C00080 + C00005 + C01342
R_GLYCL	glycine synthase; glycine cleavage	FALSE	Nitrogen metabolism	1.4.4.2	0	96.210791		[c] : C00037 + C00003 + C00101 --> C00011 + C00143 + C00004 + C01342
R_R01342	D-Amino-acid:(acceptor) oxidore	FALSE	Nitrogen metabolism	1.4.99.1	0	0		[c] : C05167 + C00001 + C00028 <==> C00161 + C01342 + C00030
R_R00790	Ammonia:ferredoxin oxidoreduct	TRUE	Nitrogen metabolism	1.7.7.1	0	0		[c] : C01342 + 2 C00001 + 6 C00139 <==> C00088 + 6 C00138 + 7 C00080
R_GLYCL	glycine synthase; glycine cleavage	FALSE	Nitrogen metabolism	1.8.1.4	0	96.210791		[c] : C00037 + C00003 + C00101 --> C00011 + C00143 + C00004 + C01342
R_GLYCL	glycine synthase; glycine cleavage	FALSE	Nitrogen metabolism	2.1.2.10	0	96.210791		[c] : C00037 + C00003 + C00101 --> C00011 + C00143 + C00004 + C01342
R_H2CO3D	Carbonic acid hydro-lyase	TRUE	Nitrogen metabolism	4.2.1.1	11.512011	0.1		[c] : C00011 + C00001 <==> C01353
R_GLNS	L-Glutamate:ammonia ligase (AD	FALSE	Nitrogen metabolism	6.3.1.2	42.29953	0.3	48.2844654	[c] : C00002 + C00025 + C01342 --> C00008 + C00064 + C00080 + C00009
R_ASNS1	L-aspartate:L-glutamine amido-li	FALSE	Nitrogen metabolism	6.3.5.4	4.4077087	0		[c] : C00049 + C00002 + C00064 + C00001 --> C00020 + C00152 + C00025 + C00080 + C0
R_PPND	Prephenate:NAD+ oxidoreductase	FALSE	Novobiocin biosynthesis	1.3.1.12	0	0		[c] : C00003 + C00254 --> C01179 + C00011 + C00004
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Novobiocin biosynthesis	2.6.1.1	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Novobiocin biosynthesis	2.6.1.5	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Novobiocin biosynthesis	2.6.1.57	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Novobiocin biosynthesis	2.6.1.9	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_UDPGDr	UDPglucose:NAD+ oxidoreductas	TRUE	Nucleotide sugars metabolism	1.1.1.22	0	0	-1000	[c] : C00001 + 2 C00003 + C00029 <==> 3 C00080 + 2 C00004 + C00167
R_GALUi	UTP:alpha-D-glucose-1-phosphat	FALSE	Nucleotide sugars metabolism	2.7.7.9	0	0.1	0	[c] : C00103 + C00080 + C00075 --> C00013 + C00029
R_R02984	dTDPglucose 4-epimerase	TRUE	Nucleotide sugars metabolism	5.1.3.2	0	0		[c] : C00842 <==> C02097
R_UDPG4E	UDPglucose 4-epimerase	TRUE	Nucleotide sugars metabolism	5.1.3.2	0	0	0	[c] : C00029 <==> C00052
R_TMDS	thymidylatesynthase	TRUE	Nucleotides	2.1.1.45	-0.962382	0		[c] : C00365 + C00143 <==> C00415 + C00364
R_MTHFR3	5-methyltetrahydrofolate:NADP+	FALSE	One carbon pool by folate	1.5.1.20	0.9623818	0.1		[c] : 2 C00080 + C00143 + C00005 --> C00440 + C00006
R_MTHFR2	5-methyltetrahydrofolate:NAD+	FALSE	One carbon pool by folate	1.5.1.20	0	192.321582	332.050472	[c] : C00080 + C00143 + C00004 --> C00440 + C00003
R_MTHFD	5,10-methylenetetrahydrofolate:	TRUE	One carbon pool by folate	1.5.1.5	19.551518	0.1		[c] : C00143 + C00006 <==> C00445 + C00005
R_METS	5-Methyltetrahydrofolate:L-homo	FALSE	One carbon pool by folate	2.1.1.13	0	192.421582	330.800298	[c] : C00440 + C05330 --> C00080 + C00073 + C00101
R_R06613	5,10-methylenetetrahydrofolate,	TRUE	One carbon pool by folate	2.1.1.148	1.4377984	0	0.61758589	[c] : C00143 + C00365 + C01352 <==> C00101 + C00364 + C00016
R_GHMT2r	5,10-Methylenetetrahydrofolate:	TRUE	One carbon pool by folate	2.1.2.1	20.791836	96.210791	179.709014	[c] : C00716 + C00101 <==> C00037 + C00001 + C00143
R_GCCbim	S-aminomethyldihydrolipoylprot	FALSE	One carbon pool by folate	2.1.2.10	0.1986164	0.1	0	[c] : C01242 + C00101 --> C02972 + C00143 + C01342
R_THFATm	S-Aminomethyldihydrolipoylprot	FALSE	One carbon pool by folate	2.1.2.10	0	0	0	[c] : C00001 + C00445 --> C03479 + C00080
R_GARFT	10-Formyltetrahydrofolate:5'-ph	TRUE	One carbon pool by folate	2.1.2.2	9.3910951	6.00E-11	-987.80205	[c] : C00234 + C03838 <==> C04376 + C00080 + C00101
R_AICART	10-Formyltetrahydrofolate:5'-ph	TRUE	One carbon pool by folate	2.1.2.3	11.123382	1.05E-10	14.4482595	[c] : C00234 + C04677 <==> C04734 + C00101
R_FMETTRS	10-Formyltetrahydrofolate:L-met	FALSE	One carbon pool by folate	2.1.2.9	0	0	0	[c] : C00234 + C02430 --> C03294 + C00080 + C00101
R_FTHFD	10-Formyltetrahydrofolate amido	FALSE	One carbon pool by folate	3.5.1.10	0	0.2	0	[c] : C00234 + C00001 --> C00058 + C00080 + C00101
R_MTHFCm	5,10-Methenyltetrahydrofolate 5-	TRUE	One carbon pool by folate	3.5.4.9	19.551518	0.1		[c] : C00001 + C00445 <==> C00234 + C00080
R_R03051	2,3-Dihydroxy-3-methylbutanoat	TRUE	Pantothenate and CoA biosynthesis	1.1.1.86	703.88647	-0.2		[c] : C00900 + C00005 + C00080 <==> C04039 + C00006
R_MOHMT	5,10-Methylenetetrahydrofolate:	FALSE	Pantothenate and CoA biosynthesis	2.1.2.11	0.0011356	0	0	[c] : C00141 + C00001 + C00143 --> C00966 + C00101
R_R00006	2-Acetolactate pyruvate-lyase (ca	TRUE	Pantothenate and CoA biosynthesis	2.2.1.6	296.11353	0.1		[c] : C00900 + C00011 <==> 2 C00022
R_VALTAm	L-Valine:2-oxoglutarate aminotra	TRUE	Pantothenate and CoA biosynthesis	2.6.1.42	-7.73755	0.3	0	[c] : C00026 + C00183 <==> C00141 + C00025

R_VALTAm	L-Valine:2-oxoglutarate aminotra	TRUE	Pantothenate and CoA biosynthesis	2.6.1.6	-7.73755	0.3	0	[c] : C00026 + C00183 <==> C00141 + C00025
R_DPCOAKr	ATP:dephospho-CoA 3'-phosphot	FALSE	Pantothenate and CoA biosynthesis	2.7.1.24	0.0011356	0	0	[c] : C00002 + C00882 --> C00008 + C00010 + C00080
R_PNTK	ATP:pantothenate 4'-phosphotra	FALSE	Pantothenate and CoA biosynthesis	2.7.1.33	0.0011356	0	0	[c] : C00002 + C00864 --> C03492 + C00008 + C00080
R_R02971	ATP:pantothenate 4'-phosphotra	TRUE	Pantothenate and CoA biosynthesis	2.7.1.33	0	0		[c] : C00002 + C00831 <==> C00008 + C01134
R_R04391	ATP:pantothenate 4'-phosphotra	TRUE	Pantothenate and CoA biosynthesis	2.7.1.33	0	0		[c] : C00002 + C04079 <==> C00008 + C04352
R_R02971	ATP:pantothenate 4'-phosphotra	TRUE	Pantothenate and CoA biosynthesis	2.7.1.34	0	0		[c] : C00002 + C00831 <==> C00008 + C01134
R_PTPAT	ATP:pantetheine-4'-phosphate ad	TRUE	Pantothenate and CoA biosynthesis	2.7.7.3	0.0011356	0	-1000	[c] : C00002 + C00080 + C01134 <==> C00882 + C00013
R_PPCDC	N-[(R)-4'-Phosphopantothenoyl]-	FALSE	Pantothenate and CoA biosynthesis	4.1.1.36	0.0011356	0		[c] : C04352 + C00080 --> C00011 + C01134
R_R01209	2,3-Dihydroxy-3-methylbutanoat	TRUE	Pantothenate and CoA biosynthesis	4.2.1.9	7.7386855	-0.4		[c] : C04039 <==> C00141 + C00001
R_PANTS	(R)-Pantoate:beta-alanine ligase (	FALSE	Pantothenate and CoA biosynthesis	6.3.2.1	0.0011356	0	0	[c] : C00099 + C00002 + C00522 --> C00020 + C00080 + C00864 + C00013
R_PPNCL2	(R)-4'-Phosphopantothenate:L-cy	FALSE	Pantothenate and CoA biosynthesis	6.3.2.5	0.0011356	0		[c] : C03492 + C00063 + C00097 --> C04352 + C00055 + C00080 + C00013
R_PPNCL3	(R)-4'-Phosphopantothenate:L-cy	FALSE	Pantothenate and CoA biosynthesis	6.3.2.5	0	0		[c] : C03492 + C00002 + C00097 --> C04352 + C00020 + C00080 + C00013
R_R01542	2-Dehydro-3-deoxy-D-gluconate:	TRUE	Pentose and glucuronate interconver	1.1.1.125	0	0		[c] : C00204 + C00003 <==> C04349 + C00004 + C00080
R_R01542	2-Dehydro-3-deoxy-D-gluconate:	TRUE	Pentose and glucuronate interconver	1.1.1.127	0	0		[c] : C00204 + C00003 <==> C04349 + C00004 + C00080
R_UDPGDr	UDPglucose:NAD+ oxidoreductas	TRUE	Pentose and glucuronate interconver	1.1.1.22	0	0	-1000	[c] : C00001 + 2 C00003 + C00029 <==> 3 C00080 + 2 C00004 + C00167
R_XYLK	ATP:D-xylulose 5-phosphotransfe	FALSE	Pentose and glucuronate interconver	2.7.1.17	0	0	1.25017387	[c] : C00002 + C00310 --> C00008 + C00080 + C00231
R_DDGLK	ATP:2-dehydro-3-deoxy-D-glucor	FALSE	Pentose and glucuronate interconver	2.7.1.45	0	0		[c] : C00204 + C00002 --> C04442 + C00008 + C00080
R_GALUi	UTP:alpha-D-glucose-1-phosphat	FALSE	Pentose and glucuronate interconver	2.7.7.9	0	0.1	0	[c] : C00103 + C00080 + C00075 --> C00013 + C00029
R_EDA	2-dehydro-3-deoxy-D-gluconate-(	FALSE	Pentose and glucuronate interconver	4.1.2.-	0	0	0	[c] : C04442 --> C00118 + C00022
R_EDA	2-dehydro-3-deoxy-D-gluconate-(	FALSE	Pentose and glucuronate interconver	4.1.2.14	0	0	0	[c] : C04442 --> C00118 + C00022
R_RPE	D-Ribulose-5-phosphate 3-epime	TRUE	Pentose and glucuronate interconver	5.1.3.1	-346.3031	-64.5405273	-13.32852	[c] : C00199 <==> C00231
R_XYLI1	D-xylose aldose-ketose-isomerase	TRUE	Pentose and glucuronate interconver	5.3.1.5	0	0	0	[c] : C01394 <==> C00310
R_GND	6-phospho-D-gluconate:NADP+ 2	FALSE	Pentose phosphate pathway	1.1.1.44	0	0.1		[c] : C00345 + C00006 --> C00011 + C00005 + C00199
R_R02736	beta-D-Glucose-6-phosphate:NAD	TRUE	Pentose phosphate pathway	1.1.1.49	0	0.1	1000	[c] : C01172 + C00006 <==> C01236 + C00005 + C00080
R_R01641	Sedoheptulose-7-phosphate:D-gly	TRUE	Pentose phosphate pathway	2.2.1.1	-329.0234	-64.6405273		[c] : C05382 + C00118 <==> C03736 + C00231
R_R01830	beta-D-Fructose 6-phosphate:D-g	TRUE	Pentose phosphate pathway	2.2.1.1	-324.6349	-64.7405273		[c] : f6p-B + C00118 <==> C00279 + C00231
R_R01827	sedoheptulose-7-phosphate:D-gly	TRUE	Pentose phosphate pathway	2.2.1.2	329.02341	64.6405273		[c] : C05382 + C00118 <==> C00279 + f6p-B
R_GNK	ATP:D-Gluconate 6-phosphotrans	FALSE	Pentose phosphate pathway	2.7.1.12	0	0	0	[c] : C00002 + C00257 --> C00345 + C00008 + C00080
R_DRBK	.	FALSE	Pentose phosphate pathway	2.7.1.15	0	0		[c] : C00002 + C01801 --> C00673 + C00008 + C00080
R_R01051	ATP:D-ribose 5-phosphotransfera	TRUE	Pentose phosphate pathway	2.7.1.15	0	0.1		[c] : C00002 + C00121 <==> C00008 + C03736
R_DDGLK	ATP:2-dehydro-3-deoxy-D-glucor	FALSE	Pentose phosphate pathway	2.7.1.45	0	0		[c] : C00204 + C00002 --> C04442 + C00008 + C00080
R_R01049	ATP:D-ribose-5-phosphate dipho	TRUE	Pentose phosphate pathway	2.7.6.1	17.279354	0.1		[c] : C00002 + C03736 <==> C00020 + C00119
R_PGLer	6-Phospho-D-glucono-1,5-lactone	FALSE	Pentose phosphate pathway	3.1.1.31	0	0.1	0	[c] : C01236 + C00001 --> C00345 + C00080
R_R04780	beta-D-Fructose 1,6-bisphosphate	TRUE	Pentose phosphate pathway	3.1.3.11	-1000	-581.564746		[c] : C05378 + C00001 <==> f6p-B + C00009
R_EDA	2-dehydro-3-deoxy-D-gluconate-(	FALSE	Pentose phosphate pathway	4.1.2.-	0	0	0	[c] : C04442 --> C00118 + C00022
R_R01070	beta-D-fructose-1,6-bisphosphate	TRUE	Pentose phosphate pathway	4.1.2.13	674.41127	-31.2202637		[c] : C05378 <==> C00111 + C00118
R_EDA	2-dehydro-3-deoxy-D-gluconate-(	FALSE	Pentose phosphate pathway	4.1.2.14	0	0	0	[c] : C04442 --> C00118 + C00022
R_RPE	D-Ribulose-5-phosphate 3-epime	TRUE	Pentose phosphate pathway	5.1.3.1	-346.3031	-64.5405273	-13.32852	[c] : C00199 <==> C00231
R_R02739	alpha-D-Glucose 6-phosphate ket	TRUE	Pentose phosphate pathway	5.1.3.15	1000	0.1		[c] : C00668 <==> C01172
R_R01056	D-ribose-5-phosphate aldose-ket	TRUE	Pentose phosphate pathway	5.3.1.6	-346.3028	-64.6405273	-13.32802	[c] : C03736 <==> C00199
R_R02740	alpha-D-Glucose 6-phosphate ket	TRUE	Pentose phosphate pathway	5.3.1.9	-1000	-0.1		[c] : C00668 <==> f6p-B
R_R02739	alpha-D-Glucose 6-phosphate ket	TRUE	Pentose phosphate pathway	5.3.1.9	1000	0.1		[c] : C00668 <==> C01172
R_R05027	.	TRUE	Peptidoglycan biosynthesis	2.4.1.227	0	0		[c] : C05888 + C00043 <==> C05889 + C00015
R_R05662	.	TRUE	Peptidoglycan biosynthesis	2.4.1.227	0	0		[c] : C04851 + C00043 <==> C05893 + C00015
R_R05032	.	TRUE	Peptidoglycan biosynthesis	2.4.1.227	0	0		[c] : C05897 + C00043 <==> C05898 + C00015
R_PAPPT3	UDPMurAc(oyl-L-Ala-D-gamma-(	FALSE	Peptidoglycan biosynthesis	2.7.8.13	0	0	0	[c] : C17556 + C04882 --> C05897 + C00105
R_R05629	UDPMurAc(oyl-L-Ala-D-gamma-(	TRUE	Peptidoglycan biosynthesis	2.7.8.13	0	0		[c] : C04702 + C17556 <==> C00105 + C04851
R_R05628	UDPMurAc(oyl-L-Ala-D-gamma-(	TRUE	Peptidoglycan biosynthesis	2.7.8.13	0	0		[c] : C04846 + C17556 <==> C00105 + C05888
R_AMAA	N-Acetylmuramoyl-Ala amidohyd	FALSE	Peptidoglycan biosynthesis	3.5.1.28	0	0		[c] : C02999 + C00001 --> C02713 + C00041
R_R05627	Undecaprenyl-diphosphate phosp	TRUE	Peptidoglycan biosynthesis	3.6.1.27	0	0	-1000	[c] : C04574 + C00001 <==> C17556 + C00009
R_R05028	Undecaprenyl-diphospho-N-acety	TRUE	Peptidoglycan biosynthesis	6.3.1.2	0	0		[c] : C00002 + C05889 + C01342 <==> C00008 + C00009 + C05890
R_R05030	Undecaprenyl-diphospho-N-acety	TRUE	Peptidoglycan biosynthesis	6.3.1.2	0	0		[c] : C00002 + C05893 + C01342 <==> C00008 + C00009 + C05894
R_R05033	Undecaprenyl-diphospho-N-acety	TRUE	Peptidoglycan biosynthesis	6.3.1.2	0	0		[c] : C00002 + C05898 + C01342 <==> C00008 + C00009 + C05899
R_UGMDDS	UDP-N-acetylmuramoyl-L-alanyl-	FALSE	Peptidoglycan biosynthesis	6.3.2.10	0	2.25E-11		[c] : C00993 + C00002 + C04877 --> C00008 + C00080 + C00009 + C04882
R_R04573	UDP-N-acetylmuramoyl-L-alanyl-	TRUE	Peptidoglycan biosynthesis	6.3.2.10	0	0		[c] : C00002 + C05892 + C00993 <==> C00008 + C00009 + C04702
R_R04572	UDP-N-acetylmuramoyl-L-alanyl-	TRUE	Peptidoglycan biosynthesis	6.3.2.10	0	0		[c] : C00002 + C04700 + C00993 <==> C00008 + C00009 + C04846
R_UAAGDS	UDP-N-acetylmuramoyl-L-alanyl-	FALSE	Peptidoglycan biosynthesis	6.3.2.13	0	1.50E-11	0	[c] : C00680 + C00002 + C00692 --> C00008 + C00080 + C00009 + C04877
R_ALAALAr	D-alanine:D-alanine ligase (ADP-f	TRUE	Peptidoglycan biosynthesis	6.3.2.4	0	2.25E-11	0	[c] : 2 C00133 + C00002 <==> C00008 + C00993 + C00080 + C00009
R_UAMAS	UDP-N-acetylmuramate:L-alanine	FALSE	Peptidoglycan biosynthesis	6.3.2.8	0	1.50E-11	0	[c] : C00041 + C00002 + C01050 --> C00008 + C00080 + C00009 + C01212

R_UAMAGS	UDP-N-acetylmuramoyl-L-alanine	FALSE	Peptidoglycan biosynthesis	6.3.2.9	0	1.50E-11	0	[c] : C00002 + C00217 + C01212 --> C00008 + C00080 + C00009 + C00692
R_CINNDO	trans-cinnamate,NADH:oxygen ox	FALSE	Phenylalanine metabolism	1.14.12.19	0	0		[c] : C00423 + C00080 + C00004 + C00007 --> C12622 + C00003
R_R06782	3-phenylpropanoate,NADH:oxyge	TRUE	Phenylalanine metabolism	1.14.12.19	0	0		[c] : C05629 + C00007 + C00004 + C00080 <==> C11588 + C00003
R_R05001	.	TRUE	Phenylalanine metabolism	1.14.13.-	0	0		[c] : 2hyoxplac <==> C06207
R_R01374	D-phenylalanine:acceptor oxidore	TRUE	Phenylalanine metabolism	1.4.99.1	0	0		[c] : C02265 + C00001 + C00028 <==> C00166 + C01342 + C00030
R_PHETA1	L-Phenylalanine:2-oxoglutarate a	TRUE	Phenylalanine metabolism	2.6.1.1	-3.387584	0	-4.400612	[c] : C00026 + C00079 <==> C00025 + C00166
R_PHETA1	L-Phenylalanine:2-oxoglutarate a	TRUE	Phenylalanine metabolism	2.6.1.5	-3.387584	0	-4.400612	[c] : C00026 + C00079 <==> C00025 + C00166
R_PHETA1	L-Phenylalanine:2-oxoglutarate a	TRUE	Phenylalanine metabolism	2.6.1.57	-3.387584	0	-4.400612	[c] : C00026 + C00079 <==> C00025 + C00166
R_PHETA1	L-Phenylalanine:2-oxoglutarate a	TRUE	Phenylalanine metabolism	2.6.1.9	-3.387584	0	-4.400612	[c] : C00026 + C00079 <==> C00025 + C00166
R_NBAH	N-Benzoylglycine amidohydrolas	TRUE	Phenylalanine metabolism	3.5.1.32	0	0	0	[c] : C01586 + C00001 <==> C00180 + C00037
R_AMID2	2-phenylacetamide amidohydrola	FALSE	Phenylalanine metabolism	3.5.1.4	0	0	0	[c] : C00001 + C02505 --> C01342 + C07086
R_SHK3Dr	Shikimate:NADP+ 3-oxidoreducta	TRUE	Phenylalanine, tyrosine and tryptoph	1.1.1.25	4.3499658	5.00E-11	-992.99903	[c] : C02637 + C00080 + C00005 <==> C00006 + C00493
R_SHK3Dr	Shikimate:NADP+ 3-oxidoreducta	TRUE	Phenylalanine, tyrosine and tryptoph	1.1.1.282	4.3499658	5.00E-11	-992.99903	[c] : C02637 + C00080 + C00005 <==> C00006 + C00493
R_PPND	Prephenate:NAD+ oxidoreductase	FALSE	Phenylalanine, tyrosine and tryptoph	1.3.1.12	0	0		[c] : C00003 + C00254 --> C01179 + C00011 + C00004
R_ANPRT	N-(5-Phospho-D-ribosyl)anthrani	FALSE	Phenylalanine, tyrosine and tryptoph	2.4.2.18	0	7.00E-11	1.35018778	[c] : C00108 + C00119 --> C00013 + C04302
R_PSCVT	Phosphoenolpyruvate:3-phospho	TRUE	Phenylalanine, tyrosine and tryptoph	2.5.1.19	4.3499658	5.00E-11		[c] : C00074 + C03175 <==> C01269 + C00009
R_DDPAm	Phosphoenolpyruvate:D-erythros	FALSE	Phenylalanine, tyrosine and tryptoph	2.5.1.54	4.3499658	5.00E-11		[c] : C00279 + C00001 + C00074 --> C04691 + C00009
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Phenylalanine, tyrosine and tryptoph	2.6.1.1	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_PHETA1	L-Phenylalanine:2-oxoglutarate a	TRUE	Phenylalanine, tyrosine and tryptoph	2.6.1.1	-3.387584	0	-4.400612	[c] : C00026 + C00079 <==> C00025 + C00166
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Phenylalanine, tyrosine and tryptoph	2.6.1.5	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_PHETA1	L-Phenylalanine:2-oxoglutarate a	TRUE	Phenylalanine, tyrosine and tryptoph	2.6.1.5	-3.387584	0	-4.400612	[c] : C00026 + C00079 <==> C00025 + C00166
R_PHETA1	L-Phenylalanine:2-oxoglutarate a	TRUE	Phenylalanine, tyrosine and tryptoph	2.6.1.57	-3.387584	0	-4.400612	[c] : C00026 + C00079 <==> C00025 + C00166
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Phenylalanine, tyrosine and tryptoph	2.6.1.57	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Phenylalanine, tyrosine and tryptoph	2.6.1.9	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_PHETA1	L-Phenylalanine:2-oxoglutarate a	TRUE	Phenylalanine, tyrosine and tryptoph	2.6.1.9	-3.387584	0	-4.400612	[c] : C00026 + C00079 <==> C00025 + C00166
R_SHKK	ATP:shikimate 3-phosphotransfe	FALSE	Phenylalanine, tyrosine and tryptoph	2.7.1.71	4.3499658	5.00E-11	7.0009737	[c] : C00002 + C00493 --> C00008 + C00080 + C03175
R_R03508	1-(2-Carboxyphenylamino)-1-dec	TRUE	Phenylalanine, tyrosine and tryptoph	4.1.1.48	0	7.00E-11	-505.76115	[c] : C01302 <==> C03506 + C00011 + C00001
R_TRPS3	(1S,2R)-1-C-(indol-3-yl)glycerol 3	FALSE	Phenylalanine, tyrosine and tryptoph	4.1.2.8	0	3.50E-11	0	[c] : C03506 --> C00118 + C00463
R_ANS2	chorismate pyruvate-lyase (amin	FALSE	Phenylalanine, tyrosine and tryptoph	4.1.3.27	0	4.00E-11		[c] : C00251 + C01342 --> C00108 + C00080 + C00001 + C00022
R_ANS	Chorismate pyruvate-lyase (amin	FALSE	Phenylalanine, tyrosine and tryptoph	4.1.3.27	0	4.00E-11	1.35018778	[c] : C00251 + C00064 --> C00108 + C00025 + C00080 + C00022
R_DHQD	3-Dehydroquinate hydro-lyase	TRUE	Phenylalanine, tyrosine and tryptoph	4.2.1.10	4.3499658	5.00E-11	-992.99903	[c] : C00944 <==> C02637 + C00001
R_TRPS2	L-Serine hydro-lyase (adding ind	FALSE	Phenylalanine, tyrosine and tryptoph	4.2.1.20	0	3.50E-11	0	[c] : C00463 + C00716 --> C00001 + C00078
R_TRPS1	L-Serine hydro-lyase (adding ind	FALSE	Phenylalanine, tyrosine and tryptoph	4.2.1.20	0	3.50E-11	1.35018778	[c] : C03506 + C00716 --> C00118 + C00001 + C00078
R_TRPS3	(1S,2R)-1-C-(indol-3-yl)glycerol 3	FALSE	Phenylalanine, tyrosine and tryptoph	4.2.1.20	0	3.50E-11	0	[c] : C03506 --> C00118 + C00463
R_PPNDH	prephenate hydro-lyase (decarbo	FALSE	Phenylalanine, tyrosine and tryptoph	4.2.1.51	3.387584	0	4.40061204	[c] : C00080 + C00254 --> C00011 + C00001 + C00166
R_R00691	L-Arogenate hydro-lyase (decarb	TRUE	Phenylalanine, tyrosine and tryptoph	4.2.1.51	0	0		[c] : C00826 <==> C00079 + C00001 + C00011
R_R00691	L-Arogenate hydro-lyase (decarb	TRUE	Phenylalanine, tyrosine and tryptoph	4.2.1.91	0	0		[c] : C00826 <==> C00079 + C00001 + C00011
R_PPNDH	prephenate hydro-lyase (decarbo	FALSE	Phenylalanine, tyrosine and tryptoph	4.2.1.91	3.387584	0	4.40061204	[c] : C00080 + C00254 --> C00011 + C00001 + C00166
R_DHQS	2-Dehydro-3-deoxy-D-arabino-he	FALSE	Phenylalanine, tyrosine and tryptoph	4.2.3.4	4.3499658	5.00E-11	7.0009737	[c] : C04691 --> C00944 + C00009
R_CHORS	5-O-(1-Carboxyvinyl)-3-phospho	FALSE	Phenylalanine, tyrosine and tryptoph	4.2.3.5	4.3499658	5.00E-11	7.0009737	[c] : C01269 --> C00251 + C00009
R_R03509	N-(5-Phospho-beta-D-ribosyl)ant	TRUE	Phenylalanine, tyrosine and tryptoph	5.3.1.24	0	7.00E-11	1.35018778	[c] : C04302 <==> C01302
R_CHORM	Chorismate pyruvatemutase	FALSE	Phenylalanine, tyrosine and tryptoph	5.4.99.5	3.387584	0	4.40061204	[c] : C00251 --> C00254
R_TYRTRSn	L-Tyrosine:tRNA(Tyr) ligase (AM	FALSE	Phenylalanine, tyrosine and tryptoph	6.1.1.1	0	0	0	[c] : C00002 + C00787 + C00082 --> C00020 + C00013 + C02839
R_PHETRSn	L-Phenylalanine:tRNA(Ala) ligase	FALSE	Phenylalanine, tyrosine and tryptoph	6.1.1.20	0	0	0	[c] : C00002 + C00079 + C01648 --> C00020 + C03511 + C00013
R_MFAPS_S	methylene-fatty-acyl-phospholipi	TRUE	Phospholipid Biosynthesis	2.1.1.16	1.692606	194.365234		[c] : C00019 + 0.01 C01241 <==> C00021 + C00080 + 0.01 C04308
R_R07412	.	TRUE	Porphyrin and chlorophyll metabolisı	.	0	0		[c] : C15672 <==> hemeA_1
R_R05217	precorrin-3A,NADH:oxygen oxido	TRUE	Porphyrin and chlorophyll metabolisı	1.14.13.83	0	0		[c] : C05772 + C00007 + C00004 + C00080 <==> C06406 + C00003 + C00001
R_R03683	Hemoglobin:oxygen oxidoreducta	TRUE	Porphyrin and chlorophyll metabolisı	1.14.99.3	0	0		[c] : C01708 + C01352 + 3 C00007 <==> C06258 + biliverd + C00237 + C14819 + C00016 +
R_R05218	cob(II)yrinic acid-a,c-diamide:FM	TRUE	Porphyrin and chlorophyll metabolisı	1.16.8.1	0	0		[c] : 2 C06504 + C01847 <==> 2 C06505 + C00061 + 2 C00080
R_GLUTRR	L-glutamate-semialdehyde: NADF	FALSE	Porphyrin and chlorophyll metabolisı	1.2.1.70	0	2.80E-10		[c] : C02987 + C00080 + C00005 --> C03741 + C00006 + C01641
R_CPC6R	.	FALSE	Porphyrin and chlorophyll metabolisı	1.3.1.54	0	0	0	[c] : C11542 + C00080 + C00005 --> C11543 + C00006
R_R05150	precorrin-6Y:NADP+ oxidoreduct	TRUE	Porphyrin and chlorophyll metabolisı	1.3.1.54	0	0		[c] : C06319 + C00006 <==> C06320 + C00005 + C00080
R_SHCHD2	S-Adenosyl-L-methionine:uropor	FALSE	Porphyrin and chlorophyll metabolisı	1.3.1.76	0	1.00E-11		[c] : dscl + C00003 --> C00080 + C00004 + C05778
R_PPPGOm	Protoporphyrinogen-IX:oxygen o	FALSE	Porphyrin and chlorophyll metabolisı	1.3.3.4	0	1.25E-11		[c] : 3 C00007 + 2 C01079 --> 6 C00001 + 2 C02191
R_R06895	coproporphyrinogen-III:S-adenos	TRUE	Porphyrin and chlorophyll metabolisı	1.3.99.22	0	2.50E-11		[c] : C03263 + 2 C00019 <==> C01079 + 2 C00011 + 2 C00073 + 2 C05198
R_UPP3MT	S-Adenosyl-L-methionine:uropor	FALSE	Porphyrin and chlorophyll metabolisı	2.1.1.107	0	1.00E-11	0	[c] : 2 C00019 + C01051 --> 2 C00021 + dscl + C00080
R_R03948	S-Adenosyl-L-methionine:precorı	TRUE	Porphyrin and chlorophyll metabolisı	2.1.1.130	0	0		[c] : C00019 + dscl <==> C00021 + C05772 + C00080
R_CPC3MT	.	FALSE	Porphyrin and chlorophyll metabolisı	2.1.1.131	0	0		[c] : C00019 + C11539 --> C00021 + C11540
R_R05180	S-Adenosyl-L-methionine:precorı	TRUE	Porphyrin and chlorophyll metabolisı	2.1.1.131	0	0		[c] : C00019 + C06406 <==> C00021 + C06407

R_R05149	S-Adenosyl-L-methionine:1-precc	TRUE	Porphyrin and chlorophyll metabolisı	2.1.1.132	0	0		[c] : 2 C00019 + C06319 <==> 2 C00021 + C06408 + C00011
R_R05810	cobalt-precorrin-4 methyltransfe	TRUE	Porphyrin and chlorophyll metabolisı	2.1.1.133	0	0		[c] : C11540 + C00019 <==> C16242 + C00021
R_R05181	S-adenosyl-L-methionine:precorr	TRUE	Porphyrin and chlorophyll metabolisı	2.1.1.133	0	0		[c] : C00019 + C06407 <==> C00021 + C06416
R_R05219	.	TRUE	Porphyrin and chlorophyll metabolisı	2.1.1.152	0	0		[c] : C06320 + C00033 + C00021 <==> C06416 + C00019 + C00001
R_R07411	.	TRUE	Porphyrin and chlorophyll metabolisı	2.5.1.-	0	0		[c] : C00032 <==> C15672
R_R07268	ATP:cobinamide Cobeta-adenosyl	TRUE	Porphyrin and chlorophyll metabolisı	2.5.1.17	0	0		[c] : C00002 + C05774 <==> C00536 + C06508
R_R05220	ATP:cob(I)yrinic acid-a,c-diamide	TRUE	Porphyrin and chlorophyll metabolisı	2.5.1.17	0	0		[c] : C06505 + C00002 <==> C06506 + C00536
R_HMBS	Porphobilinogen ammonia-lyase	FALSE	Porphyrin and chlorophyll metabolisı	2.5.1.61	0	3.50E-11		[c] : C00001 + 4 C00931 --> C01024 + 4 C01342
R_R06558	.	TRUE	Porphyrin and chlorophyll metabolisı	2.7.1.156	0	-1000		[c] : C06508 + C00044 <==> C06509 + C00035
R_ADOCBIK	.	FALSE	Porphyrin and chlorophyll metabolisı	2.7.1.156	0	1000		[c] : C06508 + C00002 --> C06509 + C00008 + C00080
R_ACBIPGT	.	FALSE	Porphyrin and chlorophyll metabolisı	2.7.7.62	0	0		[c] : C06509 + C00044 + C00080 --> C06510 + C00013
R_ADOCBLS	.	FALSE	Porphyrin and chlorophyll metabolisı	2.7.8.26	0	0		[c] : C06510 + C05775 --> C00194 + C00144 + C00080
R_UPPDC2	Uroporphyrinogen I carboxy-lyas	FALSE	Porphyrin and chlorophyll metabolisı	4.1.1.37	0	0	0	[c] : 4 C00080 + C05766 --> 4 C00011 + C05768
R_UPPDC1	Uroporphyrinogen-III carboxy-ly	FALSE	Porphyrin and chlorophyll metabolisı	4.1.1.37	0	2.50E-11	0	[c] : 4 C00080 + C01051 --> 4 C00011 + C03263
R_PPBNGS	5-Aminolevulinate hydro-lyase(a	FALSE	Porphyrin and chlorophyll metabolisı	4.2.1.24	0	1.40E-10	0	[c] : 2 C00430 --> C00080 + 2 C00001 + C00931
R_UPP3S	Hydroxymethylbilane hydro-lyas	FALSE	Porphyrin and chlorophyll metabolisı	4.2.1.75	0	3.50E-11		[c] : C01024 --> C00001 + C01051
R_FCLTm	Protoporphyrin ferro-lyase	FALSE	Porphyrin and chlorophyll metabolisı	4.99.1.1	0	5.00E-12	0	[c] : C14818 + C02191 --> 2 C00080 + C00032
R_SHCHF	S-Adenosyl-L-methionine:uropor	FALSE	Porphyrin and chlorophyll metabolisı	4.99.1.4	0	0		[c] : C14818 + C05778 --> 3 C00080 + C00748
R_CPC8MM	.	TRUE	Porphyrin and chlorophyll metabolisı	5.4.1.2	0	0		[c] : C11545 <==> C05773
R_R05177	Precorrin 8X 11,12-methylmutas	TRUE	Porphyrin and chlorophyll metabolisı	5.4.1.2	0	0		[c] : C06408 <==> C06399
R_G1SATi	(S)-4-Amino-5-oxopentanoate 4,5	FALSE	Porphyrin and chlorophyll metabolisı	5.4.3.8	0	2.80E-10	0	[c] : C03741 --> C00430
R_GLUTRS	L-Glutamate:tRNA(Glu) ligase (AI	FALSE	Porphyrin and chlorophyll metabolisı	6.1.1.17	0	2.80E-10	0	[c] : C00002 + C00025 + C01641 --> C00020 + C02987 + C00013
R_GLUTRS	L-Glutamate:tRNA(Glu) ligase (AI	FALSE	Porphyrin and chlorophyll metabolisı	6.1.1.24	0	2.80E-10	0	[c] : C00002 + C00025 + C01641 --> C00020 + C02987 + C00013
R_R07302	adenosylcobyric acid:(R)-1-amino	TRUE	Porphyrin and chlorophyll metabolisı	6.3.1.10	0	0		[c] : C00002 + C06507 + C03194 <==> C00008 + C00009 + C06508
R_ADCPS2	adenosylcobyric acid:(R)-1-amino	FALSE	Porphyrin and chlorophyll metabolisı	6.3.1.10	0	0		[c] : C06507 + C04122 + C00002 --> C06509 + C00008 + C00080 + C00009
R_ADCYRS	.	FALSE	Porphyrin and chlorophyll metabolisı	6.3.5.10	0	0		[c] : C06506 + 4 C00002 + 4 C00064 + 4 C00001 --> C06507 + 4 C00008 + 4 C00025 + 4 C0
R_R05224	.	TRUE	Porphyrin and chlorophyll metabolisı	6.3.5.9	0	0		[c] : C06399 + 2 C00064 + 2 C00002 + 2 C00001 <==> C06503 + 2 C00009 + 2 C00025 + 2
R_MPML	Magnesium-protoporphyrin IX ch	TRUE	Porphyrin and chlorophyll metabolisı	6.6.1.1	0	0		[c] : C00002 + C00001 + C00305 + C02191 <==> C00008 + 3 C00080 + C03516 + C00009
R_COCHL	hydrogenobyrinic-acid-a,c-diamid	FALSE	Porphyrin and chlorophyll metabolisı	6.6.1.2	0	0		[c] : C00002 + C00175 + C00001 + C06503 --> C00008 + C06504 + 2 C00080 + C00009
R_R00935	(S)-Methylmalonate semialdehyd	TRUE	Propanoate metabolism	1.2.1.27	0	0		[c] : C06002 + C00010 + C00003 <==> C00100 + C00011 + C00004 + C00080
R_R02940	2-Propyn-1-al:NAD+ oxidoreduct	TRUE	Propanoate metabolism	1.2.1.3	0	0		[c] : C05985 + C00003 + C00001 <==> C00804 + C00004 + C00080
R_R00919	.	TRUE	Propanoate metabolism	1.3.1.-	0	0		[c] : C00100 + C00006 <==> prpncoa + C00005 + C00080
R_R04432	Propanoyl-CoA:(acceptor) 2,3-oxi	TRUE	Propanoate metabolism	1.3.99.3	0	0		[c] : etfox + C00100 <==> etfrd + prpncoa
R_ACACT1m	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Propanoate metabolism	2.3.1.16	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_ACACT1m	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Propanoate metabolism	2.3.1.9	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_APAT2rm	3-Aminopropanoate:2-oxoglutara	TRUE	Propanoate metabolism	2.6.1.19	0	0.1	0	[c] : C00026 + C00099 <==> C00025 + C00222
R_APAT2rm	3-Aminopropanoate:2-oxoglutara	TRUE	Propanoate metabolism	2.6.1.55	0	0.1	0	[c] : C00026 + C00099 <==> C00025 + C00222
R_PPAKr	ATP:propanoate phosphotransfer	TRUE	Propanoate metabolism	2.7.2.1	0	0	0	[c] : C00008 + C02876 <==> C00002 + C00163
R_PPAKr	ATP:propanoate phosphotransfer	TRUE	Propanoate metabolism	2.7.2.15	0	0	0	[c] : C00008 + C02876 <==> C00002 + C00163
R_PRPNCOA	3-Hydroxypropionyl-CoA hydro-l	FALSE	Propanoate metabolism	4.2.1.17	0	0	0	[c] : C00001 + prpncoa --> 3hpcoa
R_MMEm	Methylmalonyl-CoA epimerase	TRUE	Propanoate metabolism	5.1.99.1	0	-0.1	0	[c] : C01213 <==> C00683
R_MMMm	(R)-Methylmalonyl-CoA CoA-carb	TRUE	Propanoate metabolism	5.4.99.2	0	0.1	0	[c] : C01213 <==> C00091
R_R01354	ATP:propanoate adenyltransferas	TRUE	Propanoate metabolism	6.2.1.1	0	0.1		[c] : C00002 + C00163 <==> C00013 + C05983
R_R00926	Propionyladenylate:CoA propiony	TRUE	Propanoate metabolism	6.2.1.1	0	0.1		[c] : C05983 + C00010 <==> C00020 + C00100
R_R01354	ATP:propanoate adenyltransferas	TRUE	Propanoate metabolism	6.2.1.17	0	0.1		[c] : C00002 + C00163 <==> C00013 + C05983
R_R00926	Propionyladenylate:CoA propiony	TRUE	Propanoate metabolism	6.2.1.17	0	0.1		[c] : C05983 + C00010 <==> C00020 + C00100
R_SUCOAS	Succinate:CoA ligase (ADP-formi	TRUE	Propanoate metabolism	6.2.1.5	350.86382	96.810791	0	[c] : C00002 + C00010 + C00042 <==> C00008 + C00009 + C00091
R_PPCOACm	Propanoyl-CoA:carbon-dioxide lig	FALSE	Propanoate metabolism	6.4.1.3	0	0.1	0	[c] : C00002 + C01353 + C00100 --> C00008 + C00080 + C00683 + C00009
R_IMPD	IMP:NAD+ oxidoreductase	FALSE	Purine metabolism	1.1.1.205	5.3587345	6.98E-25	6.96121817	[c] : C00001 + C00130 + C00003 --> C00080 + C00004 + C00655
R_RNDR1	2'-Deoxyadenosine 5'-diphosphat	FALSE	Purine metabolism	1.17.4.1	0.667893	0	0.86762067	[c] : C00008 + C00342 --> C00206 + C00001 + C00343
R_RNDR2	2'-Deoxyguanosine 5'-diphosphat	FALSE	Purine metabolism	1.17.4.1	0.48889	0	0.63508833	[c] : C00035 + C00342 --> C00361 + C00001 + C00343
R_GARFT	10-Formyltetrahydrofolate:5'-ph	TRUE	Purine metabolism	2.1.2.2	9.3910951	6.00E-11	-987.80205	[c] : C00234 + C03838 <==> C04376 + C00080 + C00101
R_IMPC	IMP 1,2-hydrolase (decyclizing)	TRUE	Purine metabolism	2.1.2.3	-11.12338	-1.05E-10		[c] : C00001 + C00130 <==> C04734
R_AICART	10-Formyltetrahydrofolate:5'-ph	TRUE	Purine metabolism	2.1.2.3	11.123382	1.05E-10	14.4482595	[c] : C00234 + C04677 <==> C04734 + C00101
R_PUNP7	Xanthosine:orthophosphate ribos	TRUE	Purine metabolism	2.4.2.1	1000	1000	0	[c] : C00009 + C01762 <==> C00620 + C00385
R_PUNP1m	Adenosine:phosphate alpha-D-rib	TRUE	Purine metabolism	2.4.2.1	0	-999.9	0	[c] : C00212 + C00009 <==> C00147 + C00620
R_PUNP5	inosine:phosphate alpha-D-ribosy	TRUE	Purine metabolism	2.4.2.1	690.2974	1000	0	[c] : C00294 + C00009 <==> C00262 + C00620
R_PUNP6	Deoxyinosine:orthophosphate rib	TRUE	Purine metabolism	2.4.2.1	0	0	0	[c] : C05512 + C00009 <==> C00672 + C00262
R_PUNP3	guanosine:orthophosphate ribosy	TRUE	Purine metabolism	2.4.2.1	-1000	-0.1	0	[c] : C00387 + C00009 <==> C00242 + C00620

R_PUNP4	Deoxyguanosine:orthophosphate	TRUE	Purine metabolism	2.4.2.1	0	0	0	[c] : C00330 + C00009 <==> C00672 + C00242
R_PUNP2	Deoxyadenosine:orthophosphate	TRUE	Purine metabolism	2.4.2.1	0	0	0	[c] : C00559 + C00009 <==> C00672 + C00147
R_GLUPRT	5-phosphoribosylamine:diphospl	FALSE	Purine metabolism	2.4.2.14	9.3910951	6.00E-11	12.1979465	[c] : C00064 + C00001 + C00119 --> C00025 + C00013 + C03090
R_PUNP5	inosine:phosphate alpha-D-ribosy	TRUE	Purine metabolism	2.4.2.15	690.2974	1000	0	[c] : C00294 + C00009 <==> C00262 + C00620
R_PUNP3	guanosine:orthophosphate ribosy	TRUE	Purine metabolism	2.4.2.15	-1000	-0.1	0	[c] : C00387 + C00009 <==> C00242 + C00620
R_GUAPRT	GMP:diphosphate 5-phospho-alpl	FALSE	Purine metabolism	2.4.2.22	0	0	0	[c] : C00242 + C00119 --> C00144 + C00013
R_XPPT	XMP:pyrophosphate phosphoribo	FALSE	Purine metabolism	2.4.2.22	0	0		[c] : C00119 + C00385 --> C00013 + C00655
R_PUNP4	Deoxyguanosine:orthophosphate	TRUE	Purine metabolism	2.4.2.4	0	0	0	[c] : C00330 + C00009 <==> C00672 + C00242
R_PUNP6	Deoxyinosine:orthophosphate rib	TRUE	Purine metabolism	2.4.2.4	0	0	0	[c] : C05512 + C00009 <==> C00672 + C00262
R_GUAPRT	GMP:diphosphate 5-phospho-alpl	FALSE	Purine metabolism	2.4.2.7	0	0	0	[c] : C00242 + C00119 --> C00144 + C00013
R_ADPT	AMP:pyrophosphate phosphoribo	FALSE	Purine metabolism	2.4.2.7	0	0.1	0	[c] : C00147 + C00119 --> C00020 + C00013
R_R04378	1-(5'-Phosphoribosyl)-5-amino-4	TRUE	Purine metabolism	2.4.2.7	0	0		[c] : C04677 + C00013 <==> C04051 + C00119
R_ADPT	AMP:pyrophosphate phosphoribo	FALSE	Purine metabolism	2.4.2.8	0	0.1	0	[c] : C00147 + C00119 --> C00020 + C00013
R_HXPRT	IMP:diphosphate phospho-D-ribo	FALSE	Purine metabolism	2.4.2.8	0	5.00E-12	0	[c] : C00262 + C00119 --> C00130 + C00013
R_GUAPRT	GMP:diphosphate 5-phospho-alpl	FALSE	Purine metabolism	2.4.2.8	0	0	0	[c] : C00242 + C00119 --> C00144 + C00013
R_XPPT	XMP:pyrophosphate phosphoribo	FALSE	Purine metabolism	2.4.2.8	0	0		[c] : C00119 + C00385 --> C00013 + C00655
R_ADNK1m	ATP:adenosine 5'-phosphotransfe	FALSE	Purine metabolism	2.7.1.20	1.67568	192.321582		[c] : C00212 + C00002 --> C00008 + C00020 + C00080
R_ADSK	ATP:adenylylsulfate 3'-phosphotr	FALSE	Purine metabolism	2.7.1.25	0	0	0	[c] : C00224 + C00002 --> C00008 + C00080 + C00053
R_R01138	dATP:pyruvate 2-O-phosphotrans	TRUE	Purine metabolism	2.7.1.40	624.73797	0.1		[c] : C00131 + C00022 <==> C00206 + C00074
R_R01858	dGTP:pyruvate 2-O-phosphotrans	TRUE	Purine metabolism	2.7.1.40	-1000	0.1		[c] : C00286 + C00022 <==> C00361 + C00074
R_PYK	ATP:pyruvate 2-O-phosphotransf	FALSE	Purine metabolism	2.7.1.40	0	1000	944.841429	[c] : C00008 + C00080 + C00074 --> C00002 + C00022
R_R00430	GTP:pyruvate 2-O-phosphotransf	TRUE	Purine metabolism	2.7.1.40	-1000	999.3		[c] : C00044 + C00022 <==> C00035 + C00074
R_ADNK1m	ATP:adenosine 5'-phosphotransfe	FALSE	Purine metabolism	2.7.1.74	1.67568	192.321582		[c] : C00212 + C00002 --> C00008 + C00020 + C00080
R_DADK	ATP:dAMP phosphotransferase	TRUE	Purine metabolism	2.7.4.11	0	0		[c] : C00002 + C00360 <==> C00008 + C00206
R_DGK1	ATP:dGMP phosphotransferase	TRUE	Purine metabolism	2.7.4.12	0	0.1	0	[c] : C00002 + C00362 <==> C00008 + C00361
R_DADK	ATP:dAMP phosphotransferase	TRUE	Purine metabolism	2.7.4.3	0	0		[c] : C00002 + C00360 <==> C00008 + C00206
R_ADK1	ATP:AMP phosphotransferase	TRUE	Purine metabolism	2.7.4.3	-336.6863	-613.38501	-13.857177	[c] : C00020 + C00002 <==> 2 C00008
R_NDPK10n	ATP:dIDP phosphotransferase	TRUE	Purine metabolism	2.7.4.6	0	0	0	[c] : C00002 + C01344 <==> C00008 + C01345
R_NDPK5	ATP:dGDP phosphotransferase	TRUE	Purine metabolism	2.7.4.6	-999.5111	0.2	0.63508833	[c] : C00002 + C00361 <==> C00008 + C00286
R_NDPK1	ATP:GDP phosphotransferase	TRUE	Purine metabolism	2.7.4.6	-0.402584	0.1	21.7417738	[c] : C00002 + C00035 <==> C00008 + C00044
R_NDPK9n	ATP:IDP phosphotransferase	TRUE	Purine metabolism	2.7.4.6	-1000	0.1	0	[c] : C00002 + C00104 <==> C00008 + C00081
R_NDPK8m	ATP:dADP phosphotransferase	TRUE	Purine metabolism	2.7.4.6	625.40587	0.1	0	[c] : C00002 + C00206 <==> C00008 + C00131
R_GK1	ATP:(d)GMP phosphotransferase	TRUE	Purine metabolism	2.7.4.8	5.3587345	0.3	1000	[c] : C00002 + C00144 <==> C00008 + C00035
R_DGK1	ATP:dGMP phosphotransferase	TRUE	Purine metabolism	2.7.4.8	0	0.1	0	[c] : C00002 + C00362 <==> C00008 + C00361
R_R01049	ATP:D-ribose-5-phosphate dipho	TRUE	Purine metabolism	2.7.6.1	17.279354	0.1		[c] : C00002 + C03736 <==> C00020 + C00119
R_GTPDPK	ATP:GTP 3'-pyrophosphotransfer	FALSE	Purine metabolism	2.7.6.5	0	0	0	[c] : C00002 + C00044 --> C00020 + C04494 + C00080
R_SADT	ATP:sulfate adenylyltransferase	FALSE	Purine metabolism	2.7.7.4	0	1.50E-11	0	[c] : C00002 + C00080 + C00059 --> C00224 + C00013
R_R01856	dGTP triphosphohydrolase	TRUE	Purine metabolism	3.1.5.1	0	0		[c] : C00286 + C00001 <==> C00330 + C00536
R_R01770	Inosine ribohydrolase	TRUE	Purine metabolism	3.2.2.1	-690.2974	-1000		[c] : C00294 + C00001 <==> C00262 + C00121
R_ADNUC	Adenosine ribohydrolase	FALSE	Purine metabolism	3.2.2.1	0	1000		[c] : C00212 + C00001 --> C00147 + C00121
R_GNNUC	Guanosine ribohydrolase	FALSE	Purine metabolism	3.2.2.1	1000	0.1		[c] : C00387 + C00001 --> C00242 + C00121
R_R02143	Xanthosine ribohydrolase	TRUE	Purine metabolism	3.2.2.1	-1000	-1000		[c] : C01762 + C00001 <==> C00385 + C00121
R_R01770	Inosine ribohydrolase	TRUE	Purine metabolism	3.2.2.2	-690.2974	-1000		[c] : C00294 + C00001 <==> C00262 + C00121
R_ADNUC	Adenosine ribohydrolase	FALSE	Purine metabolism	3.2.2.7	0	1000		[c] : C00212 + C00001 --> C00147 + C00121
R_GNNUC	Guanosine ribohydrolase	FALSE	Purine metabolism	3.2.2.8	1000	0.1		[c] : C00387 + C00001 --> C00242 + C00121
R_ADNUC	Adenosine ribohydrolase	FALSE	Purine metabolism	3.2.2.8	0	1000		[c] : C00212 + C00001 --> C00147 + C00121
R_R01770	Inosine ribohydrolase	TRUE	Purine metabolism	3.2.2.8	-690.2974	-1000		[c] : C00294 + C00001 <==> C00262 + C00121
R_IMPC	IMP 1,2-hydrolase (decyclizing)	TRUE	Purine metabolism	3.5.4.10	-11.12338	-1.05E-10		[c] : C00001 + C00130 <==> C04734
R_DADAe	Deoxyadenosine aminohydrolase	FALSE	Purine metabolism	3.5.4.4	0	0		[e] : C00559 + C00080 + C00001 --> C05512 + C01342
R_ADAe	Adenosine aminohydrolase	FALSE	Purine metabolism	3.5.4.4	0	0	0	[e] : C00212 + C00080 + C00001 --> C00294 + C01342
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.1.15	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_NTPP10	2'-Deoxyinosine-5'-triphosphate	FALSE	Purine metabolism	3.6.1.19	0	0	0	[c] : C01345 + C00001 --> C06196 + C00080 + C00013
R_NTPP1	2'-Deoxyguanosine 5'-triphospha	FALSE	Purine metabolism	3.6.1.19	0	0.1		[c] : C00286 + C00001 --> C00362 + C00080 + C00013
R_NTPP9	Inosine 5'-triphosphate pyrophos	FALSE	Purine metabolism	3.6.1.19	0	0	0	[c] : C00001 + C00081 --> C00080 + C00130 + C00013
R_NTPP11	XTP pyrophosphohydrolase	FALSE	Purine metabolism	3.6.1.19	0	0	0	[c] : C00001 + C00700 --> C00080 + C00013 + C00655
R_NTPP2	Guanosine 5'-triphosphate pyrop	FALSE	Purine metabolism	3.6.1.19	0	0.3		[c] : C00044 + C00001 --> C00144 + C00080 + C00013
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.1.3	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.1.5	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_NTPP2	Guanosine 5'-triphosphate pyrop	FALSE	Purine metabolism	3.6.1.8	0	0.3		[c] : C00044 + C00001 --> C00144 + C00080 + C00013

R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.1.8	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_NTPP9	Inosine 5'-triphosphate pyrophos	FALSE	Purine metabolism	3.6.1.8	0	0	0	[c] : C00001 + C00081 --> C00080 + C00130 + C00013
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.1	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.10	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.11	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.12	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.14	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.15	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.16	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.17	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.18	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.19	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.2	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.20	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.21	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.22	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.23	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.24	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.25	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.26	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.27	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.28	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.29	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.3	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.30	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.31	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.32	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.33	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.34	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.35	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.36	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.37	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.38	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.39	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.4	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.40	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.41	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.42	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.43	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.44	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.46	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.47	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.48	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.49	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.5	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.50	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.51	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.52	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.53	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.6	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.7	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.8	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.3.9	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.1	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.10	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.11	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.2	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.3	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.4	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009

R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.5	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.6	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.7	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.8	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_ATPM	ATP phosphohydrolase (protein-s	FALSE	Purine metabolism	3.6.4.9	0	0.1		[c] : C00002 + C00001 --> C00008 + C00080 + C00009
R_AIRCr	1-(5-Phospho-D-ribosyl)-5-amino	TRUE	Purine metabolism	4.1.1.21	9.3910951	6.00E-11	12.1979465	[c] : C03373 + C00011 <==> C04751 + C00080
R_ADSL1	N6-(1,2-dicarboxyethyl)AMP AMI	FALSE	Purine metabolism	4.3.2.2	5.7646479	1.10E-10	1000	[c] : C03794 --> C00020 + C00122
R_ADSL2r	1-(5'-Phosphoribosyl)-5-amino-4	TRUE	Purine metabolism	4.3.2.2	9.3910951	6.00E-11	12.1979465	[c] : C04823 <==> C04677 + C00122
R_GUACYC	GTP pyrophosphate-lyase (cyclizi	FALSE	Purine metabolism	4.6.1.1	0	0		[c] : C00044 --> C00942 + C00013
R_ADNCYC	ATP pyrophosphate-lyase (cyclizi	FALSE	Purine metabolism	4.6.1.1	0	0		[c] : C00002 --> C00575 + C00013
R_GUACYC	GTP pyrophosphate-lyase (cyclizi	FALSE	Purine metabolism	4.6.1.2	0	0		[c] : C00044 --> C00942 + C00013
R_PRASCS	1-(5-Phosphoribosyl)-5-amino-4-	TRUE	Purine metabolism	6.3.2.6	9.3910951	6.00E-11	12.1979465	[c] : C04751 + C00049 + C00002 <==> C04823 + C00008 + C00080 + C00009
R_PRAIS	2-(Formamido)-N1-(5-phosphori	FALSE	Purine metabolism	6.3.3.1	9.3910951	6.00E-11	12.1979465	[c] : C00002 + C04640 --> C00008 + C03373 + 2 C00080 + C00009
R_GMPS	Xanthosine-5'-phosphate:ammon	FALSE	Purine metabolism	6.3.4.1	5.3587345	0		[c] : C00002 + C01342 + C00655 --> C00020 + C00144 + 2 C00080 + C00013
R_PRAGS	5-Phospho-D-ribosylamine:glycin	FALSE	Purine metabolism	6.3.4.13	9.3910951	6.00E-11	1000	[c] : C00002 + C00037 + C03090 --> C00008 + C03838 + C00080 + C00009
R_ADSS	IMP:L-aspartate ligase (GDP-form	FALSE	Purine metabolism	6.3.4.4	5.7646479	1.10E-10	7.4870413	[c] : C00049 + C00044 + C00130 --> C03794 + C00035 + 2 C00080 + C00009
R_GMPS	Xanthosine-5'-phosphate:ammon	FALSE	Purine metabolism	6.3.5.2	5.3587345	0		[c] : C00002 + C01342 + C00655 --> C00020 + C00144 + 2 C00080 + C00013
R_GMPS2	Xanthosine-5'-phosphate:L-glutar	FALSE	Purine metabolism	6.3.5.2	0	0	6.96121817	[c] : C00002 + C00064 + C00001 + C00655 --> C00020 + C00025 + C00144 + 2 C00080 + C
R_PRFGS	5'-Phosphoribosylformylglycinan	FALSE	Purine metabolism	6.3.5.3	9.3910951	6.00E-11	12.1979465	[c] : C00002 + C04376 + C00064 + C00001 --> C00008 + C04640 + C00025 + C00080 + C0
R_RNDR4n	2'-Deoxyuridine 5'-diphosphate:d	FALSE	Pyrimidine metabolism	1.17.4.1	0.4754166	0	0	[c] : C00342 + C00015 --> C01346 + C00001 + C00343
R_RNDR3	2'-Deoxycytidine diphosphate:oxi	FALSE	Pyrimidine metabolism	1.17.4.1	0.48889	0	0.63508833	[c] : C00112 + C00342 --> C00705 + C00001 + C00343
R_DHORD	(S)-Dihydroorotate:oxygen oxido	TRUE	Pyrimidine metabolism	1.3.3.1	6.1034255	1.50E-11	-307.69568	[c] : C00337 + C00007 <==> C00027 + C00295
R_TRDRm	NADPH:oxidized-thioredoxin oxid	FALSE	Pyrimidine metabolism	1.8.1.9	2.1210895	0	0	[c] : C00080 + C00005 + C00343 --> C00006 + C00342
R_R06613	5,10-methylenetetrahydrofolate,I	TRUE	Pyrimidine metabolism	2.1.1.148	1.4377984	0	0.61758589	[c] : C00143 + C00365 + C01352 <==> C00101 + C00364 + C00016
R_ASPCTn	carbamoyl-phosphate:L-aspartate	FALSE	Pyrimidine metabolism	2.1.3.2	6.1034255	1.50E-11	0	[c] : C00049 + C00169 --> C00438 + C00080 + C00009
R_DURIPP	deoxyuridine:orthophosphate 2-d	TRUE	Pyrimidine metabolism	2.4.2.1	0	0		[c] : C00526 + C00009 <==> C00672 + C00106
R_ORPT	Orotidine-5'-phosphate:diphosph	TRUE	Pyrimidine metabolism	2.4.2.10	-6.103426	-1.50E-11	0	[c] : C01103 + C00013 <==> C00295 + C00119
R_DURIPP	deoxyuridine:orthophosphate 2-d	TRUE	Pyrimidine metabolism	2.4.2.23	0	0		[c] : C00526 + C00009 <==> C00672 + C00106
R_DURIPP	deoxyuridine:orthophosphate 2-d	TRUE	Pyrimidine metabolism	2.4.2.4	0	0		[c] : C00526 + C00009 <==> C00672 + C00106
R_UPPRT	UMP:diphosphate phospho-alpha	FALSE	Pyrimidine metabolism	2.4.2.9	0	0		[c] : C00119 + C00106 --> C00013 + C00105
R_DTMPK	ATP:dTMP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.12	0.4754166	0	0.61758589	[c] : C00002 + C00364 <==> C00008 + C00363
R_UMPK	ATP:nucleoside-phosphate phosp	TRUE	Pyrimidine metabolism	2.7.4.14	6.1034255	0.1		[c] : C00002 + C00105 <==> C00008 + C00015
R_CYTK2n	ATP:dCMP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.14	0	0		[c] : C00002 + C00239 <==> C00008 + C00705
R_CYTK1	ATP:CMP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.14	0.0011356	0		[c] : C00002 + C00055 <==> C00008 + C00112
R_UMPK	ATP:nucleoside-phosphate phosp	TRUE	Pyrimidine metabolism	2.7.4.22	6.1034255	0.1		[c] : C00002 + C00105 <==> C00008 + C00015
R_URIDK2m	ATP:dUMP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.4	-0.475417	0.1		[c] : C00002 + C00365 <==> C00008 + C01346
R_UMPK	ATP:nucleoside-phosphate phosp	TRUE	Pyrimidine metabolism	2.7.4.4	6.1034255	0.1		[c] : C00002 + C00105 <==> C00008 + C00015
R_NDPK2m	ATP:UDP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.6	5.570266	0.2	0	[c] : C00002 + C00015 <==> C00008 + C00075
R_NDPK6	ATP:dUDP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.6	0	0.1	0.61758589	[c] : C00002 + C01346 <==> C00008 + C00460
R_NDPK4	ATP:dTDP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.6	0.4754166	0	0.61758589	[c] : C00002 + C00363 <==> C00008 + C00459
R_NDPK3n	ATP:CDP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.6	-0.487754	0	0	[c] : C00002 + C00112 <==> C00008 + C00063
R_NDPK7n	ATP:dCDP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.6	0.48889	0	0	[c] : C00002 + C00705 <==> C00008 + C00458
R_URIDK2m	ATP:dUMP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.9	-0.475417	0.1		[c] : C00002 + C00365 <==> C00008 + C01346
R_DTMPK	ATP:dTMP phosphotransferase	TRUE	Pyrimidine metabolism	2.7.4.9	0.4754166	0	0.61758589	[c] : C00002 + C00364 <==> C00008 + C00363
R_DHORTSn	(S)-dihydroorotate amidohydrola	TRUE	Pyrimidine metabolism	3.5.2.3	-6.103426	-1.50E-11	0	[c] : C00337 + C00001 <==> C00438 + C00080
R_CSND	Cytosine aminohydrolase	FALSE	Pyrimidine metabolism	3.5.4.1	0	0		[c] : C00380 + C00080 + C00001 --> C01342 + C00106
R_R01411	5-Methylcytosine aminohydrolase	TRUE	Pyrimidine metabolism	3.5.4.1	0	0		[c] : C02376 + C00001 <==> C00178 + C01342
R_DCTPD2	CTP aminohydrolase	FALSE	Pyrimidine metabolism	3.5.4.13	0	0.2	4.14307622	[c] : C00063 + C00080 + C00001 --> C01342 + C00075
R_DCTPD	dCTP aminohydrolase	FALSE	Pyrimidine metabolism	3.5.4.13	0	0	0	[c] : C00458 + C00080 + C00001 --> C00460 + C01342
R_DUTPDPr	dUTP nucleotidohydrolase	FALSE	Pyrimidine metabolism	3.6.1.19	0	0.1	0	[c] : C00460 + C00001 --> C00365 + C00080 + C00013
R_NTPP8	Uridine triphosphate pyrophosph	FALSE	Pyrimidine metabolism	3.6.1.19	0	0.1		[c] : C00001 + C00075 --> C00080 + C00013 + C00105
R_DUTPDPr	dUTP nucleotidohydrolase	FALSE	Pyrimidine metabolism	3.6.1.23	0	0.1	0	[c] : C00460 + C00001 --> C00365 + C00080 + C00013
R_NTPP8	Uridine triphosphate pyrophosph	FALSE	Pyrimidine metabolism	3.6.1.8	0	0.1		[c] : C00001 + C00075 --> C00080 + C00013 + C00105
R_OMPDC	orotidine-5'-phosphate carboxy-l	FALSE	Pyrimidine metabolism	4.1.1.23	6.1034255	1.50E-11	0	[c] : C00080 + C01103 --> C00011 + C00105
R_CTPS2	UTP:ammonia ligase(ADP-formin	FALSE	Pyrimidine metabolism	6.3.4.2	0	0.1	0	[c] : C00002 + C00064 + C00001 + C00075 --> C00008 + C00063 + C00025 + 2 C00080 + C
R_CTPS1	UTP:ammonia ligase(ADP-formin	FALSE	Pyrimidine metabolism	6.3.4.2	2.9140922	0.1	0	[c] : C00002 + C01342 + C00075 --> C00008 + C00063 + 2 C00080 + C00009
R_CBPSn	hydrogen-carbonate:L-glutamine	FALSE	Pyrimidine metabolism	6.3.5.5	11.512011	1.50E-11	0	[c] : 2 C00002 + C00064 + C00001 + C01353 --> 2 C00008 + C00169 + C00025 + 2 C00080
R_MDHm	(S)-malate:NAD+ oxidoreductase	TRUE	Pyruvate metabolism	1.1.1.37	-308.7728	-96.210791	0	[c] : C00711 + C00003 <==> C00080 + C00004 + C00036
R_ME2	(S)-Malate:NADP+ oxidoreductas	FALSE	Pyruvate metabolism	1.1.1.38	0	0		[c] : C00711 + C00006 --> C00011 + C00005 + C00022

R_ME1	(S)-Malate:NADP+ oxidoreductas	FALSE	Pyruvate metabolism	1.1.1.38	0	0	47.0563196	[c] : C00711 + C00003 --> C00011 + C00004 + C00022
R_ME1	(S)-Malate:NADP+ oxidoreductas	FALSE	Pyruvate metabolism	1.1.1.39	0	0	47.0563196	[c] : C00711 + C00003 --> C00011 + C00004 + C00022
R_ME2	(S)-Malate:NADP+ oxidoreductas	FALSE	Pyruvate metabolism	1.1.1.39	0	0		[c] : C00711 + C00006 --> C00011 + C00005 + C00022
R_ME1	(S)-Malate:NADP+ oxidoreductas	FALSE	Pyruvate metabolism	1.1.1.40	0	0	47.0563196	[c] : C00711 + C00003 --> C00011 + C00004 + C00022
R_ME2	(S)-Malate:NADP+ oxidoreductas	FALSE	Pyruvate metabolism	1.1.1.40	0	0		[c] : C00711 + C00006 --> C00011 + C00005 + C00022
R_ALDD2y	Acetaldehyde:NADP+ oxidoreduc	FALSE	Pyruvate metabolism	1.2.1.3	0	0.1		[c] : C00084 + C00001 + C00006 --> C00033 + 2 C00080 + C00005
R_ALDD2x	Acetaldehyde:NAD+ oxidoreducta	FALSE	Pyruvate metabolism	1.2.1.3	0	0.1	0	[c] : C00084 + C00001 + C00003 --> C00033 + 2 C00080 + C00004
R_ALDD2y	Acetaldehyde:NADP+ oxidoreduc	FALSE	Pyruvate metabolism	1.2.1.5	0	0.1		[c] : C00084 + C00001 + C00006 --> C00033 + 2 C00080 + C00005
R_ALDD2x	Acetaldehyde:NAD+ oxidoreducta	FALSE	Pyruvate metabolism	1.2.1.5	0	0.1	0	[c] : C00084 + C00001 + C00003 --> C00033 + 2 C00080 + C00004
R_R03270	.	TRUE	Pyruvate metabolism	1.2.4.1	696.14778	96.910791		[c] : C05125 + C15972 <==> C16255 + C00068
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Pyruvate metabolism	1.2.4.1	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_R07618	enzyme N6-(dihydrolipoyl)lysine	TRUE	Pyruvate metabolism	1.8.1.4	-654.716	-0.1	0	[c] : C15973 + C00003 <==> C15972 + C00004 + C00080
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Pyruvate metabolism	2.2.1.6	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_R02569	acetyl-CoA:enzyme N6-(dihydroli	TRUE	Pyruvate metabolism	2.3.1.12	-696.1478	-96.910791		[c] : C00024 + C15973 <==> C00010 + C16255
R_ACACT1m	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Pyruvate metabolism	2.3.1.16	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_ACACT1m	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Pyruvate metabolism	2.3.1.9	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_IPPSm	acetyl-CoA:3-methyl-2-oxobutanc	FALSE	Pyruvate metabolism	2.3.3.13	0	0		[c] : C00141 + C00024 + C00001 --> C02504 + C00010 + C00080
R_MALS	L-Malate glyoxylate-lyase (CoA-ac	FALSE	Pyruvate metabolism	2.3.3.9	26.935296	0.2		[c] : C00024 + C00048 + C00001 --> C00010 + C00080 + C00711
R_PYK	ATP:pyruvate 2-O-phosphotransf	FALSE	Pyruvate metabolism	2.7.1.40	0	1000	944.841429	[c] : C00008 + C00080 + C00074 --> C00002 + C00022
R_R02320	NTP:pyruvate O2-phosphotransfe	TRUE	Pyruvate metabolism	2.7.1.40	0	0		[c] : C00201 + C00022 <==> C00454 + C00074
R_ACKr	ATP:acetate phosphotransferase	TRUE	Pyruvate metabolism	2.7.2.1	1000	193.921582	0	[c] : C00033 + C00002 <==> C00227 + C00008
R_ACKr	ATP:acetate phosphotransferase	TRUE	Pyruvate metabolism	2.7.2.15	1000	193.921582	0	[c] : C00033 + C00002 <==> C00227 + C00008
R_PPDK	ATP:pyruvate,orthophosphate ph	FALSE	Pyruvate metabolism	2.7.9.1	628.79312	0.1	588.40369	[c] : C00002 + C00009 + C00022 --> C00020 + C00080 + C00074 + C00013
R_ACYP_2	Acetyl phosphate phosphohydrol	FALSE	Pyruvate metabolism	3.6.1.7	0	0.1	0	[c] : C00227 + C00001 --> C00033 + C00080 + C00009
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Pyruvate metabolism	4.1.1.1	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_ME2	(S)-Malate:NADP+ oxidoreductas	FALSE	Pyruvate metabolism	4.1.1.3	0	0		[c] : C00711 + C00006 --> C00011 + C00005 + C00022
R_ME1	(S)-Malate:NADP+ oxidoreductas	FALSE	Pyruvate metabolism	4.1.1.3	0	0	47.0563196	[c] : C00711 + C00003 --> C00011 + C00004 + C00022
R_PPC	Orthophosphate:oxaloacetate car	FALSE	Pyruvate metabolism	4.1.1.31	0	0.1	0	[c] : C00011 + C00001 + C00074 --> C00080 + C00036 + C00009
R_R00726	ITP:oxaloacetate carboxy-lyase (t	TRUE	Pyruvate metabolism	4.1.1.32	-1000	0.1		[c] : C00081 + C00036 <==> C00104 + C00074 + C00011
R_PEPCK	GTP:oxaloacetate carboxy-lyase (	FALSE	Pyruvate metabolism	4.1.1.32	988.96292	0.5	0	[c] : C00044 + C00036 --> C00011 + C00035 + C00074
R_R00236	Acetyl adenylate:CoA ligase (AMP	TRUE	Pyruvate metabolism	6.2.1.1	-1000	-806.506592		[c] : C05993 + C00010 <==> C00020 + C00024
R_R00316	Acetate:CoA ligase (AMP-forming	TRUE	Pyruvate metabolism	6.2.1.1	-1000	-806.506592		[c] : C00002 + C00033 <==> C00013 + C05993
R_MDHm	(S)-malate:NAD+ oxidoreductase	TRUE	Reductive carboxylate cycle (CO2 fixa	1.1.1.37	-308.7728	-96.210791	0	[c] : C00711 + C00003 <==> C00080 + C00004 + C00036
R_ICDHyr	Isocitrate:NADP+ oxidoreductase	TRUE	Reductive carboxylate cycle (CO2 fixa	1.1.1.42	669.17303	-96.810791	26.0286951	[c] : C00311 + C00006 <==> C00026 + C00011 + C00005
R_OOR	2-oxoglutarate:ferredoxin oxidor	FALSE	Reductive carboxylate cycle (CO2 fixa	1.2.7.3	0	0		[c] : C00026 + C00010 + C00139 + C00080 --> C00011 + C00138 + C00091
R_SUCD1i	Succinate:(acceptor) oxidoreduct	FALSE	Reductive carboxylate cycle (CO2 fixa	1.3.99.1	0	0		[c] : C00016 + C00042 --> C01352 + C00122
R_ALAD_L	L-Alanine:NAD+ oxidoreductase (	FALSE	Reductive carboxylate cycle (CO2 fixa	1.4.1.1	0	482.325781	0	[c] : C00041 + C00001 + C00003 --> C00080 + C00004 + C01342 + C00022
R_PPC	Orthophosphate:oxaloacetate car	FALSE	Reductive carboxylate cycle (CO2 fixa	4.1.1.31	0	0.1	0	[c] : C00011 + C00001 + C00074 --> C00080 + C00036 + C00009
R_FUMm	(S)-malate hydro-lyase (fumarate	TRUE	Reductive carboxylate cycle (CO2 fixa	4.2.1.2	-335.7081	-96.410791	0	[c] : C00122 + C00001 <==> C00711
R_R01900	isocitrate hydro-lyase (cis-aconita	TRUE	Reductive carboxylate cycle (CO2 fixa	4.2.1.3	330.82697	96.810791		[c] : C00311 <==> C00417 + C00001
R_R01325	citrate hydro-lyase (cis-aconitate	TRUE	Reductive carboxylate cycle (CO2 fixa	4.2.1.3	-330.827	-96.810791		[c] : C00158 <==> C00417 + C00001
R_R01325	citrate hydro-lyase (cis-aconitate	TRUE	Reductive carboxylate cycle (CO2 fixa	4.2.1.4	-330.827	-96.810791		[c] : C00158 <==> C00417 + C00001
R_ACSm	Acetate:CoA ligase (AMP-forming	FALSE	Reductive carboxylate cycle (CO2 fixa	6.2.1.1	0	0.1	0	[c] : C00033 + C00002 + C00010 --> C00024 + C00020 + C00013
R_SUCOAS	Succinate:CoA ligase (ADP-formir	TRUE	Reductive carboxylate cycle (CO2 fixa	6.2.1.5	350.86382	96.810791	0	[c] : C00002 + C00010 + C00042 <==> C00008 + C00009 + C00091
R_DHPPDA	diaminohydroxyphosphoribosyla	TRUE	Riboflavin Metabolism	3.5.4.26	0.0001925	0		[c] : 25dhpp + C00080 + C00001 <==> C01268 + C01342
R_RBFSa	6,7-Dimethyl-8-(1-D-ribityl)luma	FALSE	Riboflavin metabolism	.	0.000385	0	0.00050007	[c] : C04732 + C15556 --> C04332 + 2 C00001 + C00009
R_DB4PS	3,4-Dihydroxy-2-butanone 4-pho	FALSE	Riboflavin metabolism	.	0.000385	0	0.00050007	[c] : C00199 --> C15556 + C00058 + C00080
R_APRAUR	5-amino-6-(5-phosphoribitylamir	FALSE	Riboflavin metabolism	1.1.1.193	0.0001925	0		[c] : C01268 + C00080 + C00005 --> C04454 + C00006
R_RBFSb	6,7-Dimethyl-8-(1-D-ribityl)luma	FALSE	Riboflavin metabolism	2.5.1.9	0.0001925	0	0.00025003	[c] : 2 C04332 --> C04732 + C00255
R_RBFK	ATP:riboflavin 5'-phosphotransfe	FALSE	Riboflavin metabolism	2.7.1.26	0.0001925	0	0.00025003	[c] : C00002 + C00255 --> C00008 + C00061 + C00080
R_FMNATm	ATP:FMN adenylyltransferase	FALSE	Riboflavin metabolism	2.7.7.2	0.0001925	0		[c] : C00002 + C00061 + C00080 --> C00016 + C00013
R_GTPCII	GTP 7,8-8,9-dihydrolase (pyroph	FALSE	Riboflavin metabolism	3.5.4.25	0.0001925	0	0.00025003	[c] : C00044 + 3 C00001 --> 25dhpp + C00058 + 2 C00080 + C00013
R_R04939	.	TRUE	Selenoamino acid metabolism	2.1.1.-	0	0		[c] : C05693 + C05691 <==> C05694 + seahcys
R_R03601	O3-Acetyl-L-serine acetate-lyase	TRUE	Selenoamino acid metabolism	2.5.1.47	9.3928466	290.204199		[c] : C00979 + C01528 <==> C05688 + C00033
R_R04945	O-Acetylhomoserine succinate-ly	TRUE	Selenoamino acid metabolism	2.5.1.48	0	0		[c] : C05700 + C05688 <==> selcyst + C00033
R_R04944	O-Phosphorylhomoserine succina	TRUE	Selenoamino acid metabolism	2.5.1.48	0	0		[c] : C05702 + C05688 <==> selcyst + C00009
R_R04946	O-Succinyl-L-homoserine succina	TRUE	Selenoamino acid metabolism	2.5.1.48	0	0		[c] : C05701 + C05688 <==> selcyst + C00042
R_SELMETA	ATP:L-methione S-adenosyltransf	FALSE	Selenoamino acid metabolism	2.5.1.6	0	0	0	[c] : C00002 + C00001 + C05335 --> C00009 + C00013 + C05691
R_ADSELK	ATP:adenylylsulfate 3'-phosphotr	FALSE	Selenoamino acid metabolism	2.7.1.25	0	0	0	[c] : adsel + C00002 --> 3padsel + C00008 + C00080

R_SELADT	ATP:sulfate adenylyltransferase	FALSE	Selenoamino acid metabolism	2.7.7.4	0	0	0	[c] : C00002 + C00080 + sel --> adsel + C00013
R_SEAHCYS	Se-Adenosylselenohomocysteine	FALSE	Selenoamino acid metabolism	3.3.1.1	0	0	0	[c] : C00001 + seahcys --> C00212 + selhcys
R_SELCYST	L-Serine hydro-lyase (adding hon	FALSE	Selenoamino acid metabolism	4.2.1.22	0	0	0	[c] : selhcys + C00716 --> C00001 + selcyst
R_R03599	Selenocysteine reductase	TRUE	Selenoamino acid metabolism	4.4.1.16	9.3928466	290.204199		[c] : C05688 + C00030 <==> C01528 + C00041 + C00028
R_R04773	Selenomethionine:tRNAMet ligas	TRUE	Selenoamino acid metabolism	6.1.1.10	0	0		[c] : C00002 + C05335 + C01647 <==> C00020 + C00013 + C05336
R_SRC_C003	. source flux	FALSE	SourceFlux	.	0	0		C00311[b] --> C00311[c]
R_SRC_C002	. source flux	FALSE	SourceFlux	.	0	0		C00246[b] --> C00246[c]
R_SRC_C007	. source flux	FALSE	SourceFlux	.	0	0		C00711[b] --> C00711[c]
R_SRC_C004	. source flux	FALSE	SourceFlux	.	5.3123477	5.31234766		C00407[b] --> C00407[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	0	0		C00037[b] --> C00037[c]
R_SRC_C002	. source flux	FALSE	SourceFlux	.	0	0		C00256[b] --> C00256[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	0	0		C00033[b] --> C00033[c]
R_SRC_C006	. source flux	FALSE	SourceFlux	.	92.800959	92.8009586		C00631[b] --> C00631[c]
R_SRC_C010	. source flux	FALSE	SourceFlux	.	0	0		C01089[b] --> C01089[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	0	0		C00080[b] --> C00080[c]
R_SRC_C001	. source flux	FALSE	SourceFlux	.	0	0		C00158[b] --> C00158[c]
R_SRC_C004	. source flux	FALSE	SourceFlux	.	0	0		C00469[b] --> C00469[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	1.0393724	1.03937237		C00078[b] --> C00078[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	6.2747295	6.27472948		C00047[b] --> C00047[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	0	0		C00041[b] --> C00041[c]
R_SRC_C001	. source flux	FALSE	SourceFlux	.	0	0		C00163[b] --> C00163[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	0	0		C00049[b] --> C00049[c]
R_SRC_C001	. source flux	FALSE	SourceFlux	.	0	0		C00183[b] --> C00183[c]
R_SRC_metm	. source flux	FALSE	SourceFlux	.	0	0		metmal[b] --> metmal[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	0	0		C00064[b] --> C00064[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	4.4858349	4.4858349		C00073[b] --> C00073[c]
R_SRC_C007	. source flux	FALSE	SourceFlux	.	0	0		C00719[b] --> C00719[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	0	0		C00058[b] --> C00058[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	0	0		C00042[b] --> C00042[c]
R_SRC_C001	. source flux	FALSE	SourceFlux	.	0	0		C00164[b] --> C00164[c]
R_SRC_C001	. source flux	FALSE	SourceFlux	.	0	0		C00116[b] --> C00116[c]
R_SRC_C109	. source flux	FALSE	SourceFlux	.	20.81066	20.81066		C10906[b] --> C10906[c]
R_SRC_C013	. source flux	FALSE	SourceFlux	.	1000	1000		C01342[b] --> C01342[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	2.5214404	2.52144038		C00082[b] --> C00082[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	767.76152	767.761522		C00001[b] --> C00001[c]
R_SRC_C001	. source flux	FALSE	SourceFlux	.	8.2379884	8.2379884		C00123[b] --> C00123[c]
R_SRC_C003	. source flux	FALSE	SourceFlux	.	0	0		C00334[b] --> C00334[c]
R_SRC_C002	. source flux	FALSE	SourceFlux	.	25.972915	25.9729146		C00266[b] --> C00266[c]
R_SRC_C000	. source flux	FALSE	SourceFlux	.	0	0		C00011[b] --> C00011[c]
R_SRC_pa_T	. source flux	FALSE	SourceFlux	.	0.0577429	0.05774291	0.07501043	pa_TF[b] --> pa_TF[c]
R_UDPGDr	UDPglucose:NAD+ oxidoreductas	TRUE	Starch and sucrose metabolism	1.1.1.22	0	0	-1000	[c] : C00001 + 2 C00003 + C00029 <==> 3 C00080 + 2 C00004 + C00167
R_R02111	1,4-alpha-D-Glucan:orthophospha	TRUE	Starch and sucrose metabolism	2.4.1.1	0	0.1	0.07501043	[c] : strch2_strch1 + C00009 <==> C00718 + C00103
R_R02737	UDPglucose:D-glucose-6-phospha	TRUE	Starch and sucrose metabolism	2.4.1.15	-0.057743	0.1		[c] : C00029 + C00668 <==> C00015 + C00689
R_R02110	1,4-alpha-D-Glucan:1,4-alpha-D-g	TRUE	Starch and sucrose metabolism	2.4.1.18	0	0.1	0.07501043	[c] : C00718 <==> strch2_strch1
R_R03920	ATP:D-fructose 6-phosphotransfe	TRUE	Starch and sucrose metabolism	2.7.1.1	0	-0.1		[c] : C00002 + C02336 <==> C00008 + f6p-B
R_R01786	ATP:alpha-D-glucose 6-phosphot	TRUE	Starch and sucrose metabolism	2.7.1.1	-1000	-1000		[c] : C00002 + C00267 <==> C00008 + C00668
R_R01786	ATP:alpha-D-glucose 6-phosphot	TRUE	Starch and sucrose metabolism	2.7.1.2	-1000	-1000		[c] : C00002 + C00267 <==> C00008 + C00668
R_R03920	ATP:D-fructose 6-phosphotransfe	TRUE	Starch and sucrose metabolism	2.7.1.4	0	-0.1		[c] : C00002 + C02336 <==> C00008 + f6p-B
R_R04111	Protein-N(pai)-phosphohistidine-	TRUE	Starch and sucrose metabolism	2.7.1.69	0	0		[c] : C04261 + C00208 <==> C00615 + C05737
R_R02780	.	TRUE	Starch and sucrose metabolism	2.7.1.69	0.0577429	-0.1		[c] : C01083 + C04261 <==> C00689 + C00615
R_GALUi	UTP:alpha-D-glucose-1-phosphat	FALSE	Starch and sucrose metabolism	2.7.7.9	0	0.1	0	[c] : C00103 + C00080 + C00075 --> C00013 + C00029
R_R00802	alpha-D-Glucoside glucohydrolas	TRUE	Starch and sucrose metabolism	3.2.1.20	0	-0.1		[c] : C00089 + C00001 <==> C02336 + C00267
R_R00028	alpha-D-Glucoside glucohydrolas	TRUE	Starch and sucrose metabolism	3.2.1.20	-0.057743	0.1		[c] : C00208 + C00001 <==> 2 C00267
R_R03527	D-Glucoside glucohydrolase	TRUE	Starch and sucrose metabolism	3.2.1.21	0	0		[c] : C01798 + C00001 <==> C01335 + C00267
R_R00026	beta-D-Glucoside glucohydrolase	TRUE	Starch and sucrose metabolism	3.2.1.21	0	-80.2506592		[c] : C00185 + C00001 <==> 2 C00221
R_R00802	alpha-D-Glucoside glucohydrolas	TRUE	Starch and sucrose metabolism	3.2.1.26	0	-0.1		[c] : C00089 + C00001 <==> C02336 + C00267
R_R00802	alpha-D-Glucoside glucohydrolas	TRUE	Starch and sucrose metabolism	3.2.1.48	0	-0.1		[c] : C00089 + C00001 <==> C02336 + C00267
R_R02740	alpha-D-Glucose 6-phosphate ket	TRUE	Starch and sucrose metabolism	5.3.1.9	-1000	-0.1		[c] : C00668 <==> f6p-B
R_R01557	Maltose alpha-D-glucosylmutase	TRUE	Starch and sucrose metabolism	5.4.99.16	0.0577429	-0.1		[c] : C00208 <==> C01083

R_HEX1	ATP:D-glucose 6-phosphotransfe	FALSE	Streptomycin biosynthesis	2.7.1.1	1000	1000		[c] : C00002 + C00267 --> C00008 + C00668 + C00080
R_HEX1	ATP:D-glucose 6-phosphotransfe	FALSE	Streptomycin biosynthesis	2.7.1.2	1000	1000		[c] : C00002 + C00267 --> C00008 + C00668 + C00080
R_MI1PP	1D-myo-Inositol 1-phosphate pho	FALSE	Streptomycin biosynthesis	3.1.3.25	0	0	0	[c] : C00001 + C01177 --> C00137 + C00009
R_MI1PS	1L-myo-Inositol-1-phosphate lya	FALSE	Streptomycin biosynthesis	5.5.1.4	0	0		[c] : C00668 --> C01177
R_AMID5	.	FALSE	Styrene degradation	3.5.1.4	0	0	0	[c] : C01659 + C00001 --> C00511 + C01342
R_AMID2	2-phenylacetamide amidohydrola	FALSE	Styrene degradation	3.5.1.4	0	0	0	[c] : C00001 + C02505 --> C01342 + C07086
R_PAPSR	adenosine 3',5'-bisphosphate,sulf	FALSE	Sulfur metabolism	1.8.4.8	0	0		[c] : C00053 + C00342 --> 2 C00080 + C00054 + C00094 + C00343
R_HSERTA	Acetyl-CoA:L-homoserine O-acety	TRUE	Sulfur metabolism	2.3.1.31	-330.827	-709.695801	0	[c] : C00024 + C00263 <==> C01077 + C00010
R_CYSSr	O3-Acetyl-L-serine acetate-lyase (	TRUE	Sulfur metabolism	2.5.1.47	-1000	-1000		[c] : C00979 + C00297 <==> C00033 + C00097 + C00080
R_R02508	.	TRUE	Sulfur metabolism	2.5.1.48	0	0		[c] : C00542 + C00042 <==> C01118 + C00097
R_CYSSr	O3-Acetyl-L-serine acetate-lyase (	TRUE	Sulfur metabolism	2.5.1.65	-1000	-1000		[c] : C00979 + C00297 <==> C00033 + C00097 + C00080
R_ADSK	ATP:adenylylsulfate 3'-phosphotr	FALSE	Sulfur metabolism	2.7.1.25	0	0	0	[c] : C00224 + C00002 --> C00008 + C00080 + C00053
R_SADT	ATP:sulfate adenylyltransferase	FALSE	Sulfur metabolism	2.7.7.4	0	1.50E-11	0	[c] : C00002 + C00080 + C00059 --> C00224 + C00013
R_BDHm	(R)-3-Hydroxybutanoate:NAD+ o	TRUE	Synthesis and degradation of ketone l	1.1.1.30	0	-5.00E-12		[c] : C01089 + C00003 <==> C00164 + C00080 + C00004
R_ACACT1n	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Synthesis and degradation of ketone l	2.3.1.16	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_ACACT1m	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Synthesis and degradation of ketone l	2.3.1.9	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_ALAD_L	L-Alanine:NAD+ oxidoreductase (	FALSE	Taurine and hypotaurine metabolism	1.4.1.1	0	482.325781	0	[c] : C00041 + C00001 + C00003 --> C00080 + C00004 + C01342 + C00022
R_ACKr	ATP:acetate phosphotransferase	TRUE	Taurine and hypotaurine metabolism	2.7.2.1	1000	193.921582	0	[c] : C00033 + C00002 <==> C00227 + C00008
R_ACKr	ATP:acetate phosphotransferase	TRUE	Taurine and hypotaurine metabolism	2.7.2.15	1000	193.921582	0	[c] : C00033 + C00002 <==> C00227 + C00008
R_FT	Farnesyl diphosphate:Isopenteny	FALSE	Terpenoid biosynthesis	2.5.1.-	0	0		[c] : C00448 + C00129 --> C00013 + ttc-ggdp
R_R06447	di-trans,poly-cis-Decaprenyl-diph	TRUE	Terpenoid biosynthesis	2.5.1.31	0	0		[c] : ttc-ggdp + 7 C00129 <==> C04574 + 7 C00013
R_R07461	.	TRUE	Thiamine metabolism	.	0	0		[c] : C15812 + C15813 <==> C15814
R_R07465	.	TRUE	Thiamine metabolism	.	0	-0.1		[c] : C15815 + C00082 + C15809 <==> C04327
R_R07464	.	TRUE	Thiamine metabolism	.	0	0.1		[c] : C15815 + C11437 + C00082 <==> C04327
R_R07463	glycine oxidase	TRUE	Thiamine metabolism	1.4.3.19	0	-0.1		[c] : C00037 <==> C15809
R_TMPPP	2-Methyl-4-amino-5-hydroxymet	FALSE	Thiamine metabolism	2.5.1.3	0	0	0	[c] : C04752 + C04327 + C00080 --> C00013 + C01081
R_HMPK1	ATP:4-amino-5-hydroxymethyl-2	FALSE	Thiamine metabolism	2.7.1.49	0	0		[c] : C01279 + C00002 --> C04556 + C00008 + C00080
R_TMPKr	ATP:thiamin-phosphate phospho	TRUE	Thiamine metabolism	2.7.4.16	0	0.1	0	[c] : C00002 + C01081 <==> C00008 + C00068
R_PMPK	ATP:4-amino-2-methyl-5-phosph	FALSE	Thiamine metabolism	2.7.4.7	0	0	0	[c] : C04556 + C00002 --> C04752 + C00008
R_R07460	L-cysteine:[ThiI] sulfurtransferas	TRUE	Thiamine metabolism	2.8.1.7	0	0		[c] : C15811 + C00097 <==> C15812 + C00041
R_TMN	Thiamin hydrolase	FALSE	Thiamine metabolism	3.5.99.2	0	0		[c] : C00001 + C00378 --> C01279 + C04294 + C00080
R_TDPm	Thiamin diphosphate phosphohy	FALSE	Thiamine metabolism	3.6.1.15	0	0.1		[c] : C00001 + C00068 --> C00080 + C00009 + C01081
R_R07663	.	TRUE	Toluene and xylene degradation	1.14.13.-	0	0		[c] : 2 C06677 + C00007 + 2 C00080 <==> 2 C01468 + 2 C11481
R_R07665	.	TRUE	Toluene and xylene degradation	1.14.13.-	0	0		[c] : C01467 + C00007 + C00004 + C00080 <==> C03351 + C00003 + C00001
R_R03791	mandelate racemase	TRUE	Toluene and xylene degradation	5.1.2.2	0	0		[c] : C01984 <==> C01983
R_tcyntt	tcynttransport	FALSE	Transport Database	.	0	0	0	C01755[e] --> C01755[c]
R_fumt	fumtransport	TRUE	Transport Database	.	0	0	0	C00122[c] <==> C00122[e]
R_ureat	ureatransport	FALSE	Transport Database	.	0	0	0	C00086[c] --> C00086[e]
R_lctst	lctstransport	FALSE	Transport Database	.	0	0	0	C00243[e] --> C00243[c]
R_lac_Lt	lac-Ltransport	TRUE	Transport Database	.	0	0	0	C00186[c] <==> C00186[e]
R_succt	succtransport	TRUE	Transport Database	.	0	0	0	C00042[c] <==> C00042[e]
R_phemet	phemetransport	FALSE	Transport Database	.	0	0	0	C00032[e] --> C00032[c]
R_cholt	choltransport	FALSE	Transport Database	.	0	0	0	C00114[e] --> C00114[c]
R_hxant	hxantransport	FALSE	Transport Database	.	0	0	0	C00262[e] --> C00262[c]
R_maltt	malttransport	FALSE	Transport Database	.	0	0	0	C00208[e] --> C00208[c]
R_ornt	orntransport	FALSE	Transport Database	.	0	0	0	C00077[e] --> C00077[c]
R_amett	amettransport	FALSE	Transport Database	.	0	0	0	C00019[e] --> C00019[c]
R_urat	uratransport	FALSE	Transport Database	.	0	0	0	C00106[e] --> C00106[c]
R_acact	acactransport	FALSE	Transport Database	.	0	0	0	C00164[c] --> C00164[e]
R_cd2t	cd2transport	FALSE	Transport Database	.	0	0	0	C01413[e] --> C01413[c]
R_val_Lt	val-Ltransport	FALSE	Transport Database	.	0	0	0	C00183[e] --> C00183[c]
R_xyl_Dt	xyl-Dtransport	FALSE	Transport Database	.	0	0	0	C01394[e] --> C01394[c]
R_acaldt	acaldtransport	FALSE	Transport Database	.	0	0	0	C00084[c] --> C00084[e]
R_etoht	etohtransport	FALSE	Transport Database	.	0	0	0	C00469[c] --> C00469[e]
R_thymt	thymtransport	FALSE	Transport Database	.	0	0	0	C00178[e] --> C00178[c]
R_kt	ktransport	FALSE	Transport Database	.	0	0	0	C00238[e] --> C00238[c]
R_lac_Dt	lac-Dtransport	TRUE	Transport Database	.	0	0	0	C00256[c] <==> C00256[e]
R_pydxnt	pydxntransport	FALSE	Transport Database	.	0	0	0	C00314[e] --> C00314[c]
R_gsnt	gsntransport	FALSE	Transport Database	.	0	0	0	C00387[e] --> C00387[c]

R_glu_Lt	glu-Ltransport	FALSE	Transport Database	.	0	0	0	C00025[e] --> C00025[c]
R_4abzt	4abztransport	FALSE	Transport Database	.	0	0	0	C00568[e] --> C00568[c]
R_fe3t	fe3transport	FALSE	Transport Database	.	0	0	0	C14819[e] --> C14819[c]
R_arg_Lt	arg-Ltransport	FALSE	Transport Database	.	0	0	0	C00062[e] --> C00062[c]
R_b_D_glucd	b-D-glucosetransport	FALSE	Transport Database	.	0	0	0	C00221[e] --> C00221[c]
R_arab_Dt	arab-Dtransport	FALSE	Transport Database	.	0	0	0	C00216[e] --> C00216[c]
R_pyrt	pyrtransport	TRUE	Transport Database	.	0	0	0	C00022[c] <==> C00022[e]
R_cu2t	cu2transport	FALSE	Transport Database	.	0	0	0	C00070[e] --> C00070[c]
R_ribflvt	ribflvtransport	FALSE	Transport Database	.	0	0	0	C00255[e] --> C00255[c]
R_strch1t	strch1transport	FALSE	Transport Database	.	0	0	0	C00369[e] --> C00369[c]
R_na1t	na1transport	FALSE	Transport Database	.	0	0	0	C01330[e] --> C01330[c]
R_asn_Lt	asn-Ltransport	FALSE	Transport Database	.	0	0	0	C00152[e] --> C00152[c]
R_sprmt	sprmtransport	FALSE	Transport Database	.	0	0	0	C00750[e] --> C00750[c]
R_csnt	csntransport	FALSE	Transport Database	.	0	0	0	C00380[e] --> C00380[c]
R_inst	instransport	FALSE	Transport Database	.	0	5.00E-12	0	C00294[e] --> C00294[c]
R_his_Lt	his-Ltransport	FALSE	Transport Database	.	0	0	0	C00135[e] --> C00135[c]
R_mg2t	mg2transport	FALSE	Transport Database	.	0	0	0	C00305[e] --> C00305[c]
R_gln_Lt	gln-Ltransport	FALSE	Transport Database	.	0	0	0	C00064[e] --> C00064[c]
R_asp_Lt	asp-Ltransport	FALSE	Transport Database	.	0	0	0	C00049[e] --> C00049[c]
R_cytdt	cytdtransport	FALSE	Transport Database	.	0	0	0	cytd[e] --> cytd[c]
R_xant	xantransport	FALSE	Transport Database	.	0	0	0	C00385[e] --> C00385[c]
R_ptrct	ptrctransport	FALSE	Transport Database	.	0	0	0	C00134[e] --> C00134[c]
R_gthrdt	gthrdtransport	FALSE	Transport Database	.	0	0	0	C00051[e] --> C00051[c]
R_nadt	nadtransport	FALSE	Transport Database	.	0	0	0	C00003[e] --> C00003[c]
R_zn2t	zn2transport	FALSE	Transport Database	.	0	0	0	C00038[e] --> C00038[c]
R_fmnt	fmntransport	FALSE	Transport Database	.	0	0	0	C00061[e] --> C00061[c]
R_folt	foltransport	FALSE	Transport Database	.	0	0	0	C00504[e] --> C00504[c]
R_phe_Lt	phe-Ltransport	FALSE	Transport Database	.	0	0	0	C00079[e] --> C00079[c]
R_act	actransport	TRUE	Transport Database	.	0	0	0	C00033[c] <==> C00033[e]
R_inostt	inosttransport	FALSE	Transport Database	.	0	0	0	C00137[e] --> C00137[c]
R_glyt	glytransport	FALSE	Transport Database	.	0	0	0	C00037[e] --> C00037[c]
R_vitd2t	vitd2transport	FALSE	Transport Database	.	0	0	0	vitd2[e] --> vitd2[c]
R_nmnt	nmntransport	FALSE	Transport Database	.	0	0	0	C00455[e] --> C00455[c]
R_h2ot	h2otransport	TRUE	Transport Database	.	0	-5.00E-11	92.7584442	C00001[c] <==> C00001[e]
R_strch2t	strch2transport	FALSE	Transport Database	.	0	0	0	C00369[e] --> C00369[c]
R_nh4t	nh4transport	TRUE	Transport Database	.	0	-1.00E-11	0	C01342[c] <==> C01342[e]
R_coat	coatransport	FALSE	Transport Database	.	0	0	0	C00010[e] --> C00010[c]
R_urit	uritransport	FALSE	Transport Database	.	0	0	0	C00299[e] --> C00299[c]
R_tyr_Lt	tyr-Ltransport	FALSE	Transport Database	.	0	0	0	C00082[e] --> C00082[c]
R_mobdt	mobdtransport	FALSE	Transport Database	.	0	0	0	C06232[e] --> C06232[c]
R_glc_Dt	glc-Dtransport	FALSE	Transport Database	.	0	0	0	C00267[e] --> C00267[c]
R_mn2t	mn2transport	FALSE	Transport Database	.	0	0	0	C00034[e] --> C00034[c]
R_zymstt	zymsttransport	FALSE	Transport Database	.	0	0	0	C05437[e] --> C05437[c]
R_met_Lt	met-Ltransport	FALSE	Transport Database	.	0	0	5.82581025	C00073[e] --> C00073[c]
R_a_D_glucd	a-D-glucosetransport	FALSE	Transport Database	.	0	0	92.7584442	C00267[e] --> C00267[c]
R_thft	thftransport	FALSE	Transport Database	.	0	0	0	C00101[e] --> C00101[c]
R_ni2t	ni2transport	FALSE	Transport Database	.	0	0	0	C00291[e] --> C00291[c]
R_adet	adetransport	FALSE	Transport Database	.	0	0	0	C00147[e] --> C00147[c]
R_leu_Lt	leu-Ltransport	FALSE	Transport Database	.	0	0	0	C00123[e] --> C00123[c]
R_avite1t	avite1transport	FALSE	Transport Database	.	0	0	0	avite1[e] --> avite1[c]
R_malttrt	malttrtransport	FALSE	Transport Database	.	0	0	0	C01835[e] --> C01835[c]
R_cys_Lt	cys-Ltransport	FALSE	Transport Database	.	0	0	0	C00097[e] --> C00097[c]
R_orott	orottransport	TRUE	Transport Database	.	0	0	0	C00295[c] <==> C00295[e]
R_pit	pitransport	FALSE	Transport Database	.	0	0	0	C00009[e] --> C00009[c]
R_ca2t	ca2transport	FALSE	Transport Database	.	0	0	0	C00076[e] --> C00076[c]
R_ala_Lt	ala-Ltransport	FALSE	Transport Database	.	0	0	0	C00041[e] --> C00041[c]
R_adnt	adntransport	FALSE	Transport Database	.	0	0	0	C00212[e] --> C00212[c]
R_mal_Lt	mal-Ltransport	TRUE	Transport Database	.	0	0	0	C00711[c] <==> C00711[e]
R_clt	cltransport	FALSE	Transport Database	.	0	0	0	C00698[e] --> C00698[c]

R_dribt	dribtransport	FALSE	Transport Database	.	0	0	0	C01801[e] --> C01801[c]
R_thmt	thmtransport	FALSE	Transport Database	.	0	0	0	C00378[e] --> C00378[c]
R_ncamt	ncamtransport	FALSE	Transport Database	.	0	0	415.026237	C00153[e] --> C00153[c]
R_ile_Lt	ile-Ltransport	FALSE	Transport Database	.	0	0	0	C00407[e] --> C00407[c]
R_acetonet	acetonetransport	FALSE	Transport Database	.	0	0	0	C00207[c] --> C00207[e]
R_hco3t	hco3transport	TRUE	Transport Database	.	0	0	0	C01353[c] <==> C01353[e]
R_thr_Lt	thr-Ltransport	FALSE	Transport Database	.	0	0	0	C00188[e] --> C00188[c]
R_thymdt	thymdtransport	FALSE	Transport Database	.	0	0	0	C00214[e] --> C00214[c]
R_ergstt	ergsttransport	FALSE	Transport Database	.	0	0	0	C01694[e] --> C01694[c]
R_pydxt	pydxtransport	FALSE	Transport Database	.	0	0	0	C00250[e] --> C00250[c]
R_btnt	btntransport	FALSE	Transport Database	.	0	0	0	C00120[e] --> C00120[c]
R_ascb_Lt	ascb-Ltransport	FALSE	Transport Database	.	0	0	0	C00072[e] --> C00072[c]
R_ser_Lt	ser-Ltransport	FALSE	Transport Database	.	0	0	0	C00716[e] --> C00716[c]
R_pnto_Rt	pnto-Rtransport	FALSE	Transport Database	.	0	0	0	C00864[e] --> C00864[c]
R_sucrt	sucrtransport	FALSE	Transport Database	.	0	0	0	C00089[e] --> C00089[c]
R_fe2t	fe2transport	FALSE	Transport Database	.	0	0	0	C14818[e] --> C14818[c]
R_nact	nactransport	FALSE	Transport Database	.	0	0	0	C11486[e] --> C11486[c]
R_cellobiose	cellobiosetransport	FALSE	Transport Database	.	0	0	0	C00185[e] --> C00185[c]
R_trp_Lt	trp-Ltransport	FALSE	Transport Database	.	0	0	0	C00078[e] --> C00078[c]
R_lys_Lt	lys-Ltransport	FALSE	Transport Database	.	0	0	0	C00047[e] --> C00047[c]
R_chsterolt	chsteroltransport	FALSE	Transport Database	.	0	0	0	C00187[e] --> C00187[c]
R_ht	htransport	FALSE	Transport Database	.	0	1.00E-11	1000	C00080[c] --> C00080[e]
R_retinolt	retinoltransport	FALSE	Transport Database	.	0	0	0	C00473[e] --> C00473[c]
R_galt	galtransport	FALSE	Transport Database	.	0	0	0	C00124[e] --> C00124[c]
R_o2t	o2transport	FALSE	Transport Database	.	0	0	0	C00007[e] --> C00007[c]
R_rib_Dt	rib-Dtransport	FALSE	Transport Database	.	0	0	0	C00121[e] --> C00121[c]
R_cellulose	cellulosetransport	FALSE	Transport Database	.	0	0	0	C00760[e] --> C00760[c]
R_st	stransport	FALSE	Transport Database	.	0	0	0	C00087[e] --> C00087[c]
R_pro_Lt	pro-Ltransport	FALSE	Transport Database	.	0	0	0	C00148[e] --> C00148[c]
R_mant	mantransport	FALSE	Transport Database	.	0	0	0	C00936[e] --> C00936[c]
R_so4t	so4transport	FALSE	Transport Database	.	0	0	0	C00059[e] --> C00059[c]
R_co2t	co2transport	TRUE	Transport Database	.	0	0	0	C00011[c] <==> C00011[e]
R_guat	guatransport	FALSE	Transport Database	.	0	0	0	C00242[e] --> C00242[c]
R_fort	fortransport	FALSE	Transport Database	.	0	0	0	C00058[c] --> C00058[e]
R_spmdt	spmdtransport	FALSE	Transport Database	.	0	0	0	C00315[e] --> C00315[c]
R_frut	frutransport	FALSE	Transport Database	.	0	0	0	C10906[e] --> C10906[c]
R_xylt	xylttransport	FALSE	Transport Database	.	0	0	0	C00379[e] --> C00379[c]
R_uratet	uratetransport	FALSE	Transport Database	.	0	0	0	C00366[e] --> C00366[c]
R_HACD1	(S)-3-Hydroxybutanoyl-CoA:NAD	TRUE	Tryptophan metabolism	1.1.1.35	0	0	-0.0132768	[c] : C00332 + C00080 + C00004 <==> 3hbcoa + C00003
R_R02670	Hydorogen-peroxide:hydrogen-p	TRUE	Tryptophan metabolism	1.11.1.6	0	0		[c] : 2 C00632 + 4 C00007 <==> C05640 + 2 C00704 + 2 C00027 + 2 C00080
R_TRPO2	L-tryptophan:oxygen 2,3-oxidore	FALSE	Tryptophan metabolism	1.13.11.11	0	0	0	[c] : C00007 + C00078 --> C02700
R_TRPO2	L-tryptophan:oxygen 2,3-oxidore	FALSE	Tryptophan metabolism	1.13.11.52	0	0	0	[c] : C00007 + C00078 --> C02700
R_5HOXIND	5-Hydroxyindoleacetaldehyde:NA	FALSE	Tryptophan metabolism	1.2.1.3	0	0	0	[c] : 5hoxindact + C00001 + C00003 --> 5hoxindoa + 2 C00080 + C00004
R_ALDD20x	Indole-3-acetaldehyde:NAD+ oxid	FALSE	Tryptophan metabolism	1.2.1.3	0	0		[c] : C00001 + C00637 + C00003 --> 2 C00080 + C00954 + C00004
R_2OXOAD(	2-oxoadipate dehydrogenase com	FALSE	Tryptophan metabolism	1.2.4.2	1000	0.1	0	[c] : C00322 + C00010 + C00003 --> C00011 + C00527 + C00004
R_R02488	Glutaryl-CoA:(acceptor) 2,3-oxide	TRUE	Tryptophan metabolism	1.3.99.7	0	0		[c] : C00527 + C00028 <==> b2coa + C00030 + C00011
R_2OXOAD(	2-oxoadipate dehydrogenase com	FALSE	Tryptophan metabolism	1.8.1.4	1000	0.1	0	[c] : C00322 + C00010 + C00003 --> C00011 + C00527 + C00004
R_R02912	serotonin O-methyltransferase	TRUE	Tryptophan metabolism	2.1.1.-	0	0		[c] : srtn + C00440 <==> C05659 + C00101
R_ACACT1n	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Tryptophan metabolism	2.3.1.16	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_2OXOAD(	2-oxoadipate dehydrogenase com	FALSE	Tryptophan metabolism	2.3.1.61	1000	0.1	0	[c] : C00322 + C00010 + C00003 --> C00011 + C00527 + C00004
R_ACACT1n	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Tryptophan metabolism	2.3.1.9	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_AMID3	Indole-3-acetamide amidohydrola	FALSE	Tryptophan metabolism	3.5.1.4	0	0	0	[c] : C00001 + C02693 --> C00954 + C01342
R_LFORKYN	Formylkynurenine hydrolase	FALSE	Tryptophan metabolism	3.7.1.3	0	0	0	[c] : C02700 + C00001 --> C00041 + C00080 + nformanth
R_HKYNH	3-Hydroxy-L-kynurenine hydrola	FALSE	Tryptophan metabolism	3.7.1.3	0	0	0	[c] : C00001 + C03227 --> C00632 + C00041
R_KYN	L-Kynurenine hydrolase	FALSE	Tryptophan metabolism	3.7.1.3	0	0	0	[c] : Lkynr + C00001 --> C00041 + C00108 + C00080
R_ECOAH1	(S)-3-Hydroxybutanoyl-CoA hydr	TRUE	Tryptophan metabolism	4.2.1.17	0	0	-0.0132768	[c] : 3hbcoa <==> b2coa + C00001
R_TRPTRS	L-Tryptophan -tRNA(Trp) ligase (	FALSE	Tryptophan metabolism	6.1.1.2	0	0	0	[c] : C00002 + C01652 + C00078 --> C00020 + C00013 + C03512
R_34DHOXF	3,4-Dihydroxyphenylethyleneglyc	TRUE	Tyrosine metabolism	1.1.1.1	0	0		[c] : 34dhmald + C00080 + C00004 <==> 34dhoxpeg + C00003
R_R02520	.	TRUE	Tyrosine metabolism	1.13.12.-	0	0		[c] : C00544 + C00007 <==> C05585 + C00011 + C00001

R_R02383	Monophenol,L-dopa:oxygen oxidc	TRUE	Tyrosine metabolism	1.14.13.-	0	0		[c] : C00483 + C00007 + C00004 + C00080 <==> C03758 + C00003 + C00001
R_R04306	.	TRUE	Tyrosine metabolism	1.14.13.-	0	0		[c] : C04353 + C00005 + C00080 + C00007 <==> C00650 + C00006 + 2 C00001
R_R02383	Monophenol,L-dopa:oxygen oxidc	TRUE	Tyrosine metabolism	1.14.18.1	0	0		[c] : C00483 + C00007 + C00004 + C00080 <==> C03758 + C00003 + C00001
R_SSALy	Succinate-semialdehyde:NADP+ c	FALSE	Tyrosine metabolism	1.2.1.16	0	0.1	0	[c] : C00001 + C00006 + C00232 --> 2 C00080 + C00005 + C00042
R_SSALx	Succinate-semialdehyde:NAD+ ox	FALSE	Tyrosine metabolism	1.2.1.16	0	0.1		[c] : C00001 + C00003 + C00232 --> 2 C00080 + C00004 + C00042
R_SSALx	Succinate-semialdehyde:NAD+ ox	FALSE	Tyrosine metabolism	1.2.1.24	0	0.1		[c] : C00001 + C00003 + C00232 --> 2 C00080 + C00004 + C00042
R_R03943	.	TRUE	Tyrosine metabolism	2.1.1.-	0	0		[c] : C02442 + C00019 <==> C06199 + C00021
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Tyrosine metabolism	2.6.1.1	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Tyrosine metabolism	2.6.1.5	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Tyrosine metabolism	2.6.1.57	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_TYRTAp	L-Tyrosine:2-oxoglutarate amino	TRUE	Tyrosine metabolism	2.6.1.9	0	3.00E-11		[c] : C00026 + C00082 <==> C01179 + C00025
R_R04379	5-Carboxymethyl-2-hydroxymucc	TRUE	Tyrosine metabolism	5.3.3.10	0	0		[c] : C04186 <==> C04052
R_AMMQT6	.	FALSE	Ubiquinone and menaquinone biosyn	2.1.1.-	0	0		[c] : C05818 + C00019 --> C00021 + C00080 + mqn6
R_R06859	.	TRUE	Ubiquinone and menaquinone biosyn	2.1.1.-	0	0		[c] : C13309 + C00019 <==> phyQ + C00021
R_R04990	UDP-L-rhamnose:flavonol-3-O-D-	TRUE	Ubiquinone and menaquinone biosyn	2.1.1.-	0	0		[c] : C05813 + C00019 <==> C05814 + C00021
R_R08165	2-succinyl-5-enolpyruvyl-6-hydr	TRUE	Ubiquinone and menaquinone biosyn	2.2.1.9	0	0	0	[c] : C00885 + C00026 <==> C16519 + C00011
R_R06858	.	TRUE	Ubiquinone and menaquinone biosyn	2.5.1.-	0	0		[c] : C03657 + C05427 <==> C13309 + C00011 + C00013
R_DHNAOT	.	FALSE	Ubiquinone and menaquinone biosyn	2.5.1.-	0	0		[c] : C03657 + C04146 --> C05818 + C00011 + C00080 + C00013
R_R07263	.	TRUE	Ubiquinone and menaquinone biosyn	4.1.3.36	0	0	0	[c] : C03160 <==> C15547 + C00001
R_SUCBZS	.	FALSE	Ubiquinone and menaquinone biosyn	4.2.1.113	0	0		[c] : C05817 --> C00001 + C02730
R_ICHORSi	Chorismate hydroxymutase	FALSE	Ubiquinone and menaquinone biosyn	5.4.4.2	0	0		[c] : C00251 --> C00885
R_SUCBZL	O-Succinylbenzoate:CoA ligase (A	FALSE	Ubiquinone and menaquinone biosyn	6.2.1.26	0	0		[c] : C00002 + C00010 + C02730 --> C00020 + C00013 + C03160
R_R01986	4-Aminobutyraldehyde:NAD+ oxi	TRUE	Urea cycle and metabolism of amino g	1.2.1.3	0	0		[c] : C00555 + C00006 + C00001 <==> C00334 + C00005 + C00080
R_NABTNOi	N4-Acetylaminobutanal:NAD+ ox	FALSE	Urea cycle and metabolism of amino g	1.2.1.3	0	0	0	[c] : C00001 + C05936 + C00003 --> C02946 + 2 C00080 + C00004
R_AGPR	N-Acetyl-L-glutamate-5-semialde	TRUE	Urea cycle and metabolism of amino g	1.2.1.38	-5.408586	-0.1	0	[c] : C01250 + C00006 + C00009 <==> C04133 + C00080 + C00005
R_G5SD	L-Glutamate-5-semialdehyde:NAI	FALSE	Urea cycle and metabolism of amino g	1.2.1.41	0	0.1	0	[c] : C03287 + C00080 + C00005 --> C01165 + C00006 + C00009
R_OCBT	Carbamoyl-phosphate:L-ornithin	TRUE	Urea cycle and metabolism of amino g	2.1.3.3	5.4085858	0	7.02597717	[c] : C00169 + C00077 <==> C00327 + C00080 + C00009
R_ACGSm	Acetyl-CoA:L-glutamate N-acetylt	FALSE	Urea cycle and metabolism of amino g	2.3.1.1	0	0	0	[c] : C00024 + C00025 --> C00624 + C00010 + C00080
R_ORNTACi	N2-Acetyl-L-ornithine:L-glutamat	FALSE	Urea cycle and metabolism of amino g	2.3.1.35	5.4085858	0.1		[c] : C00437 + C00025 --> C00624 + C00077
R_SPMS	S-adenosylmethioninamine:putre	FALSE	Urea cycle and metabolism of amino g	2.5.1.16	0	5.00E-12		[c] : C01137 + C00134 --> C00170 + C00080 + C00315
R_ACOTA	N2-Acetyl-L-ornithine:2-oxogluta	TRUE	Urea cycle and metabolism of amino g	2.6.1.11	-5.408586	-0.1	0	[c] : C00437 + C00026 <==> C01250 + C00025
R_GLU5Km	ATP:L-glutamate 5-phosphotrans	FALSE	Urea cycle and metabolism of amino g	2.7.2.11	0	0.1	0	[c] : C00002 + C00025 --> C00008 + C03287
R_ACGK	ATP:N-acetyl-L-glutamate 5-phos	FALSE	Urea cycle and metabolism of amino g	2.7.2.8	5.4085858	0.1	0	[c] : C00624 + C00002 --> C04133 + C00008
R_AMID	4-Guanidinobutanamide amidohy	FALSE	Urea cycle and metabolism of amino g	3.5.1.4	0	0	0	[c] : C03078 + C00001 --> 4gudbutn + C01342
R_ALPHNH	Urea-1-carboxylate amidohydrola	FALSE	Urea cycle and metabolism of amino g	3.5.1.54	0	0		[c] : C01010 + 3 C00080 + C00001 --> 2 C00011 + 2 C01342
R_ARGN	L-Arginine amidinohydrolase	FALSE	Urea cycle and metabolism of amino g	3.5.3.1	0	0		[c] : C00062 + C00001 --> C00077 + C00086
R_AGMT	Agmatine amidinohydrolase	FALSE	Urea cycle and metabolism of amino g	3.5.3.11	0	0	0	[c] : C00179 + C00001 --> C00134 + C00086
R_ARGSL	2-(Nomega-L-arginino)succinate	TRUE	Urea cycle and metabolism of amino g	4.3.2.1	0	0.1	-936.20413	[c] : C03406 <==> C00062 + C00122
R_ARGSS	L-Citrulline:L-aspartate ligase (AI	FALSE	Urea cycle and metabolism of amino g	6.3.4.5	0	0.1	0	[c] : C00049 + C00002 + C00327 --> C00020 + C03406 + C00080 + C00013
R_R03898	.	TRUE	Valine, leucine and isoleucine biosynt	.	0	0		[c] : C02226 + C00001 <==> C06032
R_IPMD	3-Isopropylmalate:NAD+ oxidore	FALSE	Valine, leucine and isoleucine biosynt	1.1.1.85	0	0	10.7014884	[c] : C04411 + C00003 --> C04236 + C00080 + C00004
R_R00994	(2R,3S)-3-methylmalate:NAD+ ox	TRUE	Valine, leucine and isoleucine biosynt	1.1.1.85	0	0		[c] : C00109 + C00011 + C00004 + C00080 <==> C06032 + C00003
R_R05069	(S)-2-Aceto-2-hydroxybutanoate:	TRUE	Valine, leucine and isoleucine biosynt	1.1.1.86	0	-3.00E-11		[c] : C00659 <==> C14463
R_R05068	(R)-2,3-Dihydroxy-3-methylpenta	TRUE	Valine, leucine and isoleucine biosynt	1.1.1.86	0	-3.50E-11		[c] : C04104 + C00006 <==> C14463 + C00005 + C00080
R_R04440	(R)-2,3-Dihydroxy-3-methylbutar	TRUE	Valine, leucine and isoleucine biosynt	1.1.1.86	696.14778	0.1		[c] : C04039 + C00006 <==> C04181 + C00005 + C00080
R_R05071	(S)-2-Acetolactate methylmutase	TRUE	Valine, leucine and isoleucine biosynt	1.1.1.86	-696.1478	-0.1		[c] : C06010 <==> C04181
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Valine, leucine and isoleucine biosynt	1.2.4.1	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Valine, leucine and isoleucine biosynt	2.2.1.6	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_R04673	(S)-2-Aceto-2-hydroxybutanoate	TRUE	Valine, leucine and isoleucine biosynt	2.2.1.6	0	-5.00E-11		[c] : C00109 + C05125 <==> C00659 + C00068
R_R04672	(S)-2-Acetolactate pyruvate-lyase	TRUE	Valine, leucine and isoleucine biosynt	2.2.1.6	696.14778	96.910791		[c] : C06010 + C00068 <==> C05125 + C00022
R_IPPSm	acetyl-CoA:3-methyl-2-oxobutanc	FALSE	Valine, leucine and isoleucine biosynt	2.3.3.13	0	0		[c] : C00141 + C00024 + C00001 --> C02504 + C00010 + C00080
R_LEUTAm	L-Leucine:2-oxoglutarate aminotı	TRUE	Valine, leucine and isoleucine biosynt	2.6.1.42	0	0		[c] : C00026 + C00123 <==> C00233 + C00025
R_ILETA	L-Isoleucine:2-oxoglutarate amin	TRUE	Valine, leucine and isoleucine biosynt	2.6.1.42	0	-2.00E-11	-6.9009598	[c] : C00026 + C00407 <==> C03465 + C00025
R_VALTAm	L-Valine:2-oxoglutarate aminotra	TRUE	Valine, leucine and isoleucine biosynt	2.6.1.42	-7.73755	0.3	0	[c] : C00026 + C00183 <==> C00141 + C00025
R_LEUTAm	L-Leucine:2-oxoglutarate aminotı	TRUE	Valine, leucine and isoleucine biosynt	2.6.1.6	0	0		[c] : C00026 + C00123 <==> C00233 + C00025
R_VALTAm	L-Valine:2-oxoglutarate aminotra	TRUE	Valine, leucine and isoleucine biosynt	2.6.1.6	-7.73755	0.3	0	[c] : C00026 + C00183 <==> C00141 + C00025
R_LEUTAm	L-Leucine:2-oxoglutarate aminotı	TRUE	Valine, leucine and isoleucine biosynt	2.6.1.67	0	0		[c] : C00026 + C00123 <==> C00233 + C00025
R_R00014	pyruvate:thiamin diphosphate ac	TRUE	Valine, leucine and isoleucine biosynt	4.1.1.1	1000	-0.1		[c] : C00022 + C00068 <==> C05125 + C00011
R_IPPMIb	2-Isopropylmalate hydro-lyase	TRUE	Valine, leucine and isoleucine biosynt	4.2.1.33	0	0	-10.701488	[c] : C02631 + C00001 <==> C02504

R_IPPMIa	3-Isopropylmalate hydro-lyase	TRUE	Valine, leucine and isoleucine biosynt	4.2.1.33	0	0	-10.701488	[c] : C04411 <==> C02631 + C00001
R_R03896	(R)-2-Methylmalate hydro-lyase	TRUE	Valine, leucine and isoleucine biosynt	4.2.1.35	0	0		[c] : C02612 <==> C02226 + C00001
R_DHAD2m	(R)-2,3-Dihydroxy-3-methylpenta	FALSE	Valine, leucine and isoleucine biosynt	4.2.1.9	0	3.00E-11		[c] : C04104 --> C03465 + C00001
R_DHAD1	(R)-2,3-Dihydroxy-3-methylbutar	FALSE	Valine, leucine and isoleucine biosynt	4.2.1.9	0	0.1	20.7528863	[c] : C04039 --> C00141 + C00001
R_THRD_Lm	L-threonine ammonia-lyase (2-ox	FALSE	Valine, leucine and isoleucine biosynt	4.3.1.19	329.15129	709.695801	0	[c] : C00188 --> C00109 + C01342
R_R05071	(S)-2-Acetolactate methylmutase	TRUE	Valine, leucine and isoleucine biosynt	5.4.99.3	-696.1478	-0.1		[c] : C06010 <==> C04181
R_R05069	(S)-2-Aceto-2-hydroxybutanoate:	TRUE	Valine, leucine and isoleucine biosynt	5.4.99.3	0	-3.00E-11		[c] : C00659 <==> C14463
R_LEUTRS	L-Leucine:tRNA(Leu) ligase (AMP	FALSE	Valine, leucine and isoleucine biosynt	6.1.1.4	0	0	0	[c] : C00002 + C00123 + C01645 --> C00020 + C02047 + C00013
R_ILETRS	L-Isoleucine:tRNA(Ile) ligase (AM	FALSE	Valine, leucine and isoleucine biosynt	6.1.1.5	0	0	0	[c] : C00002 + C00407 + C01644 --> C00020 + C03127 + C00013
R_VALTRSm	L-Valine:tRNAVal ligase (AMP-for	FALSE	Valine, leucine and isoleucine biosynt	6.1.1.9	0	0	0	[c] : C00002 + C01653 + C00183 --> C00020 + C00013 + C02554
R_HACD9m	(2S,3S)-3-hydroxy-2-methylbutar	TRUE	Valine, leucine and isoleucine degrada	1.1.1.178	0	0	0	[c] : C04405 + C00003 <==> C03344 + C00080 + C00004
R_R05066	3-Hydroxy-2-methylpropanoate:N	TRUE	Valine, leucine and isoleucine degrada	1.1.1.31	0	0		[c] : C06001 + C00003 <==> C06002 + C00004 + C00080
R_HACD9m	(2S,3S)-3-hydroxy-2-methylbutar	TRUE	Valine, leucine and isoleucine degrada	1.1.1.35	0	0	0	[c] : C04405 + C00003 <==> C03344 + C00080 + C00004
R_R05066	3-Hydroxy-2-methylpropanoate:N	TRUE	Valine, leucine and isoleucine degrada	1.1.1.35	0	0		[c] : C06001 + C00003 <==> C06002 + C00004 + C00080
R_R00935	(S)-Methylmalonate semialdehyd	TRUE	Valine, leucine and isoleucine degrada	1.2.1.27	0	0		[c] : C06002 + C00010 + C00003 <==> C00100 + C00011 + C00004 + C00080
R_R03869	(S)-Methylmalonate semialdehyd	TRUE	Valine, leucine and isoleucine degrada	1.2.1.3	0	0		[c] : C06002 + C00003 + C00001 <==> C02170 + C00004 + C00080
R_R02661	2-methylpropanoyl-CoA:(accepto	TRUE	Valine, leucine and isoleucine degrada	1.3.99.-	0	0		[c] : C00630 + C00028 <==> C03460 + C00030
R_ACOAD8r	3-Methylbutanoyl-CoA:(acceptor)	FALSE	Valine, leucine and isoleucine degrada	1.3.99.10	0	0		[c] : C00016 + C02939 --> C03069 + C01352
R_R03172	(S)-2-methylbutanoyl-CoA:accept	TRUE	Valine, leucine and isoleucine degrada	1.3.99.12	0	0		[c] : C15980 + C00028 <==> C03345 + C00030
R_R02661	2-methylpropanoyl-CoA:(accepto	TRUE	Valine, leucine and isoleucine degrada	1.3.99.12	0	0		[c] : C00630 + C00028 <==> C03460 + C00030
R_R03172	(S)-2-methylbutanoyl-CoA:accept	TRUE	Valine, leucine and isoleucine degrada	1.3.99.2	0	0		[c] : C15980 + C00028 <==> C03345 + C00030
R_R02661	2-methylpropanoyl-CoA:(accepto	TRUE	Valine, leucine and isoleucine degrada	1.3.99.2	0	0		[c] : C00630 + C00028 <==> C03460 + C00030
R_ACOAD8r	3-Methylbutanoyl-CoA:(acceptor)	FALSE	Valine, leucine and isoleucine degrada	1.3.99.3	0	0		[c] : C00016 + C02939 --> C03069 + C01352
R_R02661	2-methylpropanoyl-CoA:(accepto	TRUE	Valine, leucine and isoleucine degrada	1.3.99.3	0	0		[c] : C00630 + C00028 <==> C03460 + C00030
R_R03172	(S)-2-methylbutanoyl-CoA:accept	TRUE	Valine, leucine and isoleucine degrada	1.3.99.3	0	0		[c] : C15980 + C00028 <==> C03345 + C00030
R_R07618	enzyme N6-(dihydrolipoyl)lysine	TRUE	Valine, leucine and isoleucine degrada	1.8.1.4	-654.716	-0.1	0	[c] : C15973 + C00003 <==> C15972 + C00004 + C00080
R_ACACT10	Propanoyl-CoA:acetyl-CoA C-acyl	TRUE	Valine, leucine and isoleucine degrada	2.3.1.16	0	0	0	[c] : C03344 + C00010 <==> C00024 + C00100
R_ACACT1m	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Valine, leucine and isoleucine degrada	2.3.1.16	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_ACACT1m	Acetyl-CoA:acetyl-CoA C-acetyltra	FALSE	Valine, leucine and isoleucine degrada	2.3.1.9	0	9.00E-11	1000	[c] : 2 C00024 --> C00332 + C00010
R_LEUTAm	L-Leucine:2-oxoglutarate aminotr	TRUE	Valine, leucine and isoleucine degrada	2.6.1.42	0	0		[c] : C00026 + C00123 <==> C00233 + C00025
R_ILETA	L-Isoleucine:2-oxoglutarate amin	TRUE	Valine, leucine and isoleucine degrada	2.6.1.42	0	-2.00E-11	-6.9009598	[c] : C00026 + C00407 <==> C03465 + C00025
R_VALTAm	L-Valine:2-oxoglutarate aminotra	TRUE	Valine, leucine and isoleucine degrada	2.6.1.42	-7.73755	0.3	0	[c] : C00026 + C00183 <==> C00141 + C00025
R_VALTAm	L-Valine:2-oxoglutarate aminotra	TRUE	Valine, leucine and isoleucine degrada	2.6.1.6	-7.73755	0.3	0	[c] : C00026 + C00183 <==> C00141 + C00025
R_LEUTAm	L-Leucine:2-oxoglutarate aminotr	TRUE	Valine, leucine and isoleucine degrada	2.6.1.6	0	0		[c] : C00026 + C00123 <==> C00233 + C00025
R_LEUTAm	L-Leucine:2-oxoglutarate aminotr	TRUE	Valine, leucine and isoleucine degrada	2.6.1.67	0	0		[c] : C00026 + C00123 <==> C00233 + C00025
R_ECOAH12	(S)-3-Hydroxyisobutyryl-CoA hyd	TRUE	Valine, leucine and isoleucine degrada	4.2.1.17	0	0	0	[c] : C03460 + C00001 <==> C04047
R_ECOAH9r	(2S,3S)-3-Hydroxy-2-methylbuta	TRUE	Valine, leucine and isoleucine degrada	4.2.1.17	0	0	0	[c] : C03345 + C00001 <==> C04405
R_R04137	3-Hydroxyisopentyl-CoA hydro-ly	TRUE	Valine, leucine and isoleucine degrada	4.2.1.17	0	0		[c] : C05998 <==> C03069 + C00001
R_MMEm	Methylmalonyl-CoA epimerase	TRUE	Valine, leucine and isoleucine degrada	5.1.99.1	0	-0.1	0	[c] : C01213 <==> C00683
R_MMMm	(R)-Methylmalonyl-CoA CoA-carb	TRUE	Valine, leucine and isoleucine degrada	5.4.99.2	0	0.1	0	[c] : C01213 <==> C00091
R_PPCOACn	Propanoyl-CoA:carbon-dioxide lig	FALSE	Valine, leucine and isoleucine degrada	6.4.1.3	0	0.1	0	[c] : C00002 + C01353 + C00100 --> C00008 + C00080 + C00683 + C00009
R_R07456	.	TRUE	Vitamin B6 metabolism	.	0	0		[c] : C00118 + C00199 + C00064 <==> C00018 + C00025
R_PYDXNO	Pyridoxine:oxygen oxidoreductas	TRUE	Vitamin B6 metabolism	1.1.3.12	0	0	0	[c] : C00007 + C00314 <==> C00027 + C00250
R_R01710	Pyridoxamine:oxygen oxidoreduc	TRUE	Vitamin B6 metabolism	1.4.3.5	0	0		[c] : C00534 + C00001 + C00007 <==> C00250 + C01342 + C00027
R_PYDXNO	Pyridoxine:oxygen oxidoreductas	TRUE	Vitamin B6 metabolism	1.4.3.5	0	0	0	[c] : C00007 + C00314 <==> C00027 + C00250
R_PDX5PO	Pyridoxine 5-phosphate:oxygen o	TRUE	Vitamin B6 metabolism	1.4.3.5	0	0	0	[c] : C00007 + C00627 <==> C00027 + C00018
R_PYAM5PO	Pyridoxamine-5'-phosphate:oxyg	TRUE	Vitamin B6 metabolism	1.4.3.5	0	0	-12.201697	[c] : C00001 + C00007 + C00647 <==> C00027 + C01342 + C00018
R_OHPBAT	O-Phospho-4-hydroxy-L-threonin	TRUE	Vitamin B6 metabolism	2.6.1.52	0	0	0	[c] : C00025 + C06054 <==> C00026 + C06055
R_4HTHRS	O-Phospho-4-hydroxy-L-threonin	FALSE	Vitamin B6 metabolism	4.2.3.1	0	0		[c] : C00001 + C06055 --> C06056 + C00009
R_R07888	.	TRUE	alpha-Linolenic acid metabolism	1.3.3.6	0	0		[c] : C16327 + C00016 <==> C16328 + C01352
R_R07896	.	TRUE	alpha-Linolenic acid metabolism	1.3.3.6	0	0		[c] : C16335 + C00016 <==> C16336 + C01352
R_R07892	.	TRUE	alpha-Linolenic acid metabolism	1.3.3.6	0	0		[c] : C16331 + C00016 <==> C16332 + C01352
R_R07895	.	TRUE	alpha-Linolenic acid metabolism	2.3.1.16	0	0		[c] : C16335 + C00024 <==> C00010 + C16334
R_R07899	.	TRUE	alpha-Linolenic acid metabolism	2.3.1.16	0	0		[c] : C16339 + C00024 <==> C00010 + C16338
R_R07891	.	TRUE	alpha-Linolenic acid metabolism	2.3.1.16	0	0		[c] : C16331 + C00024 <==> C00010 + C16330
R_BAMPPAL	beta-Aminopropion aldehyde:NA	FALSE	beta-Alanine metabolism	1.2.1.3	0	0	0	[c] : bamppald + C00001 + C00003 --> C00099 + 2 C00080 + C00004
R_PPCOAOr	Propanoyl-CoA:(acceptor) 2,3-ox	FALSE	beta-Alanine metabolism	1.3.99.3	0	0	0	[c] : C00016 + C00100 --> C01352 + prpncoa
R_SPRMS	S-adenosylmethioninamine:sperr	FALSE	beta-Alanine metabolism	2.5.1.16	0	0		[c] : C01137 + C00315 --> C00170 + C00080 + C00750
R_SPRMS	S-adenosylmethioninamine:sperr	FALSE	beta-Alanine metabolism	2.5.1.22	0	0		[c] : C01137 + C00315 --> C00170 + C00080 + C00750

R_APAT2rm	3-Aminopropanoate:2-oxoglutara	TRUE	beta-Alanine metabolism	2.6.1.19	0	0.1	0	[c] : C00026 + C00099 <==> C00025 + C00222
R_APAT2rm	3-Aminopropanoate:2-oxoglutara	TRUE	beta-Alanine metabolism	2.6.1.55	0	0.1	0	[c] : C00026 + C00099 <==> C00025 + C00222
R_ASP1DC	L-Aspartate 1-carboxy-lyase	FALSE	beta-Alanine metabolism	4.1.1.11	0.0011356	0.1	0	[c] : C00049 + C00080 --> C00099 + C00011
R_ASP1DC	L-Aspartate 1-carboxy-lyase	FALSE	beta-Alanine metabolism	4.1.1.15	0.0011356	0.1	0	[c] : C00049 + C00080 --> C00099 + C00011
R_PRPNCOA	3-Hydroxypropionyl-CoA hydro-l	FALSE	beta-Alanine metabolism	4.2.1.17	0	0	0	[c] : C00001 + prpncoa --> 3hpcoa
R_PANTS	(R)-Pantoate:beta-alanine ligase (	FALSE	beta-Alanine metabolism	6.3.2.1	0.0011356	0	0	[c] : C00099 + C00002 + C00522 --> C00020 + C00080 + C00864 + C00013
R_R05265	.	TRUE	gamma-Hexachlorocyclohexane degra	1.14.-.-	0	0		[c] : C02235 + C00007 + 3 C00080 <==> C02814 + C00088 + C00001
R_R05258	.	TRUE	gamma-Hexachlorocyclohexane degra	1.14.13.-	0	0		[c] : C00472 + C00088 + C00006 + C00001 <==> 4nph + C00007 + C00005 + C00080
R_R06851	.	TRUE	gamma-Hexachlorocyclohexane degra	1.14.13.-	0	0		[c] : C02389 + C00005 + C00080 + C00007 <==> C02814 + C00006 + C00001

Appendix - C - Wild Type Cellobiose Polar Metabolites

ID	MZ_Blank	MZ_WTCb_Polar_Rep1	MZ_WTCb_Polar_Rep2	RT_blank	RT_WTCb_Polar_Rep1	RT_WTCb_Polar_Rep2	Int_blank	Int_WTCb_Polar_Rep1	Int_WTCb_Polar_Rep2	exp(mean.grp1)	exp(mean.grp2)	fold.mean	p.ttest	p.wilcox	mean_m/z	mean_rt	KEGG_ID_1	HMDB_ID_1	Match_mass_1	KEGG_ID_2	HMDB_ID_2	Match_mass_2
806	157.03619	157.03612	157.03619	2.08500	2.09400	2.08500	0.00000	15.67948	15.55854	6070858.56111	NaN	9.18287	0.01002	0.01002	157.03617	2.08800	C07931		156.03419	C14715		156.03420
489	261.14600	261.14581	261.14600	12.10500	12.10200	12.10500	0.00000	15.07800	15.14246	3649971.81053	NaN	7.54529	0.01137	0.01137	261.14594	12.10400			260.13722			260.13722
368	348.07132	348.07132	348.07132	2.55600	2.54200	2.55600	0.00000	14.27281	14.26065	1570224.68782	NaN	10.00798	0.01124	0.01124	348.07132	2.55133			347.06310	C00020	HMDB00045	347.06310
573	223.09686	223.09676	223.09686	30.13000	30.12700	30.13000	0.00000	14.15420	14.30173	1510515.81483	NaN	10.19081	0.01123	0.01123	223.09683	30.12900			222.08919			222.08919
637	203.05339	203.05338	203.05339	1.41400	1.42300	1.41400	0.00000	14.07997	14.28153	1440856.34004	NaN	8.24804	0.00971	0.00971	203.05339	1.41700	C07928		202.03970	C08010		202.03967
428	295.13010	295.12994	295.13010	13.12900	13.11400	13.12900	0.00000	13.96138	14.06422	1218096.43875	NaN	9.54727	0.00854	0.00854	295.13005	13.12400	C11045	HMDB01894	294.12160		HMDB00594	294.12158
336	365.10681	365.10675	365.10681	1.53200	1.54100	1.53200	0.00000	13.89936	13.85821	1065317.65656	NaN	8.86833	0.00880	0.00880	365.10679	1.53500	C10636		364.09470			364.09469
894	128.10820	128.10861	128.10820	15.00100	14.99800	15.00100	0.00000	13.69529	13.63592	860789.50714	NaN	11.35422	0.01056	0.01056	128.10834	15.00000			127.09971	C11519		127.09970
118	887.34241	887.34186	887.34241	9.63200	9.70000	9.63200	0.00000	13.52569	13.54566	755907.74247	NaN	8.44641	0.01049	0.01049	887.34222	9.65467		HMDB12920	886.29572			886.27429
1005	98.98505	98.98502	98.98505	1.61400	1.62300	1.61400	0.00000	13.65117	13.40976	751980.35991	NaN	10.57759	0.00918	0.00918	98.98504	1.61700	C12893		97.97701	C12554		97.97700
344	360.15152	360.15134	360.15152	1.55600	1.55300	1.55600	0.00000	13.37713	13.50122	686371.07525	NaN	7.84871	0.00984	0.00984	360.15146	1.55500			359.14926	C12650		359.14930
491	261.03818	261.03821	261.03818	1.57900	1.58800	1.57900	0.00000	13.48774	13.33675	668133.13248	NaN	9.92304	0.00829	0.00829	261.03819	1.58200	C18988		260.03059	C18984		260.03060
974	102.12861	102.12829	102.12861	2.10900	2.10600	2.10900	0.00000	13.42817	13.37563	661260.72791	NaN	10.01605	0.00975	0.00975	102.12850	2.10800			101.12045	C08347		101.12045
875	132.10245	132.10236	132.10245	3.61600	3.58900	3.61600	0.00000	13.24151	13.28193	574766.87649	NaN	10.84970	0.00819	0.00819	132.10242	3.60700	C00123	HMDB00687	131.09460	C00407	HMDB00172	131.09460
580	219.09824	219.09810	219.09824	2.13300	2.14100	2.13300	0.00000	13.25904	13.15716	544759.84868	NaN	9.51331	0.00973	0.00973	219.09819	2.13567	C03738		218.09030			218.09027
1095	81.01859	81.01856	81.01859	2.08500	2.09400	2.08500	0.00000	13.17826	13.08295	504137.23027	NaN	9.31106	0.00980	0.00980	81.01858	2.08800	C06753		80.00290	C19160		80.00290
315	395.18677	395.18695	395.18677	9.63200	9.70000	9.63200	0.00000	13.06465	13.19271	503169.67970	NaN	10.54696	0.01053	0.01053	395.18683	9.65467			394.17917			394.18524
756	177.05501	177.05493	177.05501	30.13000	30.12700	30.13000	0.00000	13.01200	13.18047	487104.59569	NaN	12.37882	0.01060	0.01060	177.05498	30.12900	C01173		176.04730	C03081		176.04730
828	148.06111	148.06131	148.06111	1.46100	1.47000	1.46100	0.00000	13.02884	13.05330	460961.08741	NaN	9.64261	0.00905	0.00905	148.06118	1.46400	C00025	HMDB00148	147.05320	C00217	HMDB03339	147.05320
898	127.12314	127.12317	127.12314	39.90100	39.91000	39.90100	0.00000	13.17750	12.66969	409871.23555	NaN	7.27013	0.01049	0.01049	127.12315	39.90400	C07287		126.10450		HMDB06024	126.10447
396	324.06033	324.05994	324.06033	1.96800	1.96500	1.96800	0.00000	12.95462	12.88257	407823.90597	NaN	9.60790	0.01115	0.01115	324.06020	1.96700	C00055	HMDB00095	323.05190	C03104	HMDB11692	323.05190
665	198.09706	198.09616	198.09706	1.45000	1.44700	1.45000	0.00000	12.88007	12.86278	389034.16729	NaN	11.26174	0.01214	0.01214	198.09676	1.44900			197.08406	C14462		197.09530
820	151.03548	151.03548	151.03542	1.04900	1.04600	1.04900	0.00000	12.88585	12.74943	368664.49838	NaN	9.69526	0.00786	0.00786	151.03544	1.04800	C02137	HMDB01587	150.03169		HMDB01973	150.03169
450	279.10156	279.10159	279.10156	9.38500	9.44100	9.38500	0.00000	12.65599	12.77131	332251.33944	NaN	7.81444	0.01059	0.01059	279.10157	9.40367			278.09365			278.09365
899	127.12300	127.12317	127.12300	7.90100	7.81600	7.90100	0.00000	12.53448	12.78059	314121.41317	NaN	9.19630	0.01151	0.01151	127.12306	7.87267	C07287		126.10450		HMDB06024	126.10447
582	219.02728	219.02742	219.02728	1.39100	1.40000	1.39100	0.00000	12.65012	12.55095	296717.76658	NaN	9.79291	0.01078	0.01078	219.02733	1.39400	C14614		218.02239	C14569		218.02240
565	226.95212	226.95203	226.95212	1.22600	1.22300	1.22600	0.00000	12.54034	12.54248	279682.89384	NaN	9.78621	0.01138	0.01138	226.95209	1.22500	C12835		225.94360	C12958		225.94358
140	707.22278	707.22247	707.22278	1.54400	1.55300	1.54400	0.00000	12.51545	12.52285	273525.37186	NaN	9.26051	0.00932	0.00932	707.22268	1.54700			706.17451			706.17451
510	249.10866	249.10852	249.10866	2.01500	2.01200	2.01500	0.00000	12.50711	12.53023	273394.69183	NaN	9.33786	0.01076	0.01076	249.10861	2.01400			248.10084			248.10084
216	496.72714	496.72653	496.72714	10.24400	10.30000	10.24400	0.00000	12.40495	12.54919	262253.91506	NaN	8.64075	0.00943	0.00943	496.72694	10.26267						
793	161.09253	161.09253	161.09253	1.48500	1.48200	1.48500	0.00000	12.42958	12.46610	254699.96745	NaN	12.54433	0.00897	0.00897	161.09253	1.48400	C02989		160.08479			160.08479
824	149.02342	149.02339	149.02342	30.13000	30.12700	30.13000	0.00000	12.30923	12.50065	244004.01411	NaN	11.73481	0.01190	0.01190	149.02341	30.12900	C01180	HMDB01553	148.01940	C01180	HMDB01553	148.01940
626	205.09763	205.09731	205.09763	11.63400	11.63100	11.63400	0.00000	12.32543	12.44035	238682.32140	NaN	8.19755	0.01021	0.01021	205.09752	11.63300	C00078	HMDB00929	204.08987	C00525	HMDB13609	204.08987
271	441.10104	441.10150	441.10104	1.55600	1.56400	1.55600	0.00000	12.30221	12.25460	215001.73373	NaN	9.42011	0.00937	0.00937	441.10120	1.55867			440.11069			440.11073
521	244.19109	244.19092	244.19109	25.11400	25.12300	25.11400	0.00000	12.12506	12.34261	205630.06463	NaN	9.67481	0.00975	0.00975	244.19103	25.11700		HMDB13286	243.18344	C07673		243.19870
965	110.00816	110.00806	110.00816	1.07300	1.08200	1.07300	0.00000	12.23135	12.23581	205577.59168	NaN	9.87585	0.00983	0.00983	110.00813	1.07600	C00519	HMDB00965	109.01970	C00519	HMDB00965	109.01975
741	182.08122	182.08131	182.08122	4.47500	4.36600	4.47500	0.00000	12.18703	12.25093	202598.86114	NaN	9.87415	0.00995	0.00995	182.08125	4.43867			181.07389	C01624		181.07389
453	277.13922	277.13953	277.13922	9.09100	9.15800	9.09100	0.00000	12.14104	12.25991	198883.42616	NaN	10.40556	0.00909	0.00909	277.13932	9.11333	C00449	HMDB00279	276.13210	C00449	HMDB00279	276.13214
933	116.06774	116.06783	116.06774	1.55600	1.56400	1.55600	0.00000	12.14502	12.23211	196528.68468	NaN	9.64543	0.00897	0.00897	116.06777	1.55867	C00148	HMDB00162	115.06330	C00763	HMDB03411	115.06330
1016	94.04579	94.04592	94.04579	1.07300	1.07000	1.07300	0.00000	12.12676	12.15185	187082.99761	NaN	9.34794	0.01171	0.01171	94.04584	1.07200	C00292	HMDB03012	93.05780	C14447		93.05780
141	695.13318	695.13306	695.13318	2.54500	2.53000	2.54500	0.00000	12.08632	12.10812	179372.11305	NaN	10.20109	0.01163	0.01163	695.13314	2.54000			694.13805			694.13813
267	444.13684	444.13709	444.13684	10.09100	10.13500	10.09100	0.00000	12.05300	12.08804	174647.00523	NaN	9.22054	0.01069	0.01069	444.13692	10.10567			443.12885	C18886		443.12480
227	478.06351	478.06247	478.06351	1.97900	2.00000	1.97900	0.00000	12.06534	12.07275	174389.34918	NaN	10.29768	0.00884	0.00884	478.06316	1.98600	C00513		477.05500			477.05496
866	135.09374	135.09361	135.09374	11.48100	11.51300	11.48100	0.00000	11.88237	12.20467	169994.58060	NaN	10.40279	0.00808	0.00808	135.09369	11.49167	C07720		134.08777	C07651		134.08780
406	311.12424	311.12408	311.12424	10.53900	10.55900	10.53900	0.00000	11.94465	12.10362	166730.21460	NaN	11.72074	0.00882	0.00882	311.12419	10.54567		HMDB11741	310.11649			310.11649
759	175.11945	175.11929	175.11945	1.37900	1.40000	1.37900	0.00000	11.98232	11.97988	159707.50477	NaN	9.01581	0.01069	0.01069	175.11940	1.38600	C00062	HMDB00517	174.11168			174.11168
217	493.25122	493.25070	493.25122	9.11400	9.17000	9.11400	0.00000	11.86593	12.04507	155671.42952	NaN	10.17717	0.00856	0.00856	493.25105	9.13267	C09086		492.23593	C09070		492.23590
153	647.11200	647.11127	647.11200	1.96800	1.96500	1.96800	0.00000	11.95283	11.93482	153864.16549	NaN	9.19498	0.01104	0.01104	647.11176	1.96700	C19965		646.19560			646.19564
393	325.11368	325.11359	325.11368	1.56700	1.56400	1.56700	0.00000	11.96048	11.90598	152242.54877	NaN	8.65713	0.00918	0.00918	325.11365	1.56600	C04333		324.10565			324.10565
800	158.96437	158.96468	158.96437	1.25000	1.25800	1.25000	0.00000	11.96680	11.82748	146845.95105	NaN	9.81288	0.00864	0.00864	158.96447	1.25267	C19212		157.97238	C19164		157.97240
848	142.94804	142.94840	142.94804	1.33200	1.36400	1.33200	0.00000	11.78704	11.96099	143489.34989	NaN	11.04282	0.01007	0.01007	142.94816	1.34267	C13558		141.94080	C13199		141.93130
421	301.21594	301.21539	301.21594	2.12100	2.11800	2.12100	0.00000	11.78583	11.89575	138800.44148	NaN	9.97860	0.01166	0.01166	301.21576	2.12000	C00777	HMDB02369	300.20890	C09188		300.20890
214	497.21838	497.21835	497.21838	10.85700	10.90100	10.85700	0.00000	11.80406	11.86084	137647.57802	NaN	8.08122	0.00811	0.00811	497.21837	10.87167			496.21443			496.19580
788	164.92860	164.92906	164.92860	1.32000	1.32900	1.32000	0.00000	11.84255	11.79721	135927.54937	NaN	9.16656	0.01046	0.01046	164.92876	1.32300	C06899		163.91990	C11150		163.91986
766	173.02126	173.02092	173.02126	1.66200	1.68200	1.66200	0.00000	11.85259	11.76775	134614.00729	NaN	10.46573	0.00915	0.00915	173.02114	1.66867	C03189	HMDB00126	172.01367	C02979	HMDB02520	172.01367
425	298.09726	298.09677	298.09726	11.55100	11.56000	11.55100	0.00000	11.70267	11.91421	134381.60387	NaN	8.60078	0.01024	0.01024	298.09710	11.55400	C00170	HMDB01173	297.08956	C00170	HMDB01173	297.08957
379	334.14099	334.14029	334.14099	14.68300	14.65600	14.68300	0.00000	11.72290	11.87520	133126.15393	NaN	8.38127	0.01028	0.01028	334.14076	14.67400			333.13247			333.13247
752	179.01704	179.01714	179.01704	2.06200	2.07100	2.06200	0.00000	11.84428	11.70375	129834.25300	NaN	10.32659	0.00901	0.00901	179.01708	2.06500	C11582		178.00650			178.00645
391	328.14218	328.14172	328.14218	27.97500	28.01900	27.97500	0.00000	11.59697	11.87261	124840.14010	NaN	10.70524	0.01055	0.01055	328.14203	27.98967			327.14304			327.14304
320	391.28412	391.28354	391.28412	39.92500	39.91000	39.92500	0.00000	10.78807	12.67101	124186.69012	NaN	10.14552	0.00990	0.00990	391.28393	39.92000			390.27699			390.27699
339	364.06494	364.06494	364.06494	3.78100	3.79000	3.78100	0.00000	11.61894	11.73446	117794.87389	NaN	11.07859	0.01020	0.01020	364.06494	3.78400			363.05800			363.05800
203	515.13745	515.13757	515.13745	1.59100	1.60000	1.59100	0.00000	11.66376	11.65579	115817.58386	NaN	9.46912	0.01014	0.01014	515.13749	1.59400	C11239		514.11520			514.11516
991	101.00354	101.00352	101.00354	2.06200	2.07100	2.06200	0.00000	11.74777	11.56041	115161.50986	NaN	9.40673	0.00979	0.00979	101.00353	2.06500	C18588		99.99370	C18675		99.99365
341	362.92685	362.92642	362.92685	1.22600	1.23500	1.22600	0.00000	11.57035	11.56006	105366.75593	NaN	10.65916	0.00957	0.00957	362.92671	1.22900	C07552		361.87572	C07552		361.87570
821	150.05841	150.05827	150.05841	2.22700	2.22400	2.22700	0.00000	11.53559	11.56560	103838.68243	NaN	9.72892	0.01020	0.01020	150.05837	2.22600	C00073	HMDB00696	149.05100	C00855		149.05100
429	294.93924	294.93927	294.93924	1.22600	1.23500	1.22600	0.00000	11.53508	11.52388	101669.22730	NaN	8.92977	0.01043	0.01043	294.93925	1.22900			293.99057			293.99057
280	430.91449	430.91412	430.91449	1.22600	1.23500	1.22600	0.00000	11.51845	11.50742	100001.07972	NaN	9.48336	0.00935	0.00935	430.91437	1.22900	C13706		429.97763			429.97769
635	204.08684	204.08681	204.08684	1.68500	1.68200	1.68500	0.00000	11.43446	11.58557	99709.07028	NaN	10.55441	0.01034	0.01034	204.08683	1.68400			203.07937	C12986		203.07940
671	196.96140	196.96129	196.96140	1.62600	1.64700	1.62600	0.00000	11.65169	11.28341	95563.66476	NaN	10.05755	0.01149	0.01149	196.96136	1.63300	C19183		195.95090	C19300		195.97160
845	145.04962	145.04979	145.04962	1.56700	1.56400	1.56700	0.00000	11.49571	11.35861	91780.97600	NaN	11.29341	0.01028	0.01028	145.04968	1.56600			144.04224			144.04224

220	490.17703	490.17682	490.17703	1.53200	1.54100	1.53200	0.00000	11.39665	11.40191	89257.43752	NaN	9.77603	0.00988	0.00988	490.17696	1.53500			489.15360			489.14553
394	325.04337	325.04352	325.04337	2.75600	2.75300	2.75600	0.00000	11.44444	11.33613	88458.25879	NaN	9.97283	0.01053	0.01053	325.04342	2.75500	C00105	HMDB00288	324.03586	C01168	HMDB01271	324.03586
1020	90.05570	90.05579	90.05570	1.43800	1.44700	1.43800	0.00000	11.43588	11.32074	87405.03325	NaN	11.03180	0.01002	0.01002	90.05573	1.44100	C00041	HMDB00161	89.04770	C00099	HMDB00056	89.04770
1053	85.02928	85.02894	85.02928	1.56700	1.57600	1.56700	0.00000	11.40445	11.29630	84997.14409	NaN	9.76756	0.01100	0.01100	85.02917	1.57000			84.02113	C05562		84.02113
519	245.09552	245.09564	245.09552	15.21300	15.19800	15.21300	0.00000	11.27750	11.40355	84164.31409	NaN	9.54950	0.01150	0.01150	245.09556	15.20800	C00120	HMDB00030	244.08817	C00120	HMDB00030	244.08817
395	325.04337	325.04327	325.04337	2.45000	2.44700	2.45000	0.00000	11.19934	11.46526	83474.79667	NaN	8.09839	0.01011	0.01011	325.04334	2.44900	C00105	HMDB00288	324.03586	C01168	HMDB01271	324.03586
167	603.15375	603.15295	603.15375	1.57900	1.58800	1.57900	0.00000	11.34396	11.31483	83232.43174	NaN	9.33984	0.00908	0.00908	603.15348	1.58200			602.16356	C17519		602.16360
1082	82.53783	82.53787	82.53783	1.03800	1.03500	1.03800	0.00000	11.43219	11.22157	83023.74183	NaN	9.26221	0.00966	0.00966	82.53784	1.03700						
409	310.11325	310.11346	310.11325	1.50900	1.50600	1.50900	0.00000	11.27965	11.31230	80496.82875	NaN	10.13495	0.01118	0.01118	310.11332	1.50800	C00270	HMDB00230	309.10598			309.10598
936	114.98743	114.98794	114.98743	1.03800	1.04600	1.03800	0.00000	11.31603	11.23152	78729.35926	NaN	11.19515	0.01021	0.01021	114.98760	1.04067	C03248		113.99530	C00975	HMDB02050	113.99531
990	101.02343	101.02382	101.02343	4.35800	4.30800	4.35800	0.00000	11.15133	11.36844	77643.49857	NaN	9.99000	0.01043	0.01043	101.02356	4.34133	C19524		100.01600	C19524		100.01604
960	112.05071	112.05093	112.05071	1.43800	1.45800	1.43800	0.00000	11.32238	11.14378	75589.96416	NaN	10.02658	0.01049	0.01049	112.05078	1.44467	C00380	HMDB00630	111.04326	C00380	HMDB00630	111.04326
211	498.90152	498.90183	498.90152	1.22600	1.23500	1.22600	0.00000	11.25458	11.20208	75231.74527	NaN	9.75093	0.00896	0.00896	498.90162	1.22900			497.89119			498.04675
403	317.17105	317.17078	317.17105	11.08000	11.11300	11.08000	0.00000	11.14704	11.30395	75018.80861	NaN	10.12262	0.00889	0.00889	317.17096	11.09100	C11863		316.16744	C04793		316.16744
283	428.03616	428.03635	428.03616	2.76800	2.76500	2.76800	0.00000	11.21356	11.23529	74938.55408	NaN	10.62259	0.00984	0.00984	428.03622	2.76700	C00008	HMDB01341	427.02940	C00054	HMDB00061	427.02940
286	423.08978	423.09012	423.08978	1.56700	1.58800	1.56700	0.00000	11.22278	11.22374	74851.61891	NaN	9.81629	0.00801	0.00801	423.08990	1.57400	C00689	HMDB01124	422.08250	C02591		422.08250
168	593.08978	593.08923	593.08978	2.03800	2.04700	2.03800	0.00000	11.21676	11.18828	73315.11376	NaN	10.84430	0.00958	0.00958	593.08960	2.04100			592.07005			592.14275
327	381.07944	381.08038	381.07944	1.54400	1.54100	1.54400	0.00000	11.21037	11.18315	72893.85102	NaN	9.09940	0.00981	0.00981	381.07975	1.54300			380.08071			380.08779
402	317.17127	317.17108	317.17127	11.45700	11.47800	11.45700	0.00000	11.00803	11.14799	64732.12939	NaN	9.01363	0.01086	0.01086	317.17120	11.46400	C11863		316.16744	C04793		316.16744
182	566.88965	566.88940	566.88965	1.22600	1.23500	1.22600	0.00000	11.10101	11.02609	63802.45899	NaN	9.13662	0.00999	0.00999	566.88957	1.22900			565.89537	C00029	HMDB00286	566.05499
199	527.15851	527.15857	527.15851	1.76800	1.78800	1.76800	0.00000	10.93582	11.11022	61268.33634	NaN	10.98570	0.00881	0.00881	527.15853	1.77467			526.14751			526.14751
499	255.23109	255.23103	255.23109	35.43900	35.46000	35.43900	0.00000	10.88614	11.15201	61027.15318	NaN	9.26244	0.01106	0.01106	255.23107	35.44600			254.22457			254.22457
529	242.92569	242.92560	242.92569	1.22600	1.23500	1.22600	0.00000	11.02845	11.00811	60978.39498	NaN	10.56871	0.01087	0.01087	242.92566	1.22900	C18251		241.89404	C18242		241.89400
861	137.04585	137.04601	137.04585	3.32200	3.29500	3.32200	0.00000	10.94029	11.06539	60044.44436	NaN	9.82110	0.01049	0.01049	137.04590	3.31300	C00262	HMDB00157	136.03850	C00262	HMDB00157	136.03851
681	190.07105	190.07092	190.07105	4.11000	4.08400	4.11000	0.00000	10.97438	11.02452	59841.20947	NaN	8.82941	0.01097	0.01097	190.07100	4.10133	C00624	HMDB01138	189.06370	C03871		189.06370
155	625.13477	625.13538	625.13477	1.57900	1.58800	1.57900	0.00000	10.99669	11.00107	59806.85755	NaN	9.75328	0.01111	0.01111	625.13497	1.58200			624.13258			624.13258
553	230.17500	230.17494	230.17500	22.93600	22.93300	22.93600	0.00000	10.86802	11.10571	59092.84948	NaN	11.36521	0.00891	0.00891	230.17498	22.93500		HMDB13267	229.16780	C11707		229.14670
398	323.06442	323.06412	323.06442	8.78400	8.88700	8.78400	0.00000	10.96222	10.99760	58683.31340	NaN	8.46967	0.01173	0.01173	323.06432	8.81833	C00364	HMDB01227	322.05660	C00364	HMDB01227	322.05661
190	546.20587	546.20728	546.20587	10.84500	10.90100	10.84500	0.00000	10.86311	10.98162	55401.67751	NaN	8.83026	0.01072	0.01072	546.20634	10.86367	C04428		545.19560	C04847		545.19560
1081	83.03643	83.04222	83.03643	0.95500	0.95200	0.95500	0.00000	11.28840	10.55437	55347.46019	NaN	8.64935	0.01100	0.01100	83.03836	0.95400		HMDB13749	82.04186	C08389		82.05310
455	276.10761	276.10803	276.10761	6.74800	6.80400	6.74800	0.00000	10.87509	10.94735	54787.54737	NaN	8.44122	0.00855	0.00855	276.10775	6.76667	C08328		275.10050	C08340		275.10050
148	655.27594	655.27478	655.27594	27.97500	28.01900	27.97500	0.00000	10.77829	11.04407	54785.60651	NaN	10.11038	0.00931	0.00931	655.27555	27.98967			654.26896			654.26896
285	423.19830	423.19727	423.19830	12.45800	12.47800	12.45800	0.00000	10.85100	10.94728	54129.77304	NaN	10.36773	0.01166	0.01166	423.19796	12.46467	C09801		422.19403			422.19403
811	156.01389	156.01401	156.01389	1.04900	1.05800	1.04900	0.00000	10.86444	10.85020	51912.59408	NaN	9.43466	0.01197	0.01197	156.01393	1.05200			155.00410			155.01379
473	268.10446	268.10397	268.10446	9.29100	9.34700	9.29100	0.00000	10.77246	10.92786	51542.52988	NaN	8.93941	0.01034	0.01034	268.10430	9.30967	C00212	HMDB00050	267.09674	C00330	HMDB00085	267.09674
825	148.09653	148.09662	148.09653	2.55600	2.55300	2.55600	0.00000	10.81015	10.88963	51528.55727	NaN	9.13227	0.00998	0.00998	148.09656	2.55500	C10144		147.08950	C10159		147.08954
872	132.99809	132.99831	132.99809	1.03800	1.04600	1.03800	0.00000	10.87038	10.82344	51375.14447	NaN	8.96680	0.01256	0.01256	132.99816	1.04067			132.00585	C03981		132.00585
794	160.99503	160.99387	160.99503	1.04900	1.05800	1.04900	0.00000	10.85617	10.80797	50618.49220	NaN	9.73954	0.01015	0.01015	160.99464	1.05200	C18300		159.98470	C19165		159.98470
919	121.05084	121.05091	121.05084	39.90100	39.91000	39.90100	0.00000	10.69714	10.90155	48988.70036	NaN	10.54364	0.01069	0.01069	121.05087	39.90400		HMDB01366	120.04359		HMDB01366	120.04360
284	423.19836	423.19778	423.19836	12.03400	12.05400	12.03400	0.00000	10.75125	10.80693	48006.34076	NaN	10.58559	0.01188	0.01188	423.19817	12.04067	C09801		422.19403			422.19403
672	195.12276	195.12262	195.12276	10.42100	10.47700	10.42100	0.00000	10.66789	10.86877	47492.57009	NaN	9.84692	0.01009	0.01009	195.12271	10.43967			194.10553			194.10553
885	130.04968	130.04977	130.04968	3.16900	3.16600	3.16900	0.00000	10.73514	10.78564	47117.09332	NaN	9.69586	0.01019	0.01019	130.04971	3.16800	C01879	HMDB00267	129.04259	C02237	HMDB00805	129.04259
192	545.71436	545.71387	545.71436	10.24400	10.30000	10.24400	0.00000	10.67178	10.82229	46492.00987	NaN	10.79456	0.01120	0.01120	545.71419	10.26267						
279	432.17203	432.17151	432.17203	1.53200	1.54100	1.53200	0.00000	10.71260	10.69113	44438.67091	NaN	9.98493	0.01155	0.01155	432.17186	1.53500			431.16925			431.16925
683	188.07082	188.07054	188.07082	11.63400	11.63100	11.63400	0.00000	10.60520	10.78865	44219.77472	NaN	10.82598	0.00980	0.00980	188.07072	11.63300	C06559		187.06250			187.06330
201	522.20300	522.20325	522.20300	1.80300	1.83500	1.80300	0.00000	10.49960	10.87626	43823.77781	NaN	10.20300	0.00977	0.00977	522.20308	1.81367			521.20968			521.20968
605	210.11581	210.11562	210.11581	3.61600	3.58900	3.61600	0.00000	10.55368	10.81963	43767.91030	NaN	10.41978	0.01084	0.01084	210.11575	3.60700	C01458		209.10520	C12231		209.10520
233	471.13394	471.13336	471.13394	9.63200	9.70000	9.63200	0.00000	10.70717	10.65905	43612.95501	NaN	11.00398	0.00990	0.00990	471.13375	9.65467	C19480		470.12980	C19531		470.12985
1096	80.98312	80.98029	80.98312	1.59100	1.61100	1.59100	0.00000	10.77729	10.58598	43548.70174	NaN	13.69693	0.00889	0.00889	80.98218	1.59767	C19201		79.96874	C19113		79.96870
487	265.01547	265.01578	265.01547	1.08500	1.08200	1.08500	0.00000	10.61933	10.68211	42223.02717	NaN	7.42708	0.01081	0.01081	265.01557	1.08400		HMDB00559	264.03037		HMDB03332	264.03037
566	226.18021	226.18004	226.18021	25.11400	25.12300	25.11400	0.00000	10.42372	10.80625	40740.84368	NaN	10.02608	0.01035	0.01035	226.18015	25.11700	C14186		225.15900	C18768		225.15900
434	291.12015	291.11914	291.12015	8.13700	8.15700	8.13700	0.00000	10.47207	10.74603	40499.74922	NaN	9.79684	0.00941	0.00941	291.11981	8.14367		HMDB12267	290.11140	C04421		290.11140
515	247.12888	247.12886	247.12888	9.60900	9.67600	9.60900	0.00000	10.52583	10.68880	40429.56506	NaN	10.18064	0.01162	0.01162	247.12887	9.63133		HMDB11166	246.12157		HMDB11172	246.12157
577	220.18227	220.18213	220.18227	11.48100	11.51300	11.48100	0.00000	10.71517	10.47880	40014.14798	NaN	9.71432	0.01034	0.01034	220.18222	11.49167	C16362		219.16231	C09961		219.16231
378	335.06644	335.06586	335.06644	1.57900	1.58800	1.57900	0.00000	10.54865	10.64249	39957.32512	NaN	8.39337	0.01078	0.01078	335.06624	1.58200	C00455	HMDB00229	334.05661	C00455	HMDB00229	334.05661
572	223.98994	223.99011	223.98994	1.08500	1.08200	1.08500	0.00000	10.65879	10.51747	39661.07189	NaN	10.36999	0.00935	0.00935	223.99000	1.08400			223.00362	C04327		223.00680
550	231.17055	231.16971	231.17055	1.95600	1.95300	1.95600	0.00000	10.58120	10.59192	39598.85403	NaN	10.57498	0.01164	0.01164	231.17027	1.95500			230.16304			230.16304
874	132.10230	132.10176	132.10230	12.10500	12.10200	12.10500	0.00000	10.50365	10.61943	38620.46028	NaN	10.85081	0.00842	0.00842	132.10212	12.10400	C00123	HMDB00687	131.09460	C00407	HMDB00172	131.09460
311	404.02573	404.02585	404.02573	1.86200	1.87000	1.86200	0.00000	10.48969	10.61679	38301.40046	NaN	8.56447	0.01040	0.01040	404.02577	1.86467	C00112	HMDB01546	403.01819	C00112	HMDB01546	403.01819
667	197.15302	197.15295	197.15302	29.72900	29.73800	29.72900	0.00000	10.44287	10.66204	38271.35303	NaN	9.99570	0.01007	0.01007	197.15300	29.73200	C08486		196.14630	C09837		196.14630
164	608.08820	608.08771	608.08820	3.03900	3.02400	3.03900	0.00000	10.61872	10.47905	38134.81670	NaN	10.53996	0.01013	0.01013	608.08803	3.03400	C00203	HMDB00304	607.08148	C00043	HMDB00290	607.08154
169	591.08527	591.08545	591.08527	34.53300	34.51800	34.53300	0.00000	10.52695	10.55816	37894.21267	NaN	9.52503	0.00932	0.00932	591.08533	34.52800			590.06432	C04630		590.10260
604	212.14912	212.14961	212.14912	10.42100	10.47700	10.42100	0.00000	10.43175	10.62012	37269.68246	NaN	9.10140	0.01027	0.01027	212.14929	10.43967	C19098		211.14330	C19103		211.14331
751	180.03870	180.03943	180.03870	30.13000	30.12700	30.13000	0.00000	10.43065	10.61245	37106.65068	NaN	9.77529	0.01149	0.01149	180.03894	30.12900	C00745	HMDB01934	179.02523	C03727		179.02520
116	922.00958	922.01025	922.00958	4.36900	4.31900	4.36900	0.00000	10.65428	10.37108	36778.84243	NaN	8.69803	0.01051	0.01051	922.00981	4.35233			921.15707	C14120		921.15710
634	204.08606	204.08644	204.08606	3.07400	3.03600	3.07400	0.00000	10.51565	10.50438	36680.99271	NaN	11.30587	0.00947	0.00947	204.08619	3.06133			203.07937	C12986		203.07940
390	328.13950	328.13895	328.13950	9.60900	9.66400	9.60900	0.00000	10.45364	10.55868	36539.79911	NaN	9.44822	0.01178	0.01178	328.13931	9.62733			327.14304			327.14304
299	408.91974	408.91885	408.91974	1.17900	1.17600	1.17900	0.00000	10.53348	10.45920	36182.81630	NaN	10.48907	0.00913	0.00913	408.91944	1.17800	C14176		407.81342	C15648		407.81342
512	248.07629	248.07640	248.07629	7.73700	7.71000	7.73700	0.00000	10.39599	10.59045	36070.12782	NaN	10.04652	0.00932	0.00932	248.07633	7.72800	C05931		247.06920			247.06920
404	315.05908	315.05969	315.05908	1.72000	1.61100	1.72000	0.00000	10.48430	10.47923	35659.35898	NaN	12.12333	0.01011	0.01011	315.05929	1.68367	C04376		314.05150		HMDB01308	314.05151
569	225.01584	225.01578	225.01584	1.61400	1.60000	1.61400	0.00000	10.54229	10.41448	35538.91093	NaN	8.82457	0.01066	0.01066	225.01582	1.60933			224.00780	C16455		224.02020
367	348.07025	348.07089	348.07025	8.14900	8.19300	8.14900	0.00000	10.35916	10.56637	34988.13281	NaN	9.43265	0.00981	0.00981	348.07047	8.16367	C00020	HMDB00045	347.06308	C00362	HMDB01044	347.06308
397	323.14459	323.14517	323.14459	1.62600	1.62300	1.62600	0.00000	10.36354	10.55160	34806.79135	NaN	10.89215	0.01009	0.01009	323.14479	1.62500	C09559		322.14160	C09568		322.14160
458	272.94449	272.94489	272.94449	1.17900	1.18800	1.17900	0.00000	10.43914	10.43692	34133.29733	NaN	9.84918	0.01062	0.01062	272.94462	1.18200	C14189		271.95620	C14737		271.95620
773	169.04550	169.04572	169.04550	1.03800	1.03500	1.03800	0.00000	10.76229	10.07837	33534.34741	NaN	10.35169	0.01009	0.01009	169.04557	1.03700			168.04224	C01839		168.04224

1012	97.02885	97.02898	97.02885	1.56700	1.57600	1.56700	0.00000	10.43325	10.40239	33450.47950	NaN	9.33305	0.01001	0.01001	97.02890	1.57000	C07090		96.02110	C14279		96.02110
364	349.05447	349.05408	349.05447	4.95800	5.02600	4.95800	0.00000	10.39245	10.44008	33398.36931	NaN	9.82255	0.01054	0.01054	349.05434	4.98067	C00130	HMDB00175	348.04709		HMDB11681	348.04709
753	178.13358	178.13377	178.13358	11.23300	11.23000	11.23300	0.00000	10.41260	10.38780	32866.14896	NaN	10.24287	0.01086	0.01086	178.13364	11.23200			177.12660	C07432		177.11540
508	250.05562	250.05585	250.05562	30.13000	30.11500	30.13000	0.00000	10.13317	10.62830	32232.53669	NaN	11.47383	0.01131	0.01131	250.05569	30.12500	C00627	HMDB01319	249.04023	C00627	HMDB01319	249.04022
412	308.18448	308.18597	308.18448	30.13000	30.12700	30.13000	0.00000	10.43489	10.31593	32061.42715	NaN	10.67293	0.01005	0.01005	308.18498	30.12900	C07219	HMDB05023	307.16850	C07219	HMDB05023	307.16846
298	412.16409	412.16531	412.16409	10.43300	10.45300	10.43300	0.00000	10.32718	10.41450	31915.17387	NaN	10.26110	0.00951	0.00951	412.16450	10.43967	C15038		411.15829	C15038		411.15830
547	233.11293	233.11330	233.11293	3.86300	3.82500	3.86300	0.00000	10.35278	10.38431	31841.98415	NaN	10.43202	0.00874	0.00874	233.11305	3.85033	C01410		232.10590	C03415		232.10590
554	230.10162	230.10216	230.10162	9.10200	9.17000	9.10200	0.00000	10.27093	10.45072	31597.27682	NaN	9.21915	0.01054	0.01054	230.10180	9.12467	C19344		229.08915	C19347		229.08915
260	454.29242	454.29144	454.29242	35.80400	35.84800	35.80400	0.00000	10.31446	10.39337	31379.74174	NaN	9.73816	0.00875	0.00875	454.29209	35.81867			453.28550			453.28550
548	233.11270	233.11365	233.11270	1.67300	1.67000	1.67300	0.00000	10.27797	10.41437	31137.50971	NaN	10.49347	0.01064	0.01064	233.11302	1.67200	C01410		232.10590	C03415		232.10590
528	243.02631	243.02622	243.02631	1.62600	1.64700	1.62600	0.00000	10.40189	10.28283	31019.21773	NaN	9.58131	0.01167	0.01167	243.02628	1.63300	C04299	HMDB01125	242.01915			242.01915
241	463.14899	463.14868	463.14899	9.63200	9.70000	9.63200	0.00000	10.30595	10.35155	30599.67838	NaN	10.05276	0.00952	0.00952	463.14889	9.65467			462.13821			462.13821
180	572.67334	572.67535	572.67334	10.24400	10.30000	10.24400	0.00000	10.33259	10.30050	30228.69236	NaN	9.92046	0.01149	0.01149	572.67401	10.26267			571.47532			
674	193.14610	193.14638	193.14610	11.48100	11.52500	11.48100	0.00000	10.36431	10.24443	29862.85894	NaN	10.72378	0.01091	0.01091	193.14620	11.49567	C07142		192.12630			192.12626
893	128.10930	128.10864	128.10930	4.25200	4.64900	4.25200	0.00000	10.41953	10.18906	29860.57947	NaN	9.67408	0.00945	0.00945	128.10908	4.38433			127.09971	C11519		127.09970
296	415.21127	415.21179	415.21127	32.87300	32.87000	32.87300	0.00000	10.14666	10.45323	29730.98207	NaN	8.25438	0.00962	0.00962	415.21145	32.87200	C10658		414.20420	C12512		414.20420
873	132.10156	132.10144	132.10156	11.65700	11.66600	11.65700	0.00000	10.24781	10.34097	29566.24332	NaN	10.82416	0.01055	0.01055	132.10152	11.66000	C00123	HMDB00687	131.09460	C00407	HMDB00172	131.09460
587	217.08209	217.08192	217.08209	1.69700	1.69400	1.69700	0.00000	10.22795	10.33435	29177.37020	NaN	10.29644	0.01086	0.01086	217.08204	1.69600	C17359		216.07460			216.07462
383	332.07550	332.07575	332.07550	5.09900	5.01400	5.09900	0.00000	10.35047	10.19285	28901.84749	NaN	9.79993	0.01038	0.01038	332.07558	5.07067	C00360	HMDB00905	331.06817	C00360	HMDB00905	331.06818
375	340.93247	340.93170	340.93247	1.19100	1.18800	1.19100	0.00000	10.28038	10.25433	28777.59232	NaN	10.46061	0.00935	0.00935	340.93221	1.19000	C11044		339.87830	C14372		339.87830
858	138.05426	138.05821	138.05426	3.01600	3.35400	3.01600	0.00000	10.21131	10.27110	28034.89962	NaN	9.37414	0.00864	0.00864	138.05558	3.12867	C00108	HMDB01123	137.04770	C00568	HMDB01392	137.04770
774	168.12338	168.12306	168.12338	8.67800	8.75800	8.67800	0.00000	10.16422	10.31759	28026.53348	NaN	9.23881	0.01019	0.01019	168.12328	8.70467	C10916		167.10590	C11006		167.10586
891	128.10867	128.10880	128.10867	4.03967	4.31950	4.03967	0.00000	10.42790	9.97499	26942.09480	NaN	9.17511	0.00975	0.00975	128.10871	4.13295			127.09971	C11519		127.09970
358	353.11432	353.11520	353.11432	30.13000	30.11500	30.13000	0.00000	9.71366	10.68055	26825.39631	NaN	8.19866	0.01192	0.01192	353.11461	30.12500			352.10930	C16672		352.10930
330	378.89981	378.90002	378.89981	1.22600	1.23500	1.22600	0.00000	10.19206	10.17660	26484.94308	NaN	11.12359	0.01024	0.01024	378.89988	1.22900	C18124		377.87063	C13718		377.87060
903	125.98605	125.98627	125.98605	1.07300	1.07000	1.07300	0.00000	10.22403	10.12483	26223.89515	NaN	11.06369	0.01034	0.01034	125.98612	1.07200	C18872		124.98690	C00245	HMDB00251	125.01466
970	105.04227	105.04260	105.04227	1.17900	1.18800	1.17900	0.00000	10.34672	9.99912	26184.44529	NaN	9.09461	0.00887	0.00887	105.04238	1.18200	C02221		104.03740	C02234		104.03740
920	121.05125	121.05112	121.05125	0.88500	0.89300	0.88500	0.00000	9.27430	11.05979	26031.10226	NaN	13.47250	0.01006	0.01006	121.05120	0.88767		HMDB01366	120.04359		HMDB01366	120.04360
969	106.95108	106.95043	106.95108	1.23800	1.24700	1.23800	0.00000	10.14490	10.18571	25985.72349	NaN	9.56387	0.00969	0.00969	106.95086	1.24100	C18765		105.94340	C19207		105.94181
627	204.95677	204.95668	204.95677	1.19100	1.19900	1.19100	0.00000	10.17482	10.14171	25803.48102	NaN	9.72172	0.00975	0.00975	204.95674	1.19367			203.97854			203.97854
171	585.14197	585.14252	585.14197	1.59100	1.60000	1.59100	0.00000	10.15457	10.14176	25544.21014	NaN	10.18969	0.00988	0.00988	585.14215	1.59400			584.11661			584.11661
200	525.18298	525.18201	525.18298	10.80900	10.85400	10.80900	0.00000	10.01931	10.20985	24700.60431	NaN	10.59355	0.01012	0.01012	525.18266	10.82400			524.15299			524.15293
265	446.88715	446.88785	446.88715	1.22600	1.23500	1.22600	0.00000	10.13611	10.06546	24362.17387	NaN	9.88598	0.00980	0.00980	446.88738	1.22900			445.96131			445.96131
865	136.07007	136.06923	136.07007	4.41700	4.34300	4.41700	0.00000	10.09926	10.06611	23925.23727	NaN	8.75989	0.00973	0.00973	136.06979	4.39233	C02505	HMDB10715	135.06840	C07565		135.06840
579	219.09837	219.09761	219.09837	9.93800	9.99400	9.93800	0.00000	10.11162	10.02379	23569.36789	NaN	8.57485	0.01040	0.01040	219.09812	9.95667	C03738		218.09030			218.09027
762	174.07620	174.07599	174.07620	13.68200	13.67900	13.68200	0.00000	9.99808	10.10470	23187.98229	NaN	9.54861	0.01098	0.01098	174.07613	13.68100	C01250		173.06880	C12121		173.06880
979	102.05528	102.05536	102.05528	1.47300	1.48200	1.47300	0.00000	10.08857	9.99305	22943.92863	NaN	10.95733	0.00938	0.00938	102.05531	1.47600			101.04768	C02948		101.04768
859	138.05791	138.05727	138.05791	3.38000	3.74200	3.38000	0.00000	9.78087	10.28696	22786.39245	NaN	9.00848	0.01014	0.01014	138.05769	3.50067			137.04882	C15533		137.04880
407	310.91248	310.91266	310.91248	1.22600	1.23500	1.22600	0.00000	10.07602	9.98541	22713.55163	NaN	9.57029	0.00967	0.00967	310.91254	1.22900			309.92993	C01151	HMDB11688	309.98547
222	485.07434	485.07443	485.07434	9.71500	9.77000	9.71500	0.00000	9.96933	10.08324	22613.17329	NaN	9.91328	0.01166	0.01166	485.07437	9.73333			484.06515	C13968		484.06000
1013	96.98912	96.98946	96.98912	1.07300	1.08200	1.07300	0.00000	10.14104	9.90862	22580.21068	NaN	10.02308	0.01119	0.01119	96.98924	1.07600	C11145		95.98810	C11261		95.98812
193	544.89526	544.89435	544.89526	1.19100	1.18800	1.19100	0.00000	10.05633	9.99030	22546.03927	NaN	9.36007	0.00895	0.00895	544.89496	1.19000			544.05223			544.05223
312	403.05689	403.05640	403.05689	2.47400	2.45900	2.47400	0.00000	9.93057	10.10776	22452.70963	NaN	11.18198	0.01004	0.01004	403.05672	2.46900	C18556		402.05380	C18556		402.05380
792	163.06044	163.06001	163.06044	1.55600	1.56400	1.55600	0.00000	10.11785	9.91695	22412.96594	NaN	10.50779	0.00701	0.00701	163.06030	1.55867	C00478		162.05280	C01088		162.05280
175	573.16602	573.16498	573.16602	10.84500	10.90100	10.84500	0.00000	9.97902	10.05150	22365.18862	NaN	9.20967	0.00832	0.00832	573.16567	10.86367			572.18932			572.18938
228	476.90707	476.90671	476.90707	1.17900	1.18800	1.17900	0.00000	10.06771	9.95282	22253.79034	NaN	11.02417	0.01060	0.01060	476.90695	1.18200			475.97188			475.97188
1080	83.05368	83.06086	83.05368	39.91300	39.56900	39.91300	0.00000	10.26113	9.71073	21718.72946	NaN	8.08616	0.00898	0.00898	83.05607	39.79833	C08389		82.05310	C19275		82.05310
309	405.00882	405.00986	405.00882	2.94500	2.91800	2.94500	0.00000	9.96608	10.00074	21663.97464	NaN	9.75102	0.00999	0.00999	405.00917	2.93600	C00015	HMDB00295	404.00220	C00015	HMDB00295	404.00220
324	388.14508	388.14447	388.14508	2.78000	2.77700	2.78000	0.00000	9.90404	10.05681	21599.49925	NaN	9.10991	0.00807	0.00807	388.14488	2.77900	C19329		387.13680	C19438		387.13675
386	331.18640	331.18695	331.18695	13.70600	13.71400	13.70600	0.00000	9.92520	10.02967	21535.02051	NaN	10.74433	0.01040	0.01040	331.18677	13.70867			330.17659			330.17659
607	207.13693	207.13776	207.13693	33.79100	33.77600	33.79100	0.00000	9.77836	10.17264	21493.39317	NaN	10.10062	0.01079	0.01079	207.13721	33.78600	C01588	HMDB01925	206.13068	C01588	HMDB01925	206.13068
343	361.10181	361.10086	361.10086	30.13000	30.11500	30.13000	0.00000	9.41147	10.53817	21478.71886	NaN	9.85239	0.00914	0.00914	361.10118	30.12500			360.09575			360.09575
362	351.20648	351.20599	351.20648	8.44300	8.51100	8.44300	0.00000	10.12639	9.82150	21459.99222	NaN	10.31763	0.01033	0.01033	351.20632	8.46567			350.19943			350.19943
971	104.10755	104.10748	104.10755	1.37900	1.37600	1.37900	0.00000	10.02113	9.92500	21441.16371	NaN	9.02223	0.01076	0.01076	104.10753	1.37800	C00114	HMDB00097	103.09971	C07727		103.09971
555	229.15451	229.15384	229.15451	10.99800	11.01800	10.99800	0.00000	9.98647	9.95832	21426.70953	NaN	10.58024	0.00997	0.00997	229.15429	11.00467		HMDB11174	228.14739		HMDB11175	228.14739
570	224.16420	224.16417	224.16420	33.77900	33.76400	33.77900	0.00000	9.98048	9.96374	21420.66903	NaN	10.99178	0.01100	0.01100	224.16419	33.77400	C10868		223.15720			223.15723
948	114.09155	114.09147	114.09155	12.08100	12.10200	12.08100	0.00000	9.90049	9.99558	20911.10531	NaN	10.07694	0.00841	0.00841	114.09152	12.08800			113.08406	C05853		113.08406
520	245.07787	245.07806	245.07787	30.13000	30.11500	30.13000	0.00000	9.61450	10.26671	20756.23939	NaN	10.89844	0.01161	0.01161	245.07793	30.12500			244.06954	C00299	HMDB00296	244.06954
1041	88.06976	88.06030	88.06976	1.42600	1.44700	1.42600	0.00000	9.92513	9.94027	20592.80321	NaN	10.21899	0.01050	0.01050	88.06661	1.43300	C00555		87.06840	C03219		87.06840
194	541.32611	541.32599	541.32611	32.87300	32.88100	32.87300	0.00000	9.97201	9.85498	20201.13330	NaN	8.70526	0.00895	0.00895	541.32607	32.87567	C17766		540.30870			540.34268
589	215.16359	215.16383	215.16359	29.74100	29.75000	29.74100	0.00000	9.71811	10.09150	20026.33827	NaN	8.17916	0.00955	0.00955	215.16367	29.74400			214.15688			214.15688
128	775.09851	775.09985	775.09851	2.62700	2.64800	2.62700	0.00000	9.93473	9.86491	19926.79501	NaN	11.03132	0.01096	0.01096	775.09896	2.63400			774.21591			774.21599
761	174.93791	174.93793	174.93791	1.23800	1.24700	1.23800	0.00000	9.97293	9.82662	19925.95028	NaN	9.41105	0.00828	0.00828	174.93792	1.24100			173.91193		HMDB00250	173.91193
633	204.08646	204.08626	204.08646	4.39300	4.34300	4.39300	0.00000	9.97856	9.80099	19727.58015	NaN	8.72536	0.00962	0.00962	204.08639	4.37633			203.07937	C12986		203.07940
884	130.05010	130.05066	130.05010	1.47300	1.49400	1.47300	0.00000	9.99670	9.78070	19706.35613	NaN	9.33273	0.00966	0.00966	130.05028	1.48000	C01879	HMDB00267	129.04259	C02237	HMDB00805	129.04259
443	283.01907	283.01914	283.01907	1.59100	1.61100	1.59100	0.00000	9.88428	9.86165	19398.74036	NaN	8.89621	0.01012	0.01012	283.01909	1.59767			282.01981			282.04228
639	201.12207	201.12201	201.12207	9.10200	9.15800	9.10200	0.00000	9.77638	9.95272	19236.15503	NaN	8.48267	0.01147	0.01147	201.12205	9.12067			200.11877			200.10620
542	236.12804	236.12863	236.12804	11.88100	11.89000	11.88100	0.00000	9.72547	9.97522	18964.88900	NaN	8.65788	0.01141	0.01141	236.12824	11.88400	C09573		235.12080	C09604		235.12084
502	253.21587	253.21489	253.21587	29.04600	29.06700	29.04600	0.00000	9.78930	9.91107	18961.88910	NaN	10.09191	0.00918	0.00918	253.21554	29.05300	C16795		252.20890			252.20892
371	345.03513	345.03452	345.03513	1.68500	1.70600	1.68500	0.00000	9.83590	9.86324	18950.20911	NaN	7.96875	0.01041	0.01041	345.03492	1.69200	C11719		344.03860			344.03863
750	180.08722	180.08653	180.08722	1.45000	1.45800	1.45000	0.00000	9.80864	9.88651	18912.43204	NaN	11.39244	0.00908	0.00908	180.08699	1.45267		HMDB02130	179.07937			179.07937
791	163.13283	163.13289	163.13283	18.09700	18.07100	18.09700	0.00000	9.71415	9.97615	18866.69528	NaN	11.27212	0.01078	0.01078	163.13285	18.08833	C00745	HMDB01934	162.11570	C06180	HMDB04350	162.11570
363	351.17624	351.17780	351.17624	9.36100	9.42900	9.36100	0.00000	9.76527	9.91805	18800.87171	NaN	9.03654	0.00977	0.00977	351.17676	9.38367	C09290		350.17290	C09297		350.17290
459	272.13303	272.13397	272.13303	1.82600	1.83500	1.82600	0.00000	9.69055	9.97419	18627.03014	NaN	9.07401	0.01034	0.01034	272.13334	1.82900	C11785		271.12084			271.12084
980	102.03452	102.03515	102.03452	1.07300	1.07000	1.07300	0.00000	9.80840	9.85091	18576.50726	NaN	9.03803	0.00952	0.00952	102.03473	1.07200			101.04768	C02948		101.04768

184	564.68640	564.68738	564.68640	10.25600	10.31200	10.25600	0.00000	9.78167	9.86690	18477.00836	NaN	11.43188	0.01008	0.01008	564.68673	10.27467		HMDB04948	563.52777		HMDB11774	563.52777
444	281.14883	281.14896	281.14883	30.13000	30.11500	30.13000	0.00000	9.89534	9.71978	18170.60159	NaN	10.05110	0.01067	0.01067	281.14888	30.12500			280.14231			280.14231
195	537.11877	537.11798	537.11877	1.52000	1.52900	1.52000	0.00000	9.79618	9.79812	17982.38218	NaN	8.40567	0.01133	0.01133	537.11851	1.52300			536.11654			536.11654
540	237.01585	237.01648	237.01585	1.65000	1.65900	1.65000	0.00000	9.84021	9.74250	17878.53573	NaN	9.28397	0.01260	0.01260	237.01606	1.65300	C07764		236.00380			236.00378
462	271.22607	271.22540	271.22607	26.20900	26.21800	26.20900	0.00000	9.62121	9.94936	17770.30023	NaN	8.90441	0.01126	0.01126	271.22585	26.21200			270.21948			270.21948
380	333.56967	333.57044	333.56967	10.57400	10.64200	10.57400	0.00000	9.70848	9.84997	17662.90286	NaN	11.44029	0.00811	0.00811	333.56993	10.59667						
755	177.07587	177.07529	177.07587	15.28300	15.26900	15.28300	0.00000	9.77960	9.76106	17506.46323	NaN	8.68958	0.00957	0.00957	177.07567	15.27833	C02123		176.06845		HMDB02025	176.06845
740	182.13709	182.13715	182.13709	10.48000	10.52400	10.48000	0.00000	9.74245	9.78184	17363.79801	NaN	9.87974	0.01010	0.01010	182.13711	10.49467			181.11028	C14090		181.11028
451	279.04776	279.04834	279.04776	1.56700	1.57600	1.56700	0.00000	9.81583	9.70484	17332.38503	NaN	10.32528	0.01013	0.01013	279.04795	1.57000	C06933		278.03540	C16551		278.03540
966	109.02826	109.02851	109.02826	1.63800	1.64700	1.63800	0.00000	9.78100	9.73166	17263.18672	NaN	9.71688	0.01022	0.01022	109.02834	1.64100	C00472	HMDB03364	108.02110	C02351	HMDB12133	108.02110
822	149.08070	149.07988	149.08070	8.09000	8.12200	8.09000	0.00000	9.58319	9.92118	17191.70129	NaN	9.21813	0.01036	0.01036	149.08043	8.10067	C00418	HMDB00227	148.07354			148.07354
385	331.18616	331.18744	331.18616	13.28200	13.27900	13.28200	0.00000	9.58145	9.91380	17113.52214	NaN	6.90914	0.00965	0.00965	331.18658	13.28100			330.17659			330.17659
401	319.12100	319.12332	319.12100	9.71500	9.77000	9.71500	0.00000	9.66524	9.80419	16894.02306	NaN	9.59885	0.00840	0.00840	319.12178	9.73333			318.11167	C18692		318.11670
204	514.87512	514.87604	514.87512	1.22600	1.23500	1.22600	0.00000	9.74633	9.69340	16644.99040	NaN	9.09822	0.00760	0.00760	514.87543	1.22900			514.04166			514.04173
423	300.08350	300.08353	300.08350	9.58500	9.68800	9.58500	0.00000	9.65766	9.75906	16454.62134	NaN	9.71957	0.00907	0.00907	300.08351	9.61933		HMDB01016	299.07700	C03492		299.07700
232	471.62537	471.62625	471.62537	10.24400	10.31200	10.24400	0.00000	9.68188	9.72784	16397.14245	NaN	11.12855	0.00894	0.00894	471.62566	10.26667						
910	122.96420	122.96362	122.96420	0.96700	0.98700	0.96700	0.00000	9.77257	9.62615	16307.14554	NaN	8.89076	0.00942	0.00942	122.96400	0.97367		HMDB12216	121.97128	C08270	HMDB12251	121.97129
157	615.15192	615.15381	615.15192	1.59100	1.60000	1.59100	0.00000	9.69338	9.69178	16196.95280	NaN	9.40782	0.01026	0.01026	615.15255	1.59400	C00128		614.14727		HMDB01176	614.14728
331	376.10181	376.10165	376.10181	9.39700	9.46400	9.39700	0.00000	9.57755	9.78118	15984.30432	NaN	12.03059	0.00910	0.00910	376.10176	9.41933			375.10665	C18571		375.07930
1047	86.09717	86.09716	86.09717	36.08700	36.37800	36.08700	0.00000	9.84101	9.49647	15815.40625	NaN	10.59290	0.01177	0.01177	86.09717	36.18400	C03219		85.08915	C01746		85.08910
277	433.05161	433.05115	433.05161	1.67300	1.68200	1.67300	0.00000	9.73457	9.57066	15562.42464	NaN	10.07755	0.00978	0.00978	433.05145	1.67600			432.04911	C05692		432.06600
418	303.04785	303.04916	303.04785	1.61400	1.63500	1.61400	0.00000	9.67043	9.60666	15344.98632	NaN	10.17445	0.01164	0.01164	303.04829	1.62100			302.04262	C00389	HMDB05794	302.04262
144	666.15906	666.16248	666.15906	1.55600	1.55300	1.55600	0.00000	9.67122	9.59816	15285.88785	NaN	9.96306	0.00987	0.00987	666.16020	1.55500			665.17170	C00004	HMDB01487	665.12480
664	198.09740	198.09689	198.09740	1.76800	1.77600	1.76800	0.00000	9.51816	9.74596	15245.77640	NaN	8.91458	0.01005	0.01005	198.09723	1.77067			197.08406	C14462		197.09530
783	166.08647	166.08650	166.08647	13.14100	13.11400	13.14100	0.00000	9.52993	9.72717	15192.33496	NaN	8.44553	0.00934	0.00934	166.08648	13.13200			165.07898	C02765	HMDB01943	165.07898
496	258.11069	258.11050	258.11069	1.43800	1.44700	1.43800	0.00000	9.61394	9.62750	15073.88242	NaN	9.26492	0.00833	0.00833	258.11063	1.44100	C00670	HMDB00086	257.10281			257.10282
100	971.29096	971.28931	971.29096	3.79300	3.74200	3.79300	0.00000	9.59742	9.64126	15053.05155	NaN	9.39204	0.00753	0.00753	971.29041	3.77600	C11502		970.28820			970.28824
563	227.19997	227.20007	227.19997	30.73000	30.73900	30.73000	0.00000	9.38894	9.84870	15045.26606	NaN	11.05317	0.00778	0.00778	227.20000	30.73300			226.19327			226.19327
767	172.05197	172.05176	172.05197	30.13000	30.12700	30.13000	0.00000	9.46846	9.75312	14924.92981	NaN	11.48389	0.01006	0.01006	172.05190	30.12900	C07515		171.03540	C14412		171.03540
947	114.08410	114.09184	114.08410	1.80300	1.78800	1.80300	0.00000	9.94006	9.25846	14753.88113	NaN	8.59151	0.00928	0.00928	114.08668	1.79800			113.08406	C05853		113.08406
523	244.11848	244.11832	244.11848	12.09300	12.09000	12.09300	0.00000	9.47104	9.69775	14536.17767	NaN	9.36220	0.01104	0.01104	244.11843	12.09200			243.10415	C02080		243.10415
278	432.23697	432.23828	432.23697	32.87300	32.88100	32.87300	0.00000	9.40906	9.75736	14518.96558	NaN	11.01518	0.01174	0.01174	432.23741	32.87567			431.22810			431.22810
575	222.09702	222.09753	222.09702	1.61400	1.61100	1.61400	0.00000	9.53613	9.62566	14485.34517	NaN	11.12025	0.00887	0.00887	222.09719	1.61300	C00140	HMDB00215	221.08990	C00645	HMDB01129	221.08990
787	165.05455	165.05547	165.05455	4.47500	4.36600	4.47500	0.00000	9.55538	9.58962	14364.31682	NaN	9.43370	0.00947	0.00947	165.05486	4.43867	C00166	HMDB00205	164.04730	C00811		164.04730
819	151.07533	151.07594	151.07533	25.17300	25.14600	25.17300	0.00000	9.30427	9.83943	14354.91335	NaN	10.67259	0.00944	0.00944	151.07554	25.16400		HMDB00635	150.06808			150.06808
328	380.09552	380.09598	380.09552	1.26100	1.28200	1.26100	0.00000	9.54326	9.59579	14321.61336	NaN	10.13716	0.00965	0.00965	380.09567	1.26800	C14651		379.08543	C14626		379.08540
215	497.12674	497.12665	497.12674	1.61400	1.62300	1.61400	0.00000	9.54834	9.53488	13927.36781	NaN	9.89349	0.01156	0.01156	497.12671	1.61700			496.11363	C13269		496.12486
419	302.24420	302.24414	302.24420	25.11400	25.12300	25.11400	0.00000	9.52697	9.55057	13887.88092	NaN	10.28798	0.01131	0.01131	302.24418	25.11700	C07171		301.24056	C08454		301.24057
183	565.18073	565.17944	565.18073	10.85700	10.90100	10.85700	0.00000	9.44796	9.61865	13812.15809	NaN	10.20889	0.01023	0.01023	565.18030	10.87167	C02879		564.16320			564.16316
461	271.22638	271.22583	271.22638	29.04600	29.05500	29.04600	0.00000	9.31606	9.74716	13788.77340	NaN	9.55368	0.00815	0.00815	271.22620	29.04900			270.21948			270.21948
384	331.18649	331.18665	331.18649	14.13000	14.10300	14.13000	0.00000	9.48699	9.56356	13701.73659	NaN	7.60348	0.01129	0.01129	331.18654	14.12100			330.17659			330.17659
422	300.18720	300.19095	300.18720	12.69300	12.70200	12.69300	0.00000	9.52468	9.52113	13669.21741	NaN	10.23012	0.01014	0.01014	300.18845	12.69600			299.18451			299.18451
632	204.08661	204.08662	204.08661	5.40600	5.33200	5.40600	0.00000	9.95460	9.08243	13609.34881	NaN	10.08760	0.01008	0.01008	204.08661	5.38133			203.07937	C12986		203.07940
114	922.01111	922.01166	922.01111	8.96100	8.94600	8.96100	0.00000	8.95937	10.07596	13597.81692	NaN	8.99023	0.01066	0.01066	922.01129	8.95600			921.15707	C14120		921.15710
229	476.37222	476.37064	476.37222	39.91300	39.91000	39.91300	0.00000	8.95650	10.05056	13407.00944	NaN	10.79836	0.00901	0.00901	476.37169	39.91200			475.36953	C13142		475.31452
417	303.15512	303.15595	303.15512	10.40900	10.45300	10.40900	0.00000	9.35675	9.64182	13350.15199	NaN	8.08203	0.01071	0.01071	303.15540	10.42367		HMDB00530	302.15179		HMDB00530	302.15179
594	214.08920	214.08931	214.08920	28.71700	28.69000	28.71700	0.00000	9.24034	9.75226	13310.38081	NaN	8.87314	0.00986	0.00986	214.08924	28.70800	C12865		213.07900	C13697		213.07900
586	217.09700	217.09709	217.09700	13.52900	13.50300	13.52900	0.00000	9.28638	9.69423	13230.80037	NaN	12.33142	0.00898	0.00898	217.09703	13.52033			216.08988	C14406		216.09390
1071	84.07880	84.07984	84.07880	1.01400	0.98700	1.01400	0.00000	9.65709	9.30212	13090.00109	NaN	9.98245	0.01181	0.01181	84.07915	1.00500			83.07350			83.07350
253	457.18167	457.18076	457.18167	13.41100	13.39700	13.41100	0.00000	9.37491	9.57282	13015.07640	NaN	10.28423	0.01037	0.01037	457.18137	13.40633			456.17573			456.17573
263	449.33603	449.33566	449.33603	39.91300	39.91000	39.91300	0.00000	8.83452	10.07128	12745.06768	NaN	9.59559	0.00866	0.00866	449.33591	39.91200			448.33526			448.33526
631	204.08696	204.08670	204.08696	5.99400	5.89700	5.99400	0.00000	9.82182	9.06679	12636.01122	NaN	11.53912	0.01013	0.01013	204.08687	5.96167			203.07937	C12986		203.07940
831	146.95680	146.95075	146.95680	1.02600	1.03500	1.02600	0.00000	9.56953	9.31577	12615.13650	NaN	9.89586	0.00968	0.00968	146.95478	1.02900	C14400		145.94570	C14402		145.94568
588	216.16000	216.15942	216.16000	20.68700	20.66100	20.68700	0.00000	9.21382	9.67059	12609.48601	NaN	11.78659	0.01118	0.01118	216.15981	20.67833	C18830		215.15210	C18856		215.15214
673	195.00314	195.00343	195.00314	1.45000	1.45800	1.45000	0.00000	9.42995	9.44117	12525.98675	NaN	9.27525	0.00959	0.00959	195.00324	1.45267	C12836		193.99820	C13342		193.99820
163	608.08936	608.08710	608.08936	3.36900	3.74200	3.36900	0.00000	8.78231	10.08307	12490.08154	NaN	9.51699	0.01112	0.01112	608.08860	3.49333	C00203	HMDB00304	607.08148	C00043	HMDB00290	607.08154
946	114.07674	114.08278	114.07674	0.88500	0.88200	0.88500	0.00000	9.79032	9.07128	12466.48496	NaN	10.01019	0.00896	0.00896	114.07875	0.88400	C00791	HMDB00562	113.05891	C19284		113.05891
1070	84.08069	84.08018	84.08069	0.17800	0.17500	0.17800	0.00000	9.62669	9.22954	12433.05766	NaN	10.82945	0.00997	0.00997	84.08052	0.17700			83.07350			83.07350
186	558.25330	558.25092	558.25330	13.12900	13.12600	13.12900	0.00000	9.35916	9.46081	12209.65967	NaN	10.00236	0.00853	0.00853	558.25250	13.12800			557.24851	C12011		557.24851
522	244.11809	244.11827	244.11809	11.64500	11.65400	11.64500	0.00000	9.32067	9.49283	12170.25881	NaN	9.02174	0.01072	0.01072	244.11815	11.64800			243.10415	C02080		243.10415
760	175.10768	175.10802	175.10768	1.77900	1.74100	1.77900	0.00000	9.37642	9.43285	12144.53873	NaN	9.31494	0.01111	0.01111	175.10779	1.76633	C00437		174.10040	C01047		174.10040
609	207.00526	207.00562	207.00526	1.62600	1.63500	1.62600	0.00000	9.43143	9.37693	12139.02909	NaN	9.72068	0.01268	0.01268	207.00538	1.62900	C18305		205.99820	C18310		205.99820
517	247.05931	247.05989	247.05931	1.57900	1.58800	1.57900	0.00000	9.37857	9.42363	12101.70550	NaN	10.47580	0.01027	0.01027	247.05950	1.58200	C02162		246.05280	C06355		246.05280
962	111.02078	111.02065	111.02078	34.58000	34.31800	34.58000	0.00000	9.43342	9.33534	11901.04219	NaN	9.95146	0.01066	0.01066	111.02073	34.49267	C18448		110.01328	C19484		110.01328
702	186.01631	186.01709	186.01631	1.41400	1.42300	1.41400	0.00000	9.35037	9.41281	11867.88630	NaN	9.85568	0.00980	0.00980	186.01657	1.41700	C01005	HMDB00272	185.00890	C02532		185.00890
1079	83.04966	83.05023	83.04966	14.68300	14.51500	14.68300	0.00000	9.41893	9.32777	11770.46750	NaN	9.20765	0.01042	0.01042	83.04985	14.62700		HMDB13749	82.04186	C08389		82.05310
1078	83.05262	83.05233	83.05262	8.71400	8.54600	8.71400	0.00000	9.60270	9.13705	11729.65785	NaN	10.95296	0.01051	0.01051	83.05252	8.65800		HMDB13749	82.04186	C08389		82.05310
226	478.14191	478.14160	478.14191	7.91300	7.92200	7.91300	0.00000	9.21247	9.52697	11727.79646	NaN	11.96693	0.00932	0.00932	478.14181	7.91600			477.12711			477.12706
374	342.13944	342.13886	342.13944	1.50900	1.52900	1.50900	0.00000	9.76555	8.91583	11392.21752	NaN	10.10193	0.01211	0.01211	342.13924	1.51567			341.13220	C15658		341.13220
812	155.15382	155.15411	155.15382	11.09200	11.08900	11.09200	0.00000	9.22712	9.42987	11254.16797	NaN	10.41049	0.00991	0.00991	155.15392	11.09100	C00843		154.13580	C01411		154.13580
758	176.05454	176.05666	176.05454	2.58000	2.57700	2.58000	0.00000	9.34215	9.30144	11178.99503	NaN	11.59970	0.00892	0.00892	176.05524	2.57900			175.04805	C05520		175.04805
725	184.13226	184.13274	184.13226	4.41700	4.31900	4.41700	0.00000	9.59097	9.01780	10986.08242	NaN	10.75433	0.00839	0.00839	184.13242	4.38433	C12452		183.12590	C12453		183.12590
439	288.08450	288.08493	288.08450	1.60300	1.60000	1.60300	0.00000	9.22347	9.37900	10951.56450	NaN	9.78430	0.01059	0.01059	288.08465	1.60200			287.07937	C13753		287.07285
552	230.24722	230.24739	230.24722	26.56200	26.52400	26.56200	0.00000	9.14767	9.45212	10936.91846	NaN	9.82803	0.00938	0.00938	230.24728	26.54933			229.24056			229.24057
1034	89.00384	89.00576	89.00384	1.06100	1.05800	1.06100	0.00000	9.36811	9.21637	10853.48088	NaN	9.00352	0.01123	0.01123	89.00448	1.06000	C19233		88.00798	C19208		88.00800

445	281.08115	281.08102	281.08115	34.10900	34.08200	34.10900	0.00000	8.98969	9.58590	10805.35646	NaN	9.15003	0.01040	0.01040	281.08111	34.10000			280.07354			280.07356
801	158.15343	158.15183	158.15343	27.44500	27.45400	27.44500	0.00000	9.06567	9.50815	10795.74565	NaN	9.81377	0.00914	0.00914	158.15289	27.44800	C07724		157.13275	C07674		157.13270
308	405.00937	405.01022	405.00937	3.40400	3.36600	3.40400	0.00000	9.19835	9.37434	10789.65806	NaN	11.62249	0.00858	0.00858	405.00965	3.39133	C00015	HMDB00295	404.00220	C00015	HMDB00295	404.00220
682	190.04782	190.04865	190.04782	1.74400	1.76500	1.74400	0.00000	9.26276	9.30287	10751.68545	NaN	8.40164	0.00834	0.00834	190.04810	1.75100	C08296		189.03860	C08373		189.03857
258	455.16003	455.16162	455.16003	9.64400	9.68800	9.64400	0.00000	9.25285	9.30854	10728.90441	NaN	10.58227	0.00996	0.00996	455.16056	9.65867			454.14885			454.14885
235	470.63034	470.62964	470.63034	9.63200	9.71200	9.63200	0.00000	9.25731	9.28763	10641.02506	NaN	9.41478	0.01077	0.01077	470.63011	9.65867	C18446		469.68850	C18481		469.68853
1090	81.52110	81.52120	81.52110	11.96300	11.97200	11.96300	0.00000	9.22796	9.31112	10609.89372	NaN	9.83439	0.00866	0.00866	81.52113	11.96600						
675	193.06876	193.06819	193.06876	7.60700	7.39200	7.60700	0.00000	8.94459	9.59377	10606.05337	NaN	9.96779	0.00868	0.00868	193.06857	7.53533	C00296	HMDB03072	192.06339	C01488		192.06339
431	294.15421	294.15411	294.15421	4.71100	4.66100	4.71100	0.00000	9.21244	9.26840	10305.36051	NaN	10.03633	0.00942	0.00942	294.15418	4.69433	C09222		293.14160	C09222		293.14158
864	136.06123	136.06183	136.06123	2.55600	2.54200	2.55600	0.00000	9.19727	9.27123	10241.96857	NaN	9.11328	0.01050	0.01050	136.06143	2.55133	C03059		135.05320	C06056		135.05320
568	225.09135	225.09155	225.09135	33.66200	33.64700	33.66200	0.00000	9.02267	9.43491	10186.16667	NaN	8.90647	0.01014	0.01014	225.09142	33.65700	C00766		224.08370	C01927		224.08370
251	461.21210	461.21137	461.21210	9.96200	10.01800	9.96200	0.00000	9.17908	9.27417	10164.18429	NaN	10.05635	0.01051	0.01051	461.21185	9.98067			460.20703			460.20703
495	258.12775	258.12601	258.12775	1.75600	1.75300	1.75600	0.00000	9.36997	9.07857	10140.26364	NaN	10.73956	0.01054	0.01054	258.12717	1.75500			257.11826			257.11757
701	186.07747	186.07925	186.07747	1.70900	1.70600	1.70900	0.00000	9.11020	9.31339	10014.56474	NaN	10.95019	0.01069	0.01069	186.07806	1.70800			185.08004	C19165		185.05891
1069	84.08001	84.08012	84.08001	0.70800	0.54000	0.70800	0.00000	9.39404	9.01023	9918.23524	NaN	9.90260	0.01044	0.01044	84.08005	0.65200			83.07350			83.07350
239	464.08148	464.08160	464.08148	10.71500	10.74800	10.71500	0.00000	9.08689	9.29717	9818.54225	NaN	11.05253	0.00892	0.00892	464.08152	10.72600	C03794	HMDB00536	463.07400	C03794	HMDB00536	463.07404
236	468.30728	468.30759	468.30728	37.64100	37.68500	37.64100	0.00000	9.06634	9.31339	9797.34095	NaN	9.71155	0.00982	0.00982	468.30738	37.65567			467.30115		HMDB10379	467.30115
945	114.09138	114.09161	114.09138	8.94900	9.01700	8.94900	0.00000	9.38674	8.97937	9730.85948	NaN	9.86709	0.01012	0.01012	114.09145	8.97167			113.08406	C05853		113.08406
961	111.02097	111.02123	111.02097	39.91300	39.89800	39.91300	0.00000	9.32817	9.03785	9730.36462	NaN	11.13840	0.01033	0.01033	111.02106	39.90800	C18448		110.01328	C19484		110.01328
129	774.55493	774.55237	774.55493	38.71200	38.62700	38.71200	0.00000	10.07374	8.26978	9621.53182	NaN	12.40642	0.01057	0.01057	774.55408	38.68367		HMDB09710	773.53595		HMDB09711	773.53595
313	401.11478	401.11359	401.11478	14.21200	14.25600	14.21200	0.00000	9.08301	9.25608	9600.25825	NaN	10.81311	0.01018	0.01018	401.11438	14.22667	C03725		400.10690			400.10692
677	192.03668	192.03714	192.03668	1.07300	1.08200	1.07300	0.00000	9.18372	9.14778	9563.86977	NaN	10.92179	0.01053	0.01053	192.03684	1.07600	C17938		191.02190			191.02186
629	204.08675	204.08704	204.08675	8.83200	8.89900	8.83200	0.00000	9.60833	8.71260	9513.47910	NaN	10.42887	0.01024	0.01024	204.08684	8.85433			203.07937	C12986		203.07940
914	121.05084	121.05080	121.05084	36.28700	36.33100	36.28700	0.00000	8.81441	9.50111	9487.79635	NaN	10.00312	0.00932	0.00932	121.05082	36.30167		HMDB01366	120.04359		HMDB01366	120.04360
166	604.29340	604.29480	604.29340	9.63200	9.71200	9.63200	0.00000	9.05478	9.25663	9468.29726	NaN	10.34535	0.00777	0.00777	604.29386	9.65867	C11365		603.28190			603.36186
454	276.11881	276.11981	276.11881	1.66200	1.67000	1.66200	0.00000	9.10804	9.17219	9321.81064	NaN	10.00464	0.01115	0.01115	276.11914	1.66467	C05283		275.11170	C18048		275.11170
457	273.03665	273.03742	273.03665	1.62600	1.63500	1.62600	0.00000	9.17599	9.09393	9273.89020	NaN	9.19255	0.00914	0.00914	273.03691	1.62900			272.03209	C07756		272.04669
749	180.15921	180.15894	180.15921	18.08500	18.05900	18.08500	0.00000	8.83509	9.42016	9206.16052	NaN	8.46836	0.01007	0.01007	180.15912	18.07633			179.16739			179.16739
860	137.04602	137.04630	137.04602	9.40800	9.46400	9.40800	0.00000	9.05733	9.19303	9183.63147	NaN	8.85884	0.00945	0.00945	137.04611	9.42667	C00262	HMDB00157	136.03850	C00262	HMDB00157	136.03851
1075	83.05085	83.05564	83.05085	5.73500	5.45000	5.73500	0.00000	9.31776	8.92466	9147.25770	NaN	10.79672	0.00886	0.00886	83.05245	5.64000		HMDB13749	82.04186	C08389		82.05310
770	171.14807	171.14769	171.14807	19.79300	19.74200	19.79300	0.00000	8.94339	9.29558	9131.47208	NaN	9.82164	0.01115	0.01115	171.14794	19.77600			170.14191	C03092		170.13070
333	372.54675	372.54691	372.54675	7.89000	7.95700	7.89000	0.00000	9.12439	9.11210	9120.18490	NaN	11.97650	0.00866	0.00866	372.54680	7.91233			371.38426			371.38395
507	251.16780	251.16701	251.16780	26.59800	26.60600	26.59800	0.00000	8.95127	9.26986	9050.41959	NaN	10.63931	0.00708	0.00708	251.16754	26.60067	C05318		250.15960	C07020		250.15690
218	493.10800	493.10846	493.10800	11.39800	11.40700	11.39800	0.00000	8.92693	9.26526	8920.40085	NaN	10.30990	0.01148	0.01148	493.10815	11.40100	C19370		492.10389	C18901		492.10390
376	340.02768	340.02554	340.02768	30.11800	30.10300	30.11800	0.00000	8.99394	9.19016	8884.38187	NaN	9.25274	0.01063	0.01063	340.02697	30.11300	C18916		339.01958	C18916		339.01960
784	166.06952	166.06947	166.06952	4.51100	4.46100	4.51100	0.00000	9.00463	9.17307	8855.97935	NaN	9.81220	0.00912	0.00912	166.06950	4.49433		HMDB13141	165.06506		HMDB01182	165.06506
934	116.05338	116.05406	116.05338	34.53300	34.49400	34.53300	0.00000	8.83717	9.32706	8796.55909	NaN	11.33050	0.01064	0.01064	116.05360	34.52000	C00148	HMDB00162	115.06330	C00763	HMDB03411	115.06330
1019	90.05534	90.05515	90.05534	1.85000	1.85900	1.85000	0.00000	9.12024	9.04146	8785.38829	NaN	9.09834	0.01074	0.01074	90.05528	1.85300	C00099	HMDB00056	89.04768	C00041	HMDB00161	89.04768
381	333.05634	333.05435	333.05634	7.96000	8.01600	7.96000	0.00000	8.69992	9.43197	8655.46988	NaN	12.53396	0.00937	0.00937	333.05567	7.97867		HMDB06555	332.05219			332.05219
240	463.64185	463.63892	463.64185	10.25600	10.32400	10.25600	0.00000	9.01117	9.11885	8647.36971	NaN	9.10406	0.00958	0.00958	463.64087	10.27867						
430	294.15503	294.15512	294.15503	5.35800	5.28500	5.35800	0.00000	9.06934	9.05248	8611.96910	NaN	9.45997	0.01013	0.01013	294.15506	5.33367	C07325	HMDB05035	293.15280	C07325	HMDB05035	293.15280
1030	89.50707	89.50726	89.50707	11.86900	11.89000	11.86900	0.00000	9.17550	8.93299	8554.75841	NaN	11.32511	0.01032	0.01032	89.50713	11.87600						
763	174.02376	174.02388	174.02376	1.04900	1.04600	1.04900	0.00000	9.16185	8.91643	8426.51905	NaN	7.61294	0.00951	0.00951	174.02380	1.04800	C06333		173.01470	C06334		173.01470
679	191.07671	191.07716	191.07671	1.28500	1.28200	1.28500	0.00000	9.04992	9.02765	8423.55867	NaN	9.53288	0.01142	0.01142	191.07686	1.28400	C17220		190.06640			190.06637
660	199.14356	199.14378	199.14356	8.96100	9.02900	8.96100	0.00000	9.27892	8.78920	8383.83247	NaN	12.05312	0.00916	0.00916	199.14363	8.98367	C06185		198.13680	C10858	HMDB06548	198.13683
452	278.06403	278.06360	278.06403	1.73200	1.74100	1.73200	0.00000	9.03612	9.03011	8375.91071	NaN	10.78476	0.01056	0.01056	278.06388	1.73500			277.05864	C08249		277.05890
145	666.13049	666.13257	666.13049	10.55000	10.60600	10.55000	0.00000	9.05665	9.00413	8353.12369	NaN	10.30320	0.01037	0.01037	666.13119	10.56867	C00004	HMDB01487	665.12476	C00004	HMDB01487	665.12478
335	368.02216	368.02121	368.02216	30.11800	30.10300	30.11800	0.00000	8.91289	9.12634	8263.58043	NaN	9.14019	0.00951	0.00951	368.02184	30.11300			367.01668			367.01668
369	347.24194	347.24249	347.24194	34.68600	34.69500	34.68600	0.00000	8.84293	9.18837	8230.88284	NaN	11.16086	0.01112	0.01112	347.24213	34.68900			346.23551			346.23551
1038	88.51086	88.51001	88.51086	1.02600	1.03500	1.02600	0.00000	9.13717	8.88568	8196.16001	NaN	10.89710	0.00922	0.00922	88.51058	1.02900						
494	258.89822	258.89996	258.89822	1.23800	1.23500	1.23800	0.00000	9.05027	8.96856	8179.71306	NaN	9.76907	0.00938	0.00938	258.89880	1.23700		HMDB12282	257.90955		HMDB12282	257.90956
150	649.07843	649.07733	649.07843	2.73300	2.74200	2.73300	0.00000	9.07640	8.94004	8169.96338	NaN	9.43430	0.00834	0.00834	649.07806	2.73600			648.08647			648.20535
130	752.07178	752.07251	752.07178	2.72100	2.71800	2.72100	0.00000	9.03425	8.96252	8090.01136	NaN	8.90737	0.00952	0.00952	752.07202	2.72000						
259	454.29236	454.29236	454.29236	35.05100	35.08300	35.05100	0.00000	8.82829	9.15015	8016.19630	NaN	10.69628	0.01098	0.01098	454.29236	35.06167			453.28550			453.28550
905	124.03671	124.03621	124.03671	1.12000	1.12900	1.12000	0.00000	9.06609	8.90804	7998.94832	NaN	10.83911	0.00879	0.00879	124.03655	1.12300	C00253	HMDB01488	123.03200	C06813		123.03200
1074	83.05180	83.05489	83.05180	6.53600	6.83900	6.53600	0.00000	9.40307	8.56704	7982.85175	NaN	10.99603	0.00894	0.00894	83.05283	6.63700		HMDB13749	82.04186	C08389		82.05310
685	187.00771	187.00803	187.00771	1.82600	1.83500	1.82600	0.00000	8.97918	8.97972	7938.24507	NaN	8.98600	0.00904	0.00904	187.00781	1.82900	C06679		185.99870			185.99868
111	922.00781	922.00928	922.00781	2.36800	2.35300	2.36800	0.00000	8.78032	9.15517	7845.91933	NaN	9.98004	0.01035	0.01035	922.00830	2.36300			921.15707	C14120		921.15710
883	130.04970	130.04997	130.04970	4.11000	4.07200	4.11000	0.00000	8.93376	8.97895	7757.00557	NaN	10.91874	0.01008	0.01008	130.04979	4.09733	C01879	HMDB00267	129.04259	C02237	HMDB00805	129.04259
134	739.17975	739.18323	739.17975	3.19200	3.16600	3.19200	0.00000	8.91378	8.99530	7742.95268	NaN	9.73921	0.00971	0.00971	739.18091	3.18333			738.20065			738.20073
1004	98.98447	98.98462	98.98447	2.34400	2.34100	2.34400	0.00000	9.02790	8.87664	7725.43358	NaN	9.24198	0.01190	0.01190	98.98452	2.34300	C00009	HMDB02142	97.97690	C00009	HMDB02142	97.97690
904	125.06234	125.07129	125.06234	9.85600	9.91200	9.85600	0.00000	8.87683	9.01516	7677.08761	NaN	9.78938	0.01032	0.01032	125.06532	9.87467	C17467	HMDB11724	124.05243			124.05243
382	332.32932	332.32947	332.32932	32.33100	32.29300	32.33100	0.00000	8.87007	9.01852	7664.03659	NaN	9.23113	0.01014	0.01014	332.32937	32.31833			331.28751			331.28751
288	422.14572	422.14374	422.14572	9.63200	9.70000	9.63200	0.00000	8.93276	8.94543	7624.30030	NaN	10.24457	0.01103	0.01103	422.14506	9.65467			421.14199			421.14199
230	476.21515	476.21393	476.21515	9.73800	9.80600	9.73800	0.00000	8.85517	9.01784	7604.55959	NaN	10.52064	0.00795	0.00795	476.21474	9.76067			475.21072			475.21072
1089	81.52113	81.52070	81.52113	9.27900	9.35800	9.27900	0.00000	8.94275	8.91008	7528.20776	NaN	8.87780	0.01061	0.01061	81.52099	9.30533						
270	441.15466	441.15363	441.15466	10.12700	10.17100	10.12700	0.00000	8.79614	9.05182	7509.92415	NaN	10.35109	0.01165	0.01165	441.15432	10.14167			440.14708			440.14708
1009	98.51241	98.51351	98.51241	0.97900	0.99900	0.97900	0.00000	9.03926	8.80114	7481.59589	NaN	11.16707	0.01021	0.01021	98.51277	0.98567						
909	122.96429	122.96366	122.96429	0.17800	0.17500	0.17800	0.00000	9.13806	8.68900	7431.84776	NaN	11.07042	0.00899	0.00899	122.96408	0.17700		HMDB12216	121.97128	C08270	HMDB12251	121.97129
877	132.00389	132.00230	132.00389	1.23800	1.25800	1.23800	0.00000	8.92037	8.84803	7217.04942	NaN	11.46328	0.01001	0.01001	132.00336	1.24467		HMDB01131	131.02184		HMDB01131	131.02185
237	468.01856	468.01889	468.01856	2.50900	2.47100	2.50900	0.00000	9.06473	8.70350	7216.41611	NaN	8.76338	0.00847	0.00847	468.01867	2.49633	C00458	HMDB00998	466.98961	C00458	HMDB00998	466.98960
578	220.11906	220.11774	220.11906	10.59800	10.61800	10.59800	0.00000	8.66907	9.07554	7131.69548	NaN	11.35683	0.00924	0.00924	220.11862	10.60467	C00864	HMDB00210	219.11070	C12276		219.11067
490	261.05188	261.05261	261.05188	30.13000	30.10300	30.13000	0.00000	8.41729	9.28703	6989.47212	NaN	10.29290	0.01005	0.01005	261.05212	30.12100	C07320		260.05070			260.05071
307	405.00980	405.00934	405.00980	3.79300	3.75400	3.79300	0.00000	8.91530	8.78434	6973.11949	NaN	8.51244	0.01150	0.01150	405.00964	3.78000	C00015	HMDB00295	404.00220	C00015	HMDB00295	404.00220
147	659.50678	659.50995	659.50678	35.91030	36.24900	35.91030	0.00000	7.54856	10.15090	6972.49219	NaN	9.55645	0.01074	0.01074	659.50783	36.02320			658.49371			658.49371

427	295.16892	295.16974	295.16892	1.68500	1.67000	1.68500	0.00000	8.91604	8.77358	6938.27393	NaN	10.01043	0.00988	0.00988	295.16919	1.68000			294.15796			294.15796
219	492.88281	492.88226	492.88281	1.17900	1.18800	1.17900	0.00000	8.95427	8.73515	6937.56167	NaN	11.72378	0.00858	0.00858	492.88263	1.18200			491.96679			491.96685
438	289.13858	289.13931	289.13858	6.57100	6.48600	6.57100	0.00000	8.70272	8.96434	6860.45516	NaN	10.47908	0.00848	0.00848	289.13882	6.54267	C17720		288.12630	C17786		288.12626
818	151.08823	151.08968	151.08823	14.91800	14.93900	14.91800	0.00000	8.61950	9.03485	6816.98567	NaN	9.03825	0.01020	0.01020	151.08871	14.92500			150.07931			150.07931
110	922.01086	922.00995	922.01086	11.88100	11.87800	11.88100	0.00000	8.86043	8.79235	6811.64978	NaN	10.78156	0.01021	0.01021	922.01056	11.88000			921.15707	C14120		921.15710
359	353.08505	353.08524	353.08505	1.60300	1.60000	1.60300	0.00000	8.83443	8.79125	6719.98977	NaN	9.31202	0.01068	0.01068	353.08511	1.60200			352.07693	C19562		352.07690
437	289.14462	289.14404	289.14462	12.75200	12.74900	12.75200	0.00000	8.67528	8.92975	6650.93951	NaN	10.14643	0.01174	0.01174	289.14443	12.75100			288.13620	C09942		288.13620
1017	93.03767	93.03690	93.03767	3.25100	3.24800	3.25100	0.00000	8.77836	8.80034	6563.96585	NaN	10.11268	0.00997	0.00997	93.03741	3.25000	C00116	HMDB00131	92.04730	C00116	HMDB00131	92.04734
106	922.01062	922.01007	922.01062	7.10100	6.86200	7.10100	0.00000	9.42109	8.15449	6553.71337	NaN	9.47496	0.00982	0.00982	922.01044	7.02133			921.15707	C14120		921.15710
742	181.98924	181.98921	181.98924	1.07300	1.04600	1.07300	0.00000	8.86922	8.69942	6531.02888	NaN	10.97899	0.00879	0.00879	181.98923	1.06400	C10996		181.00199	C10910		181.00200
684	187.12630	187.12714	187.12630	25.12600	25.09900	25.12600	0.00000	8.49139	9.07550	6525.31644	NaN	8.86009	0.00944	0.00944	187.12658	25.11700	C09089		186.11570	C14701		186.11570
1087	81.52151	81.52111	81.52151	11.43300	11.44200	11.43300	0.00000	8.99210	8.55838	6471.99733	NaN	7.80002	0.01191	0.01191	81.52138	11.43600						
436	289.13959	289.13937	289.13959	4.67600	4.62500	4.67600	0.00000	8.67210	8.87343	6456.00401	NaN	7.09751	0.00966	0.00966	289.13952	4.65900	C09943		288.13616			288.13620
254	457.11057	457.11160	457.11057	15.67200	15.69200	15.67200	0.00000	8.65273	8.88350	6426.05792	NaN	10.49338	0.00934	0.00934	457.11091	15.67867	C00061	HMDB01520	456.10460	C00061	HMDB01520	456.10461
1088	81.52148	81.52126	81.52148	8.96100	9.01700	8.96100	0.00000	8.74243	8.77709	6372.58884	NaN	9.24913	0.01018	0.01018	81.52141	8.97967						
935	115.03851	115.03899	115.03851	1.54400	1.54100	1.54400	0.00000	8.70342	8.81054	6354.89873	NaN	8.20325	0.00916	0.00916	115.03867	1.54300			114.03168			114.03168
149	655.14728	655.14734	655.14728	1.59100	1.60000	1.59100	0.00000	8.74931	8.76419	6353.41931	NaN	10.17144	0.01046	0.01046	655.14730	1.59400			654.14314			654.14321
161	608.08655	608.08832	608.08655	9.85600	9.92300	9.85600	0.00000	8.85187	8.61425	6204.68427	NaN	10.65577	0.01142	0.01142	608.08714	9.87833	C00203	HMDB00304	607.08148	C00043	HMDB00290	607.08154
968	107.06998	107.07049	107.06998	2.73300	2.71800	2.73300	0.00000	8.79774	8.66123	6182.54987	NaN	8.97176	0.00896	0.00896	107.07015	2.72800	C14743		106.06299	C14689		106.06300
472	268.14130	268.14200	268.14130	3.27500	3.23600	3.27500	0.00000	8.77822	8.67533	6165.79637	NaN	9.35214	0.01017	0.01017	268.14153	3.26200	C09160		267.13716	C09160		267.13720
988	101.06193	101.06335	101.06193	9.99700	10.02900	9.99700	0.00000	8.39018	9.05700	6146.21904	NaN	11.87950	0.00992	0.00992	101.06240	10.00767	C12518		100.05243		HMDB01862	100.05243
272	439.19251	439.19220	439.19251	9.71500	9.77000	9.71500	0.00000	8.64692	8.79840	6140.50723	NaN	11.10253	0.01006	0.01006	439.19240	9.73333			438.18092			438.18092
297	415.03836	415.04123	415.03836	1.68500	1.69400	1.68500	0.00000	8.76121	8.68272	6136.20721	NaN	9.72924	0.00889	0.00889	415.03932	1.68800			414.03223	C10943		414.04008
769	171.99353	171.99435	171.99353	1.04900	1.05800	1.04900	0.00000	8.61907	8.82406	6133.77741	NaN	11.52065	0.00822	0.00822	171.99381	1.05200	C13672		170.98445	C13058		170.98440
913	121.05090	121.05085	121.05090	9.85600	9.93500	9.85600	0.00000	7.87738	9.48861	5901.70121	NaN	7.98335	0.00958	0.00958	121.05088	9.88233		HMDB01366	120.04359		HMDB01366	120.04360
606	208.06383	208.06508	208.06383	3.15700	3.13000	3.15700	0.00000	8.61505	8.74010	5869.80199	NaN	9.86393	0.00909	0.00909	208.06425	3.14800	C14876		207.05650			207.05653
162	608.08893	608.08673	608.08893	9.31400	9.46400	9.31400	0.00000	8.71048	8.64430	5868.71113	NaN	10.71552	0.00937	0.00937	608.08820	9.36400	C00203	HMDB00304	607.08148	C00043	HMDB00290	607.08154
410	310.09580	310.09576	310.09580	16.68400	16.63400	16.68400	0.00000	8.52802	8.82459	5862.33355	NaN	9.79902	0.01096	0.01096	310.09579	16.66733	C08494		309.08490	C12255		309.08490
337	365.05014	365.04923	365.05014	7.19500	7.08600	7.19500	0.00000	8.59348	8.75176	5840.79749	NaN	10.37406	0.00866	0.00866	365.04984	7.15867	C00655	HMDB01554	364.04202			364.04202
782	166.10754	166.10802	166.10754	8.07800	8.11000	8.07800	0.00000	8.68200	8.65524	5817.47557	NaN	9.11262	0.01141	0.01141	166.10770	8.08867	C02765	HMDB01943	165.11536	C06199	HMDB04366	165.11536
221	489.14966	489.14853	489.14966	9.93800	10.01800	9.93800	0.00000	8.60187	8.71918	5770.55843	NaN	8.58088	0.01068	0.01068	489.14928	9.96467			488.13820	C10737		488.13190
202	521.06757	521.07007	521.06757	1.63800	1.64700	1.63800	0.00000	8.72465	8.59174	5757.12551	NaN	9.34704	0.00978	0.00978	521.06840	1.64100			520.07939	C10392		520.07939
630	204.08748	204.08804	204.08748	10.28000	10.31200	10.28000	0.00000	8.55357	8.74326	5701.10796	NaN	9.44038	0.00895	0.00895	204.08767	10.29067	C12986		203.07940			203.07937
1028	89.50745	89.50717	89.50745	9.87900	10.10000	9.87900	0.00000	8.55741	8.73618	5691.86787	NaN	10.00108	0.01097	0.01097	89.50736	9.95267						
723	184.13309	184.13385	184.13309	9.45600	9.52300	9.45600	0.00000	8.73411	8.55397	5676.22881	NaN	10.23745	0.01138	0.01138	184.13334	9.47833	C12452		183.12590	C12453		183.12590
628	204.08923	204.08710	204.08923	9.78500	9.85300	9.78500	0.00000	8.58550	8.69608	5657.78573	NaN	10.97374	0.01051	0.01051	204.08852	9.80767	C15383		203.08070			203.08071
827	148.06503	148.07349	148.06503	9.93800	9.99400	9.93800	0.00000	8.48423	8.77630	5598.56856	NaN	10.27209	0.01052	0.01052	148.06785	9.95667			147.06439	C08268		147.06439
1043	86.09713	86.09721	86.09713	34.28600	34.18800	34.28600	0.00000	9.02747	8.22284	5570.00753	NaN	6.39094	0.01092	0.01092	86.09716	34.25333	C03219		85.08915	C01746		85.08910
420	302.06360	302.06461	302.06360	1.62600	1.63500	1.62600	0.00000	8.60534	8.62051	5502.32649	NaN	10.55201	0.00885	0.00885	302.06394	1.62900			301.05627			301.05627
326	385.12912	385.12994	385.12912	7.59500	7.40400	7.59500	0.00000	8.37551	8.83249	5453.43466	NaN	11.14736	0.01039	0.01039	385.12940	7.53133	C00021	HMDB00939	384.12158	C00021	HMDB00939	384.12159
416	303.15247	303.15015	303.15247	15.22400	15.19800	15.22400	0.00000	8.40156	8.80499	5449.46135	NaN	10.55469	0.00976	0.00976	303.15169	15.21533	C17729		302.14191	C17729		302.14190
531	242.18332	242.18480	242.18332	9.87900	9.91200	9.87900	0.00000	8.56105	8.64248	5441.26405	NaN	9.43730	0.01078	0.01078	242.18381	9.89000			241.18305	C11788		241.18310
107	922.00989	922.01056	922.00989	9.82100	9.87600	9.82100	0.00000	8.78363	8.41719	5433.87263	NaN	10.07846	0.00911	0.00911	922.01011	9.83933			921.15707	C14120		921.15710
329	379.17166	379.17175	379.17166	9.95000	9.99400	9.95000	0.00000	8.61219	8.58220	5416.44515	NaN	10.12271	0.01032	0.01032	379.17169	9.96467			378.16782			378.16785
838	146.00140	146.00177	146.00140	0.96700	1.05800	0.96700	0.00000	8.69278	8.48532	5372.49362	NaN	10.23132	0.00895	0.00895	146.00153	0.99733	C19345		144.99460	C19324		144.99460
108	922.01093	922.01025	922.01093	11.39800	11.27700	11.39800	0.00000	8.74252	8.43399	5368.22844	NaN	9.42685	0.01045	0.01045	922.01070	11.35767			921.15707	C14120		921.15710
715	185.13059	185.13355	185.13059	0.82600	0.92900	0.82600	0.00000	8.47919	8.68678	5340.02251	NaN	8.90946	0.00847	0.00847	185.13157	0.86033	C17235		184.12520	C09633		184.12520
181	572.17328	572.17444	572.17328	10.25600	10.31200	10.25600	0.00000	8.48497	8.63877	5228.42422	NaN	10.50197	0.01089	0.01089	572.17367	10.27467	C19379		571.16010			571.16005
306	405.01022	405.00842	405.01022	8.94900	8.71100	8.94900	0.00000	8.60690	8.50891	5207.76527	NaN	11.38649	0.01102	0.01102	405.00962	8.86967	C00015	HMDB00295	404.00220	C00015	HMDB00295	404.00220
670	197.04054	197.03716	197.04054	1.07300	1.05800	1.07300	0.00000	8.46212	8.63731	5165.26290	NaN	10.07773	0.01048	0.01048	197.03941	1.06800	C09315	HMDB13727	196.03717			196.03717
624	206.11885	206.11961	206.11885	2.38000	2.35300	2.38000	0.00000	8.63468	8.43874	5098.55153	NaN	9.04249	0.01216	0.01216	206.11911	2.37100	C10846		205.11030			205.11028
581	219.08516	219.08543	219.08516	15.44800	15.39800	15.44800	0.00000	8.48673	8.58236	5087.51863	NaN	11.24052	0.00881	0.00881	219.08525	15.43133			218.07901			218.07904
546	233.12399	233.12413	233.12399	4.86400	4.67300	4.86400	0.00000	8.45162	8.60997	5068.47058	NaN	8.41329	0.00949	0.00949	233.12404	4.80033			232.11332	C17232		232.11330
146	664.11530	664.11902	664.11530	2.61500	2.57700	2.61500	0.00000	8.51655	8.53056	5031.91298	NaN	10.54604	0.00979	0.00979	664.11654	2.60233	C00003	HMDB00902	663.10913	C01221		663.24766
533	241.21515	241.21399	241.21515	33.16700	33.22300	33.16700	0.00000	8.27735	8.75577	4996.84369	NaN	8.67100	0.00891	0.00891	241.21476	33.18567	C17676		240.20890			240.20892
321	389.09677	389.09348	389.09677	1.69700	1.70550	1.69700	0.00000	8.45950	8.55606	4953.16058	NaN	10.96688	0.01041	0.01041	389.09567	1.69983			388.09067			388.09067
1003	98.98462	98.98435	98.98462	2.92100	2.87100	2.92100	0.00000	8.61370	8.39804	4943.71393	NaN	9.72634	0.00849	0.00849	98.98453	2.90433	C00009	HMDB02142	97.97690	C00009	HMDB02142	97.97690
817	151.53832	151.53954	151.53832	30.11800	30.11500	30.11800	0.00000	8.25450	8.74974	4925.18207	NaN	10.32324	0.01035	0.01035	151.53872	30.11700						
282	428.21423	428.21286	428.21423	1.61400	1.61100	1.61400	0.00000	8.67337	8.32689	4915.40782	NaN	9.34286	0.00883	0.00883	428.21378	1.61300			427.21072			427.21072
726	184.13265	184.13290	184.13265	11.96300	11.90100	11.96300	0.00000	7.91281	9.08314	4904.81311	NaN	11.77870	0.01177	0.01177	184.13273	11.94233	C12452		183.12590	C12453		183.12590
1010	97.04453	97.04298	97.04453	2.73300	2.74200	2.73300	0.00000	8.49248	8.49184	4876.37787	NaN	9.44740	0.01012	0.01012	97.04401	2.73600	C11272		96.03750	C11488		96.03753
305	405.01044	405.00824	405.01044	8.34900	8.44000	8.34900	0.00000	8.47747	8.50356	4868.36669	NaN	9.26951	0.00960	0.00960	405.00971	8.37933	C00015	HMDB00295	404.00220	C00015	HMDB00295	404.00220
662	199.14380	199.14446	199.14380	11.95100	11.89000	11.95100	0.00000	8.01738	8.96259	4865.79225	NaN	10.89220	0.01044	0.01044	199.14402	11.93067	C06185		198.13680	C10858	HMDB06548	198.13683
179	572.66351	572.66437	572.66351	10.85700	10.90100	10.85700	0.00000	8.39633	8.57847	4853.23404	NaN	10.19684	0.00947	0.00947	572.66380	10.87167			571.47532			
266	445.05585	445.05603	445.05585	1.67300	1.69400	1.67300	0.00000	8.60913	8.36454	4850.48033	NaN	8.40021	0.00884	0.00884	445.05591	1.68000			444.04057	C13962		444.01032
1065	84.08078	84.08027	84.08078	7.26600	7.22700	7.26600	0.00000	9.01352	7.91424	4740.41810	NaN	10.51216	0.01105	0.01105	84.08061	7.25300			83.07350			83.07350
1086	81.52078	81.52136	81.52078	10.02100	10.06500	10.02100	0.00000	8.71760	8.15935	4621.50886	NaN	10.03801	0.00930	0.00930	81.52097	10.03567						
238	464.11929	464.11835	464.11929	1.63800	1.64700	1.63800	0.00000	8.39025	8.47921	4604.22687	NaN	10.62546	0.01127	0.01127	464.11898	1.64100			463.11146			463.11146
1067	84.08064	84.08024	84.08064	8.10200	8.08700	8.10200	0.00000	8.50124	8.36202	4589.97627	NaN	9.49445	0.00942	0.00942	84.08050	8.09700			83.07350			83.07350
714	185.13310	185.13280	185.13310	8.97300	9.00500	8.97300	0.00000	8.29761	8.55941	4575.68337	NaN	10.90459	0.01031	0.01031	185.13300	8.98367	C17235		184.12520	C09633		184.12520
176	573.07062	573.06464	573.07062	1.65000	1.65900	1.65000	0.00000	8.52274	8.33243	4571.44189	NaN	9.26194	0.01062	0.01062	573.06862	1.65300			572.04721			572.04714
133	739.18256	739.18341	739.18256	3.59200	3.56600	3.59200	0.00000	8.22741	8.61987	4553.44247	NaN	11.90051	0.00856	0.00856	739.18284	3.58333			738.20065			738.20073
661	199.14185	199.14446	199.14185	9.27900	9.51100	9.27900	0.00000	7.91431	8.93155	4550.23414	NaN	9.79845	0.01098	0.01098	199.14272	9.35633	C06185		198.13680	C10858	HMDB06548	198.13683
943	114.09172	114.09116	114.09172	8.06600	8.08700	8.06600	0.00000	8.52941	8.29811	4508.67677	NaN	11.07312	0.00887	0.00887	114.09153	8.07300			113.08406	C05853		113.08406
856	140.96413	140.96257	140.96413	1.04900	1.04600	1.04900	0.00000	8.51540	8.30463	4491.82126	NaN	8.46130	0.00805	0.00805	140.96361	1.04800	C07294	HMDB12258	139.94550	C07295	HMDB12259	139.94547

152	647.10968	647.10974	647.10968	8.23100	8.25200	8.23100	0.00000	8.30964	8.50940	4489.59863	NaN	10.27751	0.01092	0.01092	647.10970	8.23800	C19965		646.19560			646.19564
862	136.07291	136.07326	136.07291	1.14400	1.14100	1.14400	0.00000	8.70441	8.11176	4483.18291	NaN	8.82940	0.01028	0.01028	136.07302	1.14300	C02505	HMDB10715	135.06840	C07565		135.06840
501	255.00514	255.00493	255.00514	4.35800	4.30800	4.35800	0.00000	8.37308	8.44020	4476.69581	NaN	10.04598	0.01055	0.01055	255.00507	4.34133	C18479		254.00137	C18458		254.00140
123	843.23969	843.23834	843.23969	11.38600	11.41900	11.38600	0.00000	8.28356	8.49882	4408.06063	NaN	8.64750	0.00968	0.00968	843.23924	11.39700			842.19056			842.19056
292	422.03696	422.03485	422.03696	2.98000	2.96500	2.98000	0.00000	8.38561	8.38559	4383.47827	NaN	10.07529	0.01023	0.01023	422.03626	2.97500	C07758		421.03779	C07758		421.03780
447	280.20853	280.20895	280.20853	10.40900	10.48900	10.40900	0.00000	8.42100	8.34955	4382.04116	NaN	10.24678	0.01038	0.01038	280.20867	10.43567		HMDB12535	279.19601	C09923		279.18344
656	199.14325	199.14426	199.14325	2.59200	2.58900	2.59200	0.00000	8.71475	8.05118	4371.95689	NaN	11.43276	0.00955	0.00955	199.14359	2.59100	C06185		198.13680	C10858	HMDB06548	198.13683
657	199.14388	199.14438	199.14388	30.01200	30.03200	30.01200	0.00000	8.51739	8.23655	4345.81386	NaN	10.32322	0.01078	0.01078	199.14404	30.01867	C06185		198.13680	C10858	HMDB06548	198.13683
564	227.17421	227.17429	227.17421	12.56400	12.53700	12.56400	0.00000	8.34379	8.40126	4326.55623	NaN	10.85568	0.00948	0.00948	227.17424	12.55500	C04277		226.16810			226.16813
456	274.09177	274.09079	274.09177	3.02700	3.02400	3.02700	0.00000	8.30363	8.39538	4228.09247	NaN	10.06156	0.01111	0.01111	274.09144	3.02600			273.08235	C10849		273.08570
786	165.11417	165.11351	165.11417	10.46800	10.54700	10.46800	0.00000	8.42087	8.27684	4225.35622	NaN	9.66858	0.01035	0.01035	165.11395	10.49433			164.10620			164.10485
906	123.04665	123.04019	123.04665	13.22300	13.24400	13.22300	0.00000	8.07582	8.58182	4141.51547	NaN	10.58534	0.01035	0.01035	123.04450	13.23000	C02037	HMDB11733	122.03678	C03098		122.03678
342	362.08542	362.08600	362.08542	7.90100	7.91000	7.90100	0.00000	8.14370	8.51242	4138.38965	NaN	10.44767	0.00806	0.00806	362.08561	7.90400	C11031		361.07170	C11024		361.07170
1027	89.50723	89.50687	89.50723	29.89400	29.86800	29.89400	0.00000	8.16880	8.48195	4127.27623	NaN	9.21774	0.00769	0.00769	89.50711	29.88533						
711	185.13072	185.13188	185.13072	9.27900	9.34700	9.27900	0.00000	8.35920	8.28749	4118.92115	NaN	9.71089	0.01071	0.01071	185.13111	9.30167	C17235		184.12520	C09633		184.12520
622	206.11862	206.11977	206.11862	4.38100	4.28400	4.38100	0.00000	8.33166	8.31153	4111.69588	NaN	8.38048	0.00923	0.00923	206.11900	4.34867	C10846		205.11030			205.11028
474	267.22629	267.22873	267.22629	31.44800	31.48000	31.44800	0.00000	8.20024	8.43051	4086.22776	NaN	8.23387	0.00987	0.00987	267.22710	31.45867			266.22457			266.22457
709	185.13074	185.13101	185.13074	1.83800	1.83500	1.83800	0.00000	8.40433	8.21237	4057.60696	NaN	9.62671	0.01029	0.01029	185.13083	1.83700	C17235		184.12520	C09633		184.12520
143	672.63318	672.63147	672.63318	9.63200	9.70000	9.63200	0.00000	8.34593	8.25252	4020.74910	NaN	9.62296	0.00866	0.00866	672.63261	9.65467		HMDB12321	671.53363			671.53362
103	922.00855	922.00769	922.00855	38.48900	38.79200	38.48900	0.00000	8.67890	7.91074	4003.09305	NaN	9.59459	0.00951	0.00951	922.00826	38.59000			921.15707	C14120		921.15710
165	605.27570	605.27081	605.27570	10.25600	10.30000	10.25600	0.00000	8.10652	8.47023	3977.36030	NaN	7.59360	0.01078	0.01078	605.27407	10.27067	C20137		604.25510	C08880		604.28831
322	388.94727	388.94763	388.94727	4.33400	4.29600	4.33400	0.00000	8.17396	8.39156	3955.09830	NaN	8.93761	0.00992	0.00992	388.94739	4.32133			387.96726			387.96726
160	608.08978	608.08698	608.08978	10.43300	10.46500	10.43300	0.00000	8.41818	8.13205	3924.96988	NaN	7.70435	0.00993	0.00993	608.08885	10.44367	C00203	HMDB00304	607.08148	C00043	HMDB00290	607.08154
475	267.22577	267.22690	267.22577	30.95400	31.01000	30.95400	0.00000	8.09587	8.44906	3914.57945	NaN	9.43986	0.00659	0.00659	267.22615	30.97267			266.22457			266.22457
997	100.07641	100.07675	100.07641	11.52800	11.44200	11.52800	0.00000	8.17121	8.36763	3902.67760	NaN	9.44615	0.01022	0.01022	100.07652	11.49933		HMDB11749	99.06841	C11249		99.06841
132	744.07983	744.08270	744.07983	7.87800	7.93400	7.87800	0.00000	8.26962	8.26709	3898.54017	NaN	10.31187	0.00986	0.00986	744.08079	7.89667	C00006	HMDB00217	743.07546			743.16699
814	153.04121	153.04324	153.04121	4.97000	4.86100	4.97000	0.00000	8.15960	8.37190	3888.36937	NaN	11.08899	0.01120	0.01120	153.04189	4.93367	C00385	HMDB00292	152.03343	C07599	HMDB00786	152.03343
174	575.94763	575.94794	575.94763	4.34600	4.29600	4.34600	0.00000	8.14713	8.37780	3875.62864	NaN	10.08147	0.01205	0.01205	575.94773	4.32933	C06886		575.00210	C06886		575.00215
680	190.07187	190.07268	190.07187	8.06600	8.07500	8.06600	0.00000	8.03324	8.48650	3865.57448	NaN	10.11945	0.00912	0.00912	190.07214	8.06900	C05379	HMDB03974	189.06372			189.06372
310	404.19431	404.19168	404.19431	9.64400	9.70000	9.64400	0.00000	8.21873	8.29349	3851.08557	NaN	10.32288	0.00996	0.00996	404.19343	9.66267			403.18557			403.18557
281	430.20804	430.20673	430.20804	10.45600	10.53600	10.45600	0.00000	8.18793	8.30775	3819.37525	NaN	10.49055	0.01045	0.01045	430.20760	10.48267			429.20122			429.20122
888	128.94035	128.93953	128.94035	1.02600	1.02300	1.02600	0.00000	8.47126	8.01775	3806.64462	NaN	10.05748	0.01088	0.01088	128.94008	1.02500	C19034		127.93765	C18902		127.93770
1025	89.50727	89.50734	89.50727	30.49400	30.58600	30.49400	0.00000	8.35285	8.12284	3781.38316	NaN	9.68832	0.00957	0.00957	89.50729	30.52467						
373	343.04242	343.04282	343.04242	1.65000	1.55250	1.65000	0.00000	8.07040	8.39287	3757.96054	NaN	10.81996	0.01106	0.01106	343.04255	1.61750	C18547		342.03270	C18547		342.03267
370	347.02609	347.02396	347.02609	2.73300	2.75300	2.73300	0.00000	8.32715	8.13443	3754.80259	NaN	10.25297	0.01130	0.01130	347.02538	2.73967	C18899		345.97800	C18899		345.97795
304	405.00900	405.00882	405.00900	9.43200	9.51100	9.43200	0.00000	8.24570	8.20612	3736.52076	NaN	8.21971	0.01055	0.01055	405.00894	9.45833	C00015	HMDB00295	404.00220	C00015	HMDB00295	404.00220
332	372.97546	372.97513	372.97546	4.33400	4.29600	4.33400	0.00000	8.04243	8.40395	3726.35936	NaN	11.24827	0.01041	0.01041	372.97535	4.32133	C18415		371.93514	C18404		371.93510
708	185.13072	185.13117	185.13072	8.19600	8.20500	8.19600	0.00000	8.25666	8.18959	3726.13192	NaN	10.39075	0.01120	0.01120	185.13087	8.19900	C17235		184.12520	C09633		184.12520
185	560.07684	560.07568	560.07684	2.73300	2.73000	2.73300	0.00000	8.31630	8.12662	3719.94142	NaN	8.94289	0.00784	0.00784	560.07646	2.73200		HMDB01178	559.07166		HMDB12276	559.07166
636	203.10396	203.10269	203.10396	7.26600	7.20400	7.26600	0.00000	8.05249	8.38007	3700.71279	NaN	9.46196	0.00981	0.00981	203.10354	7.24533	C06658		202.09540	C08271		202.09540
815	152.05634	152.05820	152.05634	3.72200	3.66000	3.72200	0.00000	8.18876	8.23928	3692.35595	NaN	10.34122	0.01006	0.01006	152.05696	3.70133	C00242	HMDB00132	151.04940	C00242	HMDB00132	151.04941
234	471.12198	471.12451	471.12198	10.25600	10.30000	10.25600	0.00000	8.13457	8.27263	3654.07816	NaN	7.94885	0.01004	0.01004	471.12282	10.27067			470.12125			470.12125
944	114.09003	114.09058	114.09003	2.42700	2.40000	2.42700	0.00000	8.00037	8.40057	3642.65917	NaN	8.52786	0.01022	0.01022	114.09021	2.41800			113.08406	C05853		113.08406
1064	84.08063	84.08081	84.08063	5.73500	5.70900	5.73500	0.00000	9.17466	7.21648	3624.85241	NaN	9.36214	0.01076	0.01076	84.08069	5.72633			83.07350			83.07350
955	113.05143	113.04911	113.05143	0.93200	0.92900	0.93200	0.00000	8.29112	8.07989	3588.55115	NaN	11.10055	0.00902	0.00902	113.05066	0.93100			112.03851	C01066		112.05240
816	152.05640	152.05791	152.05640	8.16000	8.19300	8.16000	0.00000	8.08043	8.28057	3570.64489	NaN	10.02718	0.00959	0.00959	152.05690	8.17100	C00242	HMDB00132	151.04940	C00242	HMDB00132	151.04941
257	456.64410	456.64453	456.64410	10.24400	10.31200	10.24400	0.00000	8.08028	8.26876	3549.35895	NaN	9.80133	0.01152	0.01152	456.64425	10.26667			455.74065	C18180		455.74070
139	712.48743	712.48596	712.48743	37.00500	36.64900	37.00500	0.00000	8.65419	7.69425	3548.27697	NaN	8.97278	0.01007	0.01007	712.48694	36.88633			711.48386			711.48386
1033	89.07188	89.07063	89.07188	2.96800	2.96500	2.96800	0.00000	8.11874	8.22033	3531.69633	NaN	10.76329	0.01040	0.01040	89.07147	2.96700	C16364		88.06366	C19299		88.06366
987	101.06408	101.06739	101.06408	9.31400	9.38200	9.31400	0.00000	7.83717	8.49475	3519.09954	NaN	9.50259	0.00996	0.00996	101.06518	9.33667	C12518		100.05243		HMDB01862	100.05243
887	130.01979	130.02206	130.01979	0.80200	1.03500	0.80200	0.00000	8.36589	7.96483	3516.98581	NaN	9.18520	0.01033	0.01033	130.02055	0.87967	C06554		129.01740	C06560		129.01744
366	348.06940	348.07040	348.06940	6.91200	6.74500	6.91200	0.00000	7.99509	8.33128	3509.34608	NaN	9.27451	0.01012	0.01012	348.06973	6.85633	C00020	HMDB00045	347.06308	C00362	HMDB01044	347.06308
104	922.01050	922.01056	922.01050	14.49500	14.19700	14.49500	0.00000	8.37729	7.93367	3482.41290	NaN	10.30488	0.01048	0.01048	922.01052	14.39567			921.15707	C14120		921.15710
941	114.09215	114.09242	114.09215	39.91300	39.91000	39.91300	0.00000	8.18404	8.11904	3468.71191	NaN	9.93361	0.00926	0.00926	114.09224	39.91200	C06593		113.08410			113.08406
836	146.06851	146.06908	146.06851	12.26900	12.26600	12.26900	0.00000	8.05195	8.24357	3455.62348	NaN	10.12032	0.00922	0.00922	146.06870	12.26800	C02796		145.05280	C06324		145.05280
659	199.14362	199.14371	199.14362	9.87900	10.02900	9.87900	0.00000	7.84107	8.43964	3430.13214	NaN	10.80829	0.01032	0.01032	199.14365	9.92900	C06185		198.13680	C10858	HMDB06548	198.13683
757	176.98030	176.98930	176.98030	1.01400	1.03500	1.01400	0.00000	7.99863	8.28132	3428.84634	NaN	8.17769	0.01053	0.01053	176.98330	1.02100	C03572		175.98760	C03585		175.98760
440	284.04761	284.05054	284.04761	1.63800	1.63500	1.63800	0.00000	8.16163	8.11215	3418.26733	NaN	9.99450	0.01074	0.01074	284.04858	1.63700	C12987		283.04570			283.04570
392	327.05017	327.05231	327.05017	1.25000	1.25800	1.25000	0.00000	8.14485	8.11817	3399.93758	NaN	10.44535	0.01075	0.01075	327.05088	1.25267			326.04265			326.04265
505	253.17712	253.17876	253.17712	10.44400	10.50000	10.44400	0.00000	8.22124	8.03650	3390.96838	NaN	9.83135	0.00990	0.00990	253.17767	10.46267	C09645		252.17250	C16504		252.17250
303	405.00806	405.00977	405.00806	4.75800	4.50800	4.75800	0.00000	8.31649	7.93735	3384.36382	NaN	8.90399	0.01066	0.01066	405.00863	4.67467	C00015	HMDB00295	404.00220	C00015	HMDB00295	404.00220
972	103.08189	103.07501	103.08189	8.07800	8.11000	8.07800	0.00000	7.87011	8.33587	3304.33692	NaN	10.56179	0.00997	0.00997	103.07960	8.08867	C00803	HMDB00892	102.06810	C08262	HMDB00718	102.06810
486	267.20642	267.20679	267.20642	0.82600	0.62300	0.82600	0.00000	7.80295	8.40193	3302.51853	NaN	9.36049	0.00910	0.00910	267.20654	0.75833			266.19943	C04834		266.18820
658	199.14455	199.14412	199.14455	11.51600	11.30100	11.51600	0.00000	7.95674	8.24025	3289.51327	NaN	9.86573	0.01046	0.01046	199.14440	11.44433	C06185		198.13680	C10858	HMDB06548	198.13683
655	199.14323	199.14314	199.14323	29.54100	29.17300	29.54100	0.00000	8.21284	7.97205	3269.67407	NaN	11.78134	0.01049	0.01049	199.14320	29.41833	C06185		198.13680	C10858	HMDB06548	198.13683
995	100.07969	100.07888	100.07969	39.91300	39.89800	39.91300	0.00000	8.18427	7.99269	3256.72788	NaN	8.84792	0.01011	0.01011	100.07942	39.90800		HMDB11749	99.06841	C11249		99.06841
973	103.03925	103.04025	103.03925	4.49900	4.48400	4.49900	0.00000	8.01803	8.15136	3244.42836	NaN	11.41924	0.00984	0.00984	103.03958	4.49400	C00109	HMDB00005	102.03170	C00164	HMDB00060	102.03170
562	227.98232	227.98270	227.98232	0.99100	1.02300	0.99100	0.00000	8.04857	8.11117	3228.81202	NaN	9.81493	0.01131	0.01131	227.98244	1.00167	C01557		226.99047	C12469		226.99850
826	148.05978	148.06128	148.05978	4.11000	4.08400	4.11000	0.00000	8.08523	8.07128	3223.59225	NaN	9.67564	0.00933	0.00933	148.06028	4.10133			147.05316			147.05316
424	298.99655	298.99747	298.99655	1.66200	1.56433	1.66200	0.00000	8.14265	8.01380	3223.49280	NaN	10.38628	0.00831	0.00831	298.99686	1.62944			297.98488	C07695		297.94900
798	158.96182	158.96223	158.96182	8.63125	8.24000	8.63125	0.00000	7.91950	8.23401	3218.76105	NaN	8.13998	0.01127	0.01127	158.96196	8.50083	C19212		157.97238	C19164		157.97240
135	729.04547	729.04395	729.04547	2.78000	2.78900	2.78000	0.00000	8.11214	8.02683	3195.45760	NaN	9.60499	0.00928	0.00928	729.04496	2.78300			728.17991			728.17999
449	279.13644	279.13535	279.13644	10.51500	10.53600	10.51500	0.00000	7.94068	8.19680	3193.08142	NaN	11.54893	0.00951	0.00951	279.13608	10.52200	C05775		278.12670	C18753		278.12670
996	100.07672	100.07689	100.07672	8.06600	7.94600	8.06600	0.00000	8.02700	8.10594	3185.83375	NaN	9.97111	0.01088	0.01088	100.07678	8.02600		HMDB11749	99.06841	C11249		99.06841
355	358.20206	358.20239	358.20206	1.82600	1.81200	1.82600	0.00000	8.07838	8.04059	3163.66753	NaN	11.56145	0.01182	0.01182	358.20217	1.82133	C09558		357.19401	C07251		357.19401

154	641.12585	641.12714	641.12585	1.63800	1.64700	1.63800	0.00000	8.07132	8.01280	3109.00775	NaN	9.93114	0.01053	0.01053	641.12628	1.64100			640.12749			640.12749
156	619.22913	619.23346	619.22913	8.00700	8.01600	8.00700	0.00000	7.88031	8.19437	3094.36404	NaN	9.46588	0.00958	0.00958	619.23057	8.01000	C08853		618.26760	C08872		618.26763
986	101.06405	101.06660	101.06405	8.14900	8.24000	8.14900	0.00000	7.95146	8.12299	3094.02323	NaN	10.90703	0.01003	0.01003	101.06490	8.17933	C12518		100.05243		HMDB01862	100.05243
268	444.03214	444.03293	444.03214	9.35000	9.41700	9.35000	0.00000	7.95978	8.09999	3071.37509	NaN	10.23392	0.01044	0.01044	444.03240	9.37233	C00035	HMDB01201	443.02434	C00035	HMDB01201	443.02432
830	146.96101	146.96330	146.96101	0.17800	0.18700	0.17800	0.00000	8.28371	7.76875	3060.19280	NaN	9.39340	0.01164	0.01164	146.96178	0.18100	C14400		145.94570	C14402		145.94568
414	306.08896	306.08649	306.08896	3.80400	3.75400	3.80400	0.00000	8.00220	8.03389	3035.23464	NaN	9.84336	0.00975	0.00975	306.08814	3.78733	C13752		305.07920	C13752		305.07919
197	536.10315	536.10693	536.10315	3.19200	3.15400	3.19200	0.00000	7.96025	8.07038	3026.96612	NaN	9.60901	0.00935	0.00935	536.10441	3.17933			535.09604	C16238		535.09600
269	444.02951	444.03174	444.02951	8.21900	8.20500	8.21900	0.00000	7.87719	8.13867	3004.68878	NaN	9.48694	0.00933	0.00933	444.03025	8.21433	C08069		443.02064	C08069		443.02060
189	555.88934	555.88721	555.88934	3.42800	3.40100	3.42800	0.00000	7.84515	8.15907	2987.25605	NaN	8.22702	0.01034	0.01034	555.88863	3.41900		HMDB11104	554.93066			554.93068
625	205.11496	205.11391	205.11496	5.11100	5.07300	5.11100	0.00000	7.95402	8.03606	2966.20509	NaN	9.01509	0.00997	0.00997	205.11461	5.09833	C03955		204.11100	C04210		204.11100
188	555.89166	555.88910	555.89166	3.02700	2.97700	3.02700	0.00000	7.98767	8.00139	2964.69210	NaN	11.90133	0.01085	0.01085	555.89081	3.01033		HMDB11104	554.93066			554.93068
797	158.96109	158.96152	158.96109	9.86800	9.93500	9.86800	0.00000	8.15605	7.81317	2935.44177	NaN	11.21684	0.00958	0.00958	158.96123	9.89033	C19212		157.97238	C19164		157.97240
483	267.20734	267.20676	267.20734	9.52600	9.57000	9.52600	0.00000	8.28915	7.67009	2920.82109	NaN	9.88058	0.01019	0.01019	267.20714	9.54067			266.19943	C04834		266.18820
415	305.17014	305.17191	305.17014	7.08900	6.96800	7.08900	0.00000	7.84562	8.11206	2918.54413	NaN	9.94365	0.00997	0.00997	305.17073	7.04867			304.16477	C01804		304.16480
354	358.20267	358.20126	358.20267	1.29700	1.29400	1.29700	0.00000	7.89460	8.02810	2867.93734	NaN	11.51494	0.00942	0.00942	358.20220	1.29600	C09558		357.19401	C07251		357.19401
926	118.08733	118.08699	118.08733	8.18400	8.19300	8.18400	0.00000	7.75274	8.16533	2861.30847	NaN	9.41808	0.01009	0.01009	118.08721	8.18700	C00183	HMDB00883	117.07900	C00431	HMDB03355	117.07900
514	247.12698	247.12837	247.12698	10.24400	10.24100	10.24400	0.00000	7.91245	7.99996	2853.21225	NaN	9.88028	0.01061	0.01061	247.12745	10.24300		HMDB11166	246.12157		HMDB11172	246.12157
1002	98.98445	98.99095	98.98445	3.39200	3.35400	3.39200	0.00000	8.10779	7.80451	2853.06670	NaN	9.65745	0.01027	0.01027	98.98662	3.37933	C12893		97.97701	C12554		97.97700
619	206.11903	206.11884	206.11903	3.59200	3.43600	3.59200	0.00000	7.93921	7.95612	2828.95059	NaN	10.57443	0.01068	0.01068	206.11897	3.54000	C10846		205.11030			205.11028
302	405.01111	405.00958	405.01111	9.86800	9.94700	9.86800	0.00000	8.03111	7.85637	2817.88688	NaN	8.42764	0.01039	0.01039	405.01060	9.89433	C00015	HMDB00295	404.00220	C00015	HMDB00295	404.00220
231	473.17789	473.17740	473.17789	10.91500	10.96000	10.91500	0.00000	7.90312	7.98369	2816.92900	NaN	10.94676	0.00821	0.00821	473.17772	10.93000			472.17329	C18681		472.17330
863	136.06241	136.06274	136.06241	5.08800	4.94300	5.08800	0.00000	7.83440	8.04881	2811.87581	NaN	11.09095	0.00997	0.00997	136.06252	5.03967	C00147	HMDB00034	135.05450	C00147	HMDB00034	135.05450
954	113.06704	113.06954	113.06704	8.12500	8.15700	8.12500	0.00000	7.82346	8.05200	2800.99525	NaN	11.40438	0.00932	0.00932	113.06787	8.13567			112.05243			112.05243
246	461.21680	461.21552	461.21680	1.80300	1.81200	1.80300	0.00000	7.94283	7.91684	2778.96366	NaN	9.76124	0.01143	0.01143	461.21637	1.80600	C10672		460.20970	C10704		460.20970
748	181.12437	181.12901	181.12437	30.65900	30.78600	30.65900	0.00000	8.01470	7.82350	2749.29042	NaN	11.51717	0.01139	0.01139	181.12592	30.70133	C04033		180.11503	C03929		180.11500
435	290.97769	290.97836	290.97769	4.35800	4.30800	4.35800	0.00000	7.80624	8.01812	2730.33124	NaN	9.53264	0.01185	0.01185	290.97792	4.34133	C17113		290.00730	C17132		290.00731
618	206.11812	206.11836	206.11812	9.55000	9.60600	9.55000	0.00000	7.94276	7.86851	2712.51277	NaN	9.13647	0.00751	0.00751	206.11820	9.56867	C10846		205.11030			205.11028
1023	89.50768	89.50742	89.50768	15.66000	15.29200	15.66000	0.00000	8.21033	7.59959	2710.68753	NaN	10.07910	0.00838	0.00838	89.50759	15.53733						
518	246.11285	246.11029	246.11285	1.69700	1.70600	1.69700	0.00000	8.03532	7.76747	2701.04403	NaN	9.06063	0.00928	0.00928	246.11200	1.70000			245.11643	C19897		245.09130
471	270.19690	270.20505	270.19690	10.58600	10.60600	10.58600	0.00000	7.86247	7.90535	2654.22533	NaN	10.54573	0.01078	0.01078	270.19962	10.59267	C05763		269.19391			269.19909
835	146.08128	146.07629	146.08128	9.44400	9.39400	9.44400	0.00000	7.88820	7.87940	2653.94569	NaN	9.09505	0.01009	0.01009	146.07962	9.42733			145.07388	C03656	HMDB12131	145.07388
250	461.21683	461.21774	461.21683	1.01400	0.62300	1.01400	0.00000	7.56179	8.19152	2635.05185	NaN	10.52420	0.00795	0.00795	461.21713	0.88367	C10672		460.20970	C10704		460.20970
413	306.13089	306.13178	306.13089	7.72500	7.65100	7.72500	0.00000	7.66969	8.07773	2627.29543	NaN	10.31948	0.01046	0.01046	306.13119	7.70033			305.12230			305.12230
574	222.10234	222.10211	222.10234	10.28000	10.31200	10.28000	0.00000	7.68013	8.04156	2593.72030	NaN	10.42663	0.00849	0.00849	222.10227	10.29067	C02587		221.09130		HMDB00389	221.09128
878	131.04637	131.04518	131.04637	8.09000	8.13400	8.09000	0.00000	7.67993	8.04162	2593.52412	NaN	9.03306	0.01054	0.01054	131.04597	8.10467	C20254		130.03780	C16483		130.04300
247	461.21863	461.21893	461.21863	10.97400	10.67700	10.97400	0.00000	7.78097	7.92074	2567.92822	NaN	8.51509	0.00812	0.00812	461.21873	10.87500	C10715		460.20972	C10831		460.20972
1024	89.50737	89.50768	89.50737	7.67800	7.41600	7.67800	0.00000	7.62586	8.06260	2550.97346	NaN	9.83429	0.01056	0.01056	89.50747	7.59067						
493	259.02210	259.02237	259.02210	1.76800	1.78800	1.76800	0.00000	7.87906	7.80930	2550.84537	NaN	10.69272	0.00811	0.00811	259.02219	1.77467	C01236		258.01410	C01286		258.01410
654	199.14342	199.14356	199.14342	10.66800	10.70000	10.66800	0.00000	7.81597	7.87223	2550.64270	NaN	10.79962	0.00951	0.00951	199.14346	10.67867	C06185		198.13680	C10858	HMDB06548	198.13683
722	184.13309	184.13399	184.13309	11.33900	11.26600	11.33900	0.00000	7.35453	8.31431	2526.06977	NaN	11.55431	0.01029	0.01029	184.13339	11.31467	C12452		183.12590	C12453		183.12590
125	800.57611	800.56891	800.57611	34.29700	34.40000	34.29700	0.00000	8.04770	7.61643	2520.11562	NaN	10.10744	0.01099	0.01099	800.57371	34.33133			799.57267			799.57267
881	130.09370	130.08592	130.09370	10.95100	10.93600	10.95100	0.00000	7.73820	7.92406	2517.76714	NaN	8.42376	0.01007	0.01007	130.09111	10.94600	C00408	HMDB00716	129.07900	C03969		129.07900
338	364.61758	364.61719	364.61758	12.87000	12.84300	12.87000	0.00000	7.54227	8.11672	2513.66584	NaN	9.95500	0.01043	0.01043	364.61745	12.86100						
567	226.15579	226.15591	226.15579	6.10000	5.86200	6.10000	0.00000	7.70239	7.94442	2498.39964	NaN	10.17107	0.00951	0.00951	226.15583	6.02067	C10965		225.15896	C18784		225.15896
646	199.98723	199.98703	199.98723	9.42000	9.51100	9.42000	0.00000	7.71507	7.91073	2472.28667	NaN	9.57724	0.00844	0.00844	199.98716	9.45033	C18905		198.97480	C19047		198.97477
939	114.09135	114.09104	114.09135	12.36400	12.46700	12.36400	0.00000	8.04188	7.57181	2457.35620	NaN	9.48577	0.01036	0.01036	114.09125	12.39833			113.08406	C05853		113.08406
196	536.09985	536.10437	536.09985	3.58100	3.56600	3.58100	0.00000	7.66015	7.93928	2439.89979	NaN	9.68528	0.00932	0.00932	536.10136	3.57600	C16238		535.09604			535.09604
847	144.07129	144.07159	144.07129	1.73200	1.72900	1.73200	0.00000	7.64188	7.95245	2433.69439	NaN	10.29374	0.01190	0.01190	144.07139	1.73100			143.05824			143.05824
964	110.01241	110.02057	110.01241	22.79500	22.69800	22.79500	0.00000	7.78914	7.80097	2428.56586	NaN	9.20461	0.01084	0.01084	110.01513	22.76267	C00519	HMDB00965	109.01970	C00519	HMDB00965	109.01975
989	101.02038	101.01852	101.02038	0.66100	1.02250	0.66100	0.00000	8.10575	7.48005	2423.32885	NaN	11.45525	0.00998	0.00998	101.01976	0.78150			100.00952	C19524		100.01600
595	213.97997	213.98062	213.97997	4.36900	4.29600	4.36900	0.00000	7.80585	7.73941	2374.71724	NaN	10.73135	0.01095	0.01095	213.98018	4.34467			212.97482	C05708		212.99040
291	422.03598	422.03473	422.03598	3.41600	3.36600	3.41600	0.00000	7.57541	7.95907	2361.94165	NaN	10.55686	0.01037	0.01037	422.03556	3.39933	C07758		421.03779	C07758		421.03780
173	578.91333	578.91577	578.91333	2.78000	2.75300	2.78000	0.00000	7.85021	7.67356	2349.32241	NaN	10.02304	0.00946	0.00946	578.91414	2.77100	C03034		578.05500	C06017		578.05500
527	243.13438	243.13667	243.13438	15.13000	15.12700	15.13000	0.00000	7.67173	7.85077	2347.83360	NaN	9.85306	0.01088	0.01088	243.13515	15.12900			242.12666			242.12666
142	676.88043	676.88886	676.88043	2.79200	2.83600	2.79200	0.00000	7.74173	7.75637	2319.36048	NaN	12.57501	0.00974	0.00974	676.88324	2.80667						
261	451.11520	451.11231	451.11520	16.63700	16.56400	16.63700	0.00000	7.79352	7.70152	2315.81223	NaN	9.17070	0.00913	0.00913	451.11424	16.61267			450.11616			450.11616
689	186.96016	186.96019	186.96016	29.97600	29.95000	29.97600	0.00000	7.76243	7.73172	2314.79138	NaN	9.14836	0.01095	0.01095	186.96017	29.96733			185.93164	C14846		185.93160
844	145.04572	145.04593	145.04572	15.29500	15.28000	15.29500	0.00000	7.71919	7.76543	2303.78423	NaN	8.73151	0.01026	0.01026	145.04579	15.29000	C07833		144.03420	C07833		144.03419
463	270.99750	270.99698	270.99750	1.65000	1.69400	1.65000	0.00000	7.85205	7.61605	2284.84267	NaN	9.15216	0.01077	0.01077	270.99733	1.66467		HMDB06343	270.01187		HMDB06343	270.01188
852	141.95902	141.95958	141.95902	9.77300	9.38200	9.77300	0.00000	7.74231	7.72303	2281.69039	NaN	9.20736	0.00823	0.00823	141.95920	9.64267	C00169	HMDB01096	140.98270	C00169	HMDB01096	140.98271
365	348.07010	348.07123	348.07010	18.76800	18.84800	18.76800	0.00000	7.76888	7.68625	2270.06863	NaN	11.56517	0.01207	0.01207	348.07048	18.79467	C00020	HMDB00045	347.06308	C00362	HMDB01044	347.06308
482	267.20584	267.21286	267.20584	30.51800	30.43250	30.51800	0.00000	7.80596	7.63827	2257.72676	NaN	9.08696	0.01082	0.01082	267.20818	30.48950			266.19943	C04834		266.18820
785	165.11897	165.12282	165.11897	11.05700	11.10100	11.05700	0.00000	7.72647	7.71160	2250.78291	NaN	9.55350	0.01028	0.01028	165.12026	11.07167			164.10620			164.10485
334	369.94196	369.94589	369.94196	4.29900	4.24900	4.29900	0.00000	7.71373	7.71930	2245.12344	NaN	9.43713	0.01096	0.01096	369.94327	4.28233	C17302		369.01466	C17167		369.01470
545	234.94493	234.94713	234.94493	4.13400	3.95400	4.13400	0.00000	8.17401	7.25827	2244.27592	NaN	8.66283	0.01095	0.01095	234.94566	4.07400			233.95416	C03575		233.95420
210	503.92865	503.92517	503.92865	9.80900	9.84100	9.80900	0.00000	7.71908	7.68242	2210.00845	NaN	10.39573	0.00926	0.00926	503.92749	9.81967			502.96420			502.97076
138	712.48621	712.48547	712.48621	34.36800	34.30600	34.36800	0.00000	7.83784	7.54750	2192.21181	NaN	11.87655	0.01037	0.01037	712.48596	34.34733			711.48386			711.48386
833	146.07544	146.07632	146.07544	8.17200	8.20500	8.17200	0.00000	7.71282	7.67150	2191.10512	NaN	11.13437	0.01070	0.01070	146.07573	8.18300			145.07388	C03656	HMDB12131	145.07388
481	267.20505	267.21146	267.20505	29.98800	29.89100	29.98800	0.00000	7.99806	7.37823	2182.32448	NaN	7.75755	0.00978	0.00978	267.20718	29.95567			266.19943	C04834		266.18820
513	247.12897	247.12849	247.12897	10.76200	10.84200	10.76200	0.00000	7.70163	7.66971	2176.92133	NaN	8.10050	0.00969	0.00969	247.12881	10.78867		HMDB11166	246.12157		HMDB11172	246.12157
551	231.14598	231.14420	231.14598	5.64100	5.41400	5.64100	0.00000	7.58214	7.78727	2174.82973	NaN	10.00192	0.01034	0.01034	231.14539	5.56533	C10758		230.14190	C10775		230.14191
804	158.00418	158.00291	158.00418	11.51600	11.50100	11.51600	0.00000	7.83191	7.53717	2174.46230	NaN	10.73062	0.00855	0.00855	158.00376	11.51100	C14407		156.99310	C14456		156.99310
377	338.07419	338.07294	338.07419	3.88700	3.79000	3.88700	0.00000	7.61435	7.75205	2171.55708	NaN	8.89330	0.01106	0.01106	338.07377	3.85467	C03997		337.06750			337.06750
615	206.11690	206.11757	206.11690	9.84400	9.91200	9.84400	0.00000	7.81018	7.54411	2158.44524	NaN	8.45909	0.00940	0.00940	206.11712	9.86667			205.11028	C10869		205.11028
448	280.19577	280.19556	280.19577	18.00300	17.92900	18.00300	0.00000	7.44794	7.89671	2148.06391	NaN	9.88499	0.00989	0.00989	280.19570	17.97833	C09923		279.18344	C09901		279.18340

834	146.07555	146.07562	146.07555	9.84400	9.93500	9.84400	0.00000	7.62754	7.71259	2143.21438	NaN	10.93281	0.00906	0.00906	146.07557	9.87433			145.07388	C03656	HMDB12131	145.07388
126	791.22284	791.22742	791.22284	3.78100	3.73100	3.78100	0.00000	7.62522	7.70546	2133.11733	NaN	9.59360	0.01043	0.01043	791.22437	3.76433	C04488		790.27860	C04488		790.27862
851	141.95851	141.95894	141.95851	11.16300	11.52500	11.16300	0.00000	7.76631	7.56013	2128.59908	NaN	9.45649	0.01158	0.01158	141.95865	11.28367	C00169	HMDB01096	140.98270	C00169	HMDB01096	140.98271
734	182.98402	182.98523	182.98402	12.23400	12.23100	12.23400	0.00000	7.74717	7.57461	2123.63607	NaN	9.15598	0.01185	0.01185	182.98443	12.23300	C07598		181.97080	C07719		181.97075
593	215.06824	215.07504	215.06824	3.31000	3.30700	3.31000	0.00000	7.74928	7.56823	2119.11692	NaN	11.90911	0.01030	0.01030	215.07051	3.30900			214.06299	C08460		214.06299
796	158.96117	158.96057	158.96117	29.96500	29.86800	29.96500	0.00000	7.48890	7.80787	2097.26085	NaN	11.34318	0.01037	0.01037	158.96097	29.93267	C19212		157.97238	C19164		157.97240
470	270.19977	270.20343	270.19977	13.60000	13.60900	13.60000	0.00000	7.56160	7.73347	2095.47165	NaN	11.86997	0.01135	0.01135	270.20099	13.60300	C05763		269.19391			269.19909
590	215.13756	215.13812	215.13756	9.30200	9.37000	9.30200	0.00000	7.58972	7.68763	2076.98845	NaN	12.07024	0.01081	0.01081	215.13775	9.32467	C01909	HMDB03581	214.13170			214.13174
127	789.16132	789.16388	789.16132	4.47500	4.33100	4.47500	0.00000	7.58911	7.68354	2072.11634	NaN	9.65691	0.01080	0.01080	789.16217	4.42700			788.17991			788.17991
638	202.11461	202.11852	202.11461	9.58500	9.65300	9.58500	0.00000	7.54904	7.72307	2071.55123	NaN	11.64049	0.00962	0.00962	202.11591	9.60767	C02691		201.11400	C05753		201.09492
652	199.14392	199.14258	199.14392	31.02400	31.12700	31.02400	0.00000	7.65700	7.59494	2050.76853	NaN	9.76099	0.01040	0.01040	199.14347	31.05833	C06185		198.13680	C10858	HMDB06548	198.13683
209	503.92740	503.92600	503.92740	11.95100	11.81900	11.95100	0.00000	7.64285	7.60241	2043.92241	NaN	10.99699	0.00984	0.00984	503.92693	11.90700			502.96420			502.97076
614	206.11931	206.12355	206.11931	13.61150	13.60900	13.61150	0.00000	7.81120	7.43209	2041.91637	NaN	8.90010	0.00895	0.00895	206.12072	13.61067			205.11365	C17225		205.11370
697	186.15094	186.15135	186.15094	11.33900	11.28900	11.33900	0.00000	7.78606	7.45483	2039.46328	NaN	8.56635	0.00916	0.00916	186.15108	11.32233	C16649		185.14158			185.15281
287	422.63797	422.63864	422.63797	10.22100	10.28800	10.22100	0.00000	7.57733	7.64535	2020.97684	NaN	11.72023	0.01171	0.01171	422.63819	10.24333	C18103		421.77960	C18103		421.77962
208	503.92621	503.92456	503.92621	12.29300	12.27800	12.29300	0.00000	7.63928	7.57479	2012.30466	NaN	9.29376	0.01022	0.01022	503.92566	12.28800			502.96420			502.97076
526	243.13860	243.14081	243.13860	14.47100	14.48000	14.47100	0.00000	7.43179	7.77002	1999.99738	NaN	9.96675	0.00988	0.00988	243.13933	14.47400	C14225		242.13070	C14898		242.13070
719	184.13364	184.13353	184.13364	18.41500	18.35300	18.41500	0.00000	7.69607	7.50057	1994.84331	NaN	8.17277	0.01153	0.01153	184.13360	18.39433	C12452		183.12590	C12453		183.12590
871	134.06712	134.07559	134.06712	10.77400	10.53600	10.77400	0.00000	7.68947	7.50630	1993.97526	NaN	12.23810	0.01015	0.01015	134.06995	10.69467			133.06400	C10901		133.06400
356	358.15305	358.14957	358.15305	9.65600	9.72300	9.65600	0.00000	7.53261	7.63388	1965.00105	NaN	10.82322	0.00887	0.00887	358.15189	9.67833	C09914		357.14240	C09924		357.14237
746	181.12592	181.12755	181.12592	31.36600	31.28000	31.36600	0.00000	7.90307	7.24798	1949.87929	NaN	11.10015	0.00944	0.00944	181.12646	31.33733	C04033		180.11503	C03929		180.11500
361	351.53647	351.53629	351.53647	6.34700	6.03800	6.34700	0.00000	7.59168	7.55255	1943.24283	NaN	9.61893	0.01168	0.01168	351.53641	6.24400			350.39125			350.39125
649	199.14430	199.14360	199.14430	28.68100	28.59600	28.68100	0.00000	7.94948	7.19304	1941.58415	NaN	10.07226	0.01017	0.01017	199.14407	28.65267	C06185		198.13680	C10858	HMDB06548	198.13683
805	158.00287	158.00293	158.00287	9.77300	9.50000	9.77300	0.00000	7.43541	7.70398	1938.54948	NaN	10.04737	0.00940	0.00940	158.00289	9.68200	C14407		156.99310	C14456		156.99310
1021	89.50710	89.50756	89.50710	16.41400	16.15200	16.41400	0.00000	8.43931	6.69071	1929.49214	NaN	10.52930	0.01013	0.01013	89.50725	16.32667						
492	260.09451	260.09253	260.09451	4.47500	4.37800	4.47500	0.00000	7.30070	7.82775	1927.97043	NaN	10.43659	0.01003	0.01003	260.09385	4.44267			259.08579	C10701		259.08450
245	461.22223	461.21964	461.22223	12.37500	12.39600	12.37500	0.00000	7.51613	7.60842	1924.22432	NaN	7.71315	0.00936	0.00936	461.22136	12.38200	C10715		460.20972	C10831		460.20972
707	185.13037	185.13168	185.13037	7.54800	7.56900	7.54800	0.00000	7.51092	7.58606	1897.87282	NaN	10.51650	0.00911	0.00911	185.13081	7.55500	C17235		184.12520	C09633		184.12520
207	503.92932	503.92676	503.92932	12.97600	12.99600	12.97600	0.00000	7.59983	7.48637	1887.67626	NaN	10.51653	0.01070	0.01070	503.92847	12.98267			502.96420			502.97076
765	173.08066	173.08752	173.08066	10.42100	10.80600	10.42100	0.00000	7.35796	7.69831	1859.63318	NaN	10.49434	0.01246	0.01246	173.08295	10.54933		HMDB00341	172.07356		HMDB04982	172.07356
405	311.94644	311.94650	311.94644	4.33400	4.28400	4.33400	0.00000	7.46907	7.58377	1856.45123	NaN	9.94534	0.00884	0.00884	311.94646	4.31733	C18941		310.93490	C18941		310.93487
721	184.13287	184.13359	184.13287	20.18100	20.21300	20.18100	0.00000	7.40715	7.63726	1848.63339	NaN	11.00670	0.00955	0.00955	184.13311	20.19167	C12452		183.12590	C12453		183.12590
539	237.08791	237.08592	237.08791	4.57000	4.50800	4.57000	0.00000	7.42112	7.61332	1839.44895	NaN	9.51263	0.00841	0.00841	237.08725	4.54933	C02700	HMDB01200	236.07970	C15605		236.07970
262	450.01813	450.01950	450.01813	2.76800	2.76500	2.76800	0.00000	7.54008	7.46457	1812.25148	NaN	9.59877	0.01064	0.01064	450.01859	2.76700			449.01630	C08106		449.03270
592	215.07997	215.08084	215.07997	4.42800	4.34300	4.42800	0.00000	7.78800	7.20773	1804.18178	NaN	10.06051	0.01117	0.01117	215.08026	4.39967			214.07021			214.07760
319	391.28445	391.28394	391.28445	3.00400	3.33000	3.00400	0.00000	6.53634	8.45872	1803.58848	NaN	8.76829	0.01069	0.01069	391.28428	3.11267			390.27699			390.27699
178	572.91260	572.91046	572.91260	2.95700	2.95400	2.95700	0.00000	7.41851	7.57053	1798.16576	NaN	10.75339	0.00993	0.00993	572.91189	2.95600			572.04714			572.04721
549	232.11855	232.11877	232.11855	3.42800	3.74200	3.42800	0.00000	7.55331	7.42250	1786.30622	NaN	11.11120	0.01086	0.01086	232.11862	3.53267			231.11067			231.11067
206	503.92804	503.92542	503.92804	10.46800	10.71200	10.46800	0.00000	7.57307	7.39927	1783.21346	NaN	8.32155	0.00882	0.00882	503.92717	10.54933			502.96420			502.97076
353	358.19800	358.19778	358.19800	14.04700	14.03200	14.04700	0.00000	7.45038	7.49595	1760.16781	NaN	9.05822	0.00971	0.00971	358.19793	14.04200			357.18999			357.18999
696	186.15578	186.15787	186.15578	29.95300	29.95000	29.95300	0.00000	7.67792	7.26610	1758.13229	NaN	10.42783	0.00764	0.00764	186.15647	29.95200			185.15281	C16649		185.14158
643	201.10255	201.10530	201.10255	11.30400	11.10100	11.30400	0.00000	7.44116	7.48806	1745.17072	NaN	10.54504	0.00930	0.00930	201.10347	11.23633	C06537		200.09500	C14759		200.09500
318	391.28214	391.28671	391.28214	3.41600	3.70700	3.41600	0.00000	6.54719	8.37150	1736.00274	NaN	10.29888	0.01057	0.01057	391.28366	3.51300			390.27699			390.27699
882	130.05733	130.06184	130.05733	15.44800	15.45700	15.44800	0.00000	7.15003	7.76325	1731.31514	NaN	10.90188	0.00908	0.00908	130.05883	15.45100	C06323		129.05780	C06413		129.05780
718	184.13394	184.13336	184.13394	8.09000	8.11000	8.09000	0.00000	7.45447	7.45588	1728.77896	NaN	11.08481	0.00920	0.00920	184.13375	8.09667			183.12593	C10865		183.12593
823	149.04237	149.04477	149.04237	4.51100	4.47200	4.51100	0.00000	7.31497	7.58689	1721.45843	NaN	8.75602	0.00824	0.00824	149.04317	4.49800		HMDB00426	148.03717		HMDB00428	148.03717
400	319.15131	319.15134	319.15131	3.98100	3.96600	3.98100	0.00000	7.32681	7.57193	1718.78102	NaN	9.15232	0.01057	0.01057	319.15132	3.97600	C09981		318.14670			318.14670
488	261.49374	261.49075	261.49374	2.75600	2.75350	2.75600	0.00000	7.35842	7.53722	1716.11695	NaN	8.36379	0.01126	0.01126	261.49275	2.75517						
159	608.09094	608.08868	608.09094	11.46900	11.48900	11.46900	0.00000	7.64152	7.25036	1712.89128	NaN	9.94178	0.01004	0.01004	608.09019	11.47567	C00043	HMDB00290	607.08160	C00203	HMDB00304	607.08160
747	181.12360	181.12955	181.12360	14.01200	14.35000	14.01200	0.00000	7.23953	7.64995	1710.83910	NaN	12.35597	0.00834	0.00834	181.12558	14.12467	C04033		180.11503	C03929		180.11500
602	213.19109	213.19397	213.19109	29.90600	29.77300	29.90600	0.00000	7.91059	6.97110	1704.19367	NaN	11.19040	0.00777	0.00777	213.19205	29.86167			212.17763			212.17763
650	199.14494	199.14465	199.14494	13.36400	13.33800	13.36400	0.00000	7.62922	7.24965	1701.78340	NaN	10.75407	0.00940	0.00940	199.14485	13.35533	C10858	HMDB06548	198.13683	C06185		198.13680
902	126.04741	126.04914	126.04741	13.01100	13.24400	13.01100	0.00000	7.52262	7.35511	1700.81871	NaN	8.49628	0.01052	0.01052	126.04799	13.08867			125.04768	C02535		125.04768
813	155.00797	155.00984	155.00797	1.17900	1.16400	1.17900	0.00000	7.33398	7.54108	1698.54508	NaN	8.99497	0.01108	0.01108	155.00859	1.17400	C02876		154.00310	C03505		154.00310
317	391.28360	391.28549	391.28360	8.09000	7.89875	8.09000	0.00000	7.28806	7.56520	1680.13684	NaN	8.54470	0.00920	0.00920	391.28423	8.02625			390.27699			390.27699
772	171.05257	171.05287	171.05257	3.26300	3.26000	3.26300	0.00000	7.45949	7.34924	1643.13585	NaN	9.83780	0.00948	0.00948	171.05267	3.26200	C05515		170.04400			170.04399
1063	84.07967	84.08067	84.07967	35.45100	35.35400	35.45100	0.00000	8.50516	6.30087	1640.92441	NaN	8.72572	0.01033	0.01033	84.08000	35.41867			83.07350			83.07350
940	114.09100	114.09090	114.09100	10.82100	10.79500	10.82100	0.00000	6.92942	7.85319	1621.82211	NaN	11.43464	0.01050	0.01050	114.09096	10.81233			113.08406	C05853		113.08406
976	102.08418	102.09204	102.08418	24.99600	25.01700	24.99600	0.00000	8.22474	6.55332	1618.13237	NaN	10.12495	0.00868	0.00868	102.08680	25.00300			101.08406	C01842		101.08406
744	181.12726	181.12866	181.12726	32.17800	32.28100	32.17800	0.00000	7.75127	7.00933	1604.06616	NaN	9.56214	0.01028	0.01028	181.12773	32.21233	C04033		180.11503	C03929		180.11500
177	572.91419	572.91431	572.91419	3.41600	3.37700	3.41600	0.00000	7.26778	7.47979	1593.64921	NaN	8.35861	0.01140	0.01140	572.91423	3.40300			572.04714			572.04721
137	712.48016	712.48291	712.48016	35.11000	35.16600	35.11000	0.00000	8.65315	6.06721	1572.11706	NaN	10.51677	0.01031	0.01031	712.48108	35.12867			711.48386			711.48386
938	114.09078	114.09158	114.09078	9.80900	9.93500	9.80900	0.00000	7.63521	7.06881	1559.32553	NaN	9.25365	0.00972	0.00972	114.09105	9.85100			113.08406	C05853		113.08406
350	358.20322	358.20282	358.20322	12.94000	12.79600	12.94000	0.00000	7.70149	6.99910	1556.65622	NaN	10.62088	0.00923	0.00923	358.20309	12.89200	C09558		357.19401	C07251		357.19401
850	141.95883	141.95903	141.95883	10.02100	9.94700	10.02100	0.00000	7.19007	7.48997	1540.74092	NaN	9.69276	0.00827	0.00827	141.95890	9.99633	C00169	HMDB01096	140.98270	C00169	HMDB01096	140.98271
264	448.95593	448.96118	448.95593	4.45200	4.34300	4.45200	0.00000	7.39553	7.27853	1536.13769	NaN	10.68880	0.01068	0.01068	448.95768	4.41567	C05837		448.06100	C05837		448.06102
754	177.07587	177.07452	177.07587	15.97800	15.68100	15.97800	0.00000	7.88789	6.78011	1531.49191	NaN	9.81127	0.00870	0.00870	177.07542	15.87900	C02123		176.06845		HMDB02025	176.06845
389	330.60733	330.60696	330.60733	34.55630	34.61200	34.55630	0.00000	8.00887	6.64899	1523.75704	NaN	10.15288	0.00985	0.00985	330.60721	34.57487						
151	647.10492	647.10736	647.10492	9.76200	9.60600	9.76200	0.00000	7.39799	7.25294	1518.48142	NaN	10.51474	0.00831	0.00831	647.10573	9.71000	C19965		646.19560			646.19564
504	253.19048	253.19128	253.19048	2.88600	2.74200	2.88600	0.00000	7.24086	7.36947	1487.96667	NaN	9.24545	0.01084	0.01084	253.19075	2.83800			252.18378			252.17255
433	291.11896	291.12045	291.11896	7.30100	7.14500	7.30100	0.00000	7.04957	7.55824	1486.08965	NaN	10.99139	0.01074	0.01074	291.11946	7.24900		HMDB12267	290.11140	C04421		290.11140
411	308.91754	308.91568	308.91754	3.48600	3.34200	3.48600	0.00000	7.54124	7.04053	1466.86305	NaN	11.56151	0.01146	0.01146	308.91692	3.43800	C18707		307.96210	C18707		307.96212
735	182.98312	182.98485	182.98312	28.49300	28.11300	28.49300	0.00000	6.96896	7.61116	1465.66317	NaN	10.57212	0.00994	0.00994	182.98370	28.36633	C07598		181.97080	C07719		181.97075
599	213.19441	213.19418	213.19441	11.25700	11.27700	11.25700	0.00000	7.77555	6.80389	1465.15444	NaN	10.62379	0.00993	0.00993	213.19434	11.26367			212.17763			212.17763
645	199.98782	199.98906	199.98782	31.20100	31.58600	31.20100	0.00000	7.30621	7.24797	1446.77182	NaN	9.98847	0.01034	0.01034	199.98824	31.32933	C18905		198.97480	C19047		198.97477

687	186.95990	186.95961	186.95990	29.60000	29.59700	29.60000	0.00000	7.35007	7.19897	1443.06195	NaN	10.22328	0.00989	0.00989	186.95980	29.59900			185.93164	C14846		185.93160
576	221.09222	221.09422	221.09222	6.64200	6.50900	6.64200	0.00000	7.20757	7.30638	1417.95827	NaN	10.33737	0.01276	0.01276	221.09289	6.59767	C00643	HMDB00472	220.08480	C01017		220.08480
538	237.08774	237.08658	237.08774	6.23000	6.07400	6.23000	0.00000	7.15118	7.35847	1414.91790	NaN	9.92048	0.01088	0.01088	237.08735	6.17800	C02700	HMDB01200	236.07970	C15605		236.07970
879	130.96619	130.96686	130.96619	0.19000	0.18700	0.19000	0.00000	7.04370	7.46081	1411.28239	NaN	10.86389	0.01162	0.01162	130.96641	0.18900	C14860		129.95880	C14867		129.95884
698	186.15425	186.15575	186.15425	30.36500	30.38600	30.36500	0.00000	6.99328	7.50192	1404.72906	NaN	11.03111	0.00893	0.00893	186.15475	30.37200	C16649		185.14158			185.15281
1006	98.51392	98.51312	98.51392	13.30500	13.39700	13.30500	0.00000	7.46900	7.01319	1395.62353	NaN	9.15436	0.01054	0.01054	98.51365	13.33567						
977	102.07099	102.07771	102.07099	10.70350	10.58300	10.70350	0.00000	7.78737	6.67551	1382.21268	NaN	9.78205	0.01130	0.01130	102.07323	10.66333	C07672		101.07010	C08063		101.07015
1007	98.51154	98.51234	98.51154	10.05600	9.84100	10.05600	0.00000	7.37267	7.06568	1365.35942	NaN	8.13823	0.01083	0.01083	98.51181	9.98433						
399	319.14945	319.14920	319.14945	7.05400	6.93300	7.05400	0.00000	6.91534	7.51042	1356.79244	NaN	10.47028	0.00914	0.00914	319.14936	7.01367	C09981		318.14670			318.14670
351	358.19525	358.20239	358.19525	12.38700	12.33700	12.38700	0.00000	7.25049	7.16877	1352.39202	NaN	9.00475	0.00952	0.00952	358.19763	12.37033			357.18999			357.18999
352	358.19678	358.20651	358.19678	13.29400	13.53800	13.29400	0.00000	6.99416	7.42453	1352.00696	NaN	9.24833	0.01056	0.01056	358.20002	13.37533	C07251		357.19400	C09558		357.19400
301	405.00952	405.00986	405.00952	10.60900	10.70000	10.60900	0.00000	7.15930	7.25237	1347.26876	NaN	10.74654	0.01136	0.01136	405.00963	10.63933	C00015	HMDB00295	404.00220	C00015	HMDB00295	404.00220
901	126.08268	126.08936	126.08268	8.12500	8.16900	8.12500	0.00000	7.36464	7.04043	1342.82893	NaN	10.88133	0.01030	0.01030	126.08491	8.13967	C02376	HMDB02894	125.05891		HMDB04339	125.05891
464	270.92352	270.91980	270.92352	4.31100	4.24900	4.31100	0.00000	7.20890	7.19048	1339.01229	NaN	12.40488	0.00915	0.00915	270.92228	4.29033	C16181		269.89400	C16193		269.89395
953	113.06964	113.06960	113.06964	13.03500	12.90200	13.03500	0.00000	6.50665	7.89094	1337.82138	NaN	8.74216	0.00982	0.00982	113.06963	12.99067			112.05243			112.05243
316	395.03357	395.04016	395.03357	1.26100	1.24700	1.26100	0.00000	7.14362	7.23521	1325.32278	NaN	9.49235	0.01047	0.01047	395.03577	1.25633			394.03581			394.03585
983	101.06364	101.06390	101.06364	38.19400	37.97900	38.19400	0.00000	6.90894	7.45104	1312.89294	NaN	10.24060	0.01119	0.01119	101.06373	38.12233	C12518		100.05243		HMDB01862	100.05243
325	386.05042	386.04742	386.05042	3.72200	3.64800	3.72200	0.00000	7.12436	7.23476	1312.32891	NaN	9.33146	0.00970	0.00970	386.04942	3.69733		HMDB12468	385.02295			385.07080
931	116.06731	116.06732	116.06731	10.99800	11.01800	10.99800	0.00000	7.39399	6.94176	1297.08507	NaN	8.67692	0.01069	0.01069	116.06732	11.00467	C00148	HMDB00162	115.06330	C00763	HMDB03411	115.06330
598	213.19089	213.19211	213.19089	28.37500	28.37200	28.37500	0.00000	7.55119	6.76696	1285.72520	NaN	10.84637	0.01043	0.01043	213.19129	28.37400			212.17763			212.17763
843	145.04598	145.04074	145.04598	11.50400	11.50100	11.50400	0.00000	7.13008	7.18647	1284.69277	NaN	10.20968	0.01152	0.01152	145.04423	11.50300	C07833		144.03420	C07833		144.03419
693	186.14883	186.14980	186.14883	10.70350	10.73600	10.70350	0.00000	7.64080	6.67574	1284.68157	NaN	10.53941	0.01079	0.01079	186.14916	10.71433	C16649		185.14158			185.15281
876	132.02176	132.02980	132.02176	0.17800	0.16350	0.17800	0.00000	7.17898	7.12604	1277.30774	NaN	10.62064	0.01049	0.01049	132.02444	0.17317		HMDB01131	131.02184		HMDB01131	131.02185
842	145.04213	145.04073	145.04213	13.01100	12.98500	13.01100	0.00000	7.12278	7.18058	1276.24395	NaN	9.72306	0.01080	0.01080	145.04166	13.00233	C07833		144.03419	C07833		144.03420
923	119.08218	119.08242	119.08218	14.82400	14.56230	14.82400	0.00000	7.38264	6.91611	1273.30702	NaN	9.77431	0.00912	0.00912	119.08226	14.73677	C02045	HMDB06293	118.07423			118.07423
1008	98.51341	98.51202	98.51341	12.29300	12.29000	12.29300	0.00000	7.11028	7.17758	1266.39768	NaN	9.69759	0.01048	0.01048	98.51295	12.29200						
1040	88.07863	88.07517	88.07863	6.18300	6.09700	6.18300	0.00000	7.31673	6.92700	1238.75937	NaN	11.18819	0.01016	0.01016	88.07747	6.15433		HMDB01080	87.06841	C00048	HMDB00119	87.06841
855	141.01729	141.01639	141.01729	4.35800	4.27200	4.35800	0.00000	7.11492	7.10141	1221.90098	NaN	10.25834	0.01067	0.01067	141.01699	4.32933			140.01096	C13637		140.01096
1094	81.03640	81.04525	81.03640	12.98800	12.98500	12.98800	0.00000	7.07625	7.13385	1218.09946	NaN	9.52840	0.00904	0.00904	81.03935	12.98700	C00396		80.03740		HMDB03361	80.03745
611	206.12245	206.11818	206.12245	14.98900	14.72700	14.98900	0.00000	7.22900	6.96899	1210.75045	NaN	9.30589	0.00811	0.00811	206.12103	14.90167			205.11365	C17225		205.11370
131	744.07599	744.08221	744.07599	5.93500	5.87300	5.93500	0.00000	6.84585	7.34675	1207.48920	NaN	10.47397	0.00840	0.00840	744.07806	5.91433	C00006	HMDB00217	743.07546			743.16699
293	419.08771	419.08756	419.08771	22.80600	23.14500	22.80600	0.00000	6.72790	7.43363	1188.87579	NaN	9.56660	0.01285	0.01285	419.08766	22.91900			418.08897	C06435		418.08900
1018	90.05520	90.05556	90.05520	9.84400	10.08800	9.84400	0.00000	7.30374	6.84412	1180.78100	NaN	9.97344	0.01044	0.01044	90.05532	9.92533	C00099	HMDB00056	89.04768	C00041	HMDB00161	89.04768
122	850.04022	850.04614	850.04022	4.40500	4.28400	4.40500	0.00000	7.32624	6.81950	1179.52851	NaN	9.24613	0.01141	0.01141	850.04220	4.36467	C04739		849.10070			849.10072
300	405.00583	405.01184	405.00583	12.48100	12.31300	12.48100	0.00000	7.11008	7.02673	1174.27408	NaN	11.63412	0.01011	0.01011	405.00783	12.42500	C00015	HMDB00295	404.00220	C00015	HMDB00295	404.00220
360	352.31738	352.32083	352.31738	0.93200	0.92900	0.93200	0.00000	7.17652	6.94588	1165.84204	NaN	11.32623	0.00887	0.00887	352.31853	0.93100			351.31372			351.31372
1037	88.50927	88.51022	88.50927	13.29400	12.98500	13.29400	0.00000	7.31403	6.80362	1163.07676	NaN	11.31411	0.01207	0.01207	88.50959	13.19100						
648	199.14397	199.14357	199.14397	31.91900	32.12800	31.91900	0.00000	6.95759	7.15770	1161.70651	NaN	10.81868	0.00989	0.00989	199.14384	31.98867	C06185		198.13680	C10858	HMDB06548	198.13683
290	422.03909	422.03415	422.03909	8.13700	8.16900	8.13700	0.00000	7.17193	6.93414	1156.35836	NaN	11.17542	0.00904	0.00904	422.03745	8.14767	C07758		421.03779	C07758		421.03780
466	270.21509	270.21692	270.21509	9.76200	9.82900	9.76200	0.00000	7.30767	6.79371	1153.65182	NaN	11.96861	0.00848	0.00848	270.21570	9.78433			269.19909	C05763		269.19391
556	229.09918	229.10107	229.09918	13.28200	13.25500	13.28200	0.00000	7.24973	6.84862	1151.90752	NaN	10.78441	0.00917	0.00917	229.09981	13.27300	C14236		228.09390	C14336		228.09390
1001	98.98573	98.98484	98.98573	12.99900	12.73700	12.99900	0.00000	6.74323	7.34758	1147.56993	NaN	10.19633	0.00986	0.00986	98.98543	12.91167	C12893		97.97701	C12554		97.97700
868	134.07167	134.07140	134.07167	13.01100	12.98500	13.01100	0.00000	7.17765	6.91300	1147.48316	NaN	8.22779	0.01060	0.01060	134.07158	13.00233			133.06400	C10901		133.06400
932	116.06742	116.06355	116.06742	13.28200	13.00800	13.28200	0.00000	7.10227	6.98747	1146.95618	NaN	9.70994	0.01126	0.01126	116.06613	13.19067	C00148	HMDB00162	115.06330	C00763	HMDB03411	115.06330
808	156.96909	156.96796	156.96909	0.92000	0.92900	0.92000	0.00000	7.02316	7.06030	1143.36368	NaN	9.62986	0.00958	0.00958	156.96871	0.92300	C11036		155.95750	C11120		155.95746
967	108.00025	108.00179	108.00025	3.60400	3.82500	3.60400	0.00000	6.99426	7.06934	1132.07042	NaN	9.50873	0.00871	0.00871	108.00077	3.67767			107.01379	C19178		107.01379
158	613.92316	613.91919	613.92316	3.88700	3.71900	3.88700	0.00000	7.12087	6.93221	1126.12426	NaN	9.93340	0.01081	0.01081	613.92183	3.83100						
807	156.96751	156.96707	156.96751	0.19000	0.18700	0.19000	0.00000	7.03443	7.01667	1125.01528	NaN	9.73280	0.00774	0.00774	156.96737	0.18900	C11036		155.95750	C11120		155.95746
446	280.20245	280.20233	280.20245	2.74500	2.70600	2.74500	0.00000	7.10918	6.93383	1120.47030	NaN	9.65869	0.00869	0.00869	280.20241	2.73200		HMDB12535	279.19601	C09923		279.18344
198	533.95435	533.96344	533.95435	3.74500	3.77800	3.74500	0.00000	6.95131	7.08374	1116.02378	NaN	9.17896	0.00884	0.00884	533.95738	3.75600			533.08118			533.08118
544	234.94803	234.94830	234.94803	9.79700	9.87600	9.79700	0.00000	7.06658	6.93501	1097.50193	NaN	10.57165	0.00976	0.00976	234.94812	9.82333			233.95416	C03575		233.95420
642	201.10280	201.10176	201.10280	16.27200	16.58700	16.27200	0.00000	6.96703	7.02500	1092.27146	NaN	10.70503	0.00957	0.00957	201.10245	16.37700	C06537		200.09496			200.09496
950	113.06855	113.06924	113.06855	27.29200	26.95980	27.29200	0.00000	7.84792	6.13251	1085.95555	NaN	11.21247	0.00908	0.00908	113.06878	27.18127			112.05243			112.05243
1084	81.52095	81.52121	81.52095	7.53600	7.92200	7.53600	0.00000	7.07741	6.88938	1078.56955	NaN	11.36963	0.01069	0.01069	81.52104	7.66467						
922	119.08404	119.08118	119.08404	12.98800	12.98500	12.98800	0.00000	7.08711	6.87216	1074.52243	NaN	9.11188	0.00945	0.00945	119.08308	12.98700	C02045	HMDB06293	118.07423			118.07423
1060	84.96046	84.96563	84.96046	11.49200	11.50100	11.49200	0.00000	6.92806	7.00332	1059.64230	NaN	10.63004	0.00912	0.00912	84.96218	11.49500	C02271		83.95340	C02390		83.95336
1059	84.95779	84.96182	84.95779	13.01100	12.98500	13.01100	0.00000	7.03844	6.85832	1041.46038	NaN	9.86250	0.00949	0.00949	84.95913	13.00233	C02390		83.95336	C02271		83.95340
841	145.04329	145.04182	145.04329	12.26900	12.30200	12.26900	0.00000	6.80124	7.09124	1039.23499	NaN	8.84164	0.00968	0.00968	145.04280	12.28000	C07833		144.03420	C07833		144.03419
790	163.94647	163.95601	163.94647	1.00200	0.99900	1.00200	0.00000	7.10488	6.78096	1035.78541	NaN	10.68506	0.01079	0.01079	163.94965	1.00100	C01152	HMDB00479	162.97016			162.97617
930	116.97788	116.97817	116.97788	0.19000	0.18700	0.19000	0.00000	6.71897	7.14134	1022.64908	NaN	10.72018	0.00716	0.00716	116.97798	0.18900	C00122	HMDB00134	116.01096	C01384	HMDB00176	116.01096
121	850.04950	850.04407	850.04950	12.34000	12.32500	12.34000	0.00000	7.04044	6.81295	1019.11805	NaN	10.27717	0.00993	0.00993	850.04769	12.33500	C04739		849.10070			849.10072
120	850.04871	850.04639	850.04871	0.17800	0.17500	0.17800	0.00000	7.06988	6.71762	986.09479	NaN	9.99998	0.01052	0.01052	850.04793	0.17700	C04739		849.10070			849.10072
585	218.11589	218.10635	218.11589	4.02800	3.94300	4.02800	0.00000	6.70354	7.08174	984.99913	NaN	10.34437	0.01028	0.01028	218.11271	3.99967			217.10626			217.10626
388	330.60858	330.60718	330.60858	33.62600	33.56400	33.62600	0.00000	7.28837	6.49229	982.72363	NaN	10.24073	0.01199	0.01199	330.60811	33.60533						
205	513.11395	513.10999	513.11395	3.80400	3.75400	3.80400	0.00000	6.81462	6.92931	964.84214	NaN	10.18808	0.01146	0.01146	513.11263	3.78733			512.10597			512.13503
694	186.15291	186.15855	186.15291	29.15200	28.93700	29.15200	0.00000	7.02349	6.71623	962.81617	NaN	10.32708	0.01093	0.01093	186.15479	29.08033	C16649		185.14158			185.15281
937	114.09172	114.09185	114.09172	20.77000	20.43700	20.77000	0.00000	7.04402	6.68880	959.49480	NaN	11.35486	0.00956	0.00956	114.09176	20.65900			113.08406	C05853		113.08406
535	238.15550	238.15599	238.15550	10.02100	9.82900	10.02100	0.00000	7.14393	6.57705	953.83674	NaN	10.92564	0.00934	0.00934	238.15567	9.95700			237.15175	C05314		237.15180
1058	84.96788	84.96219	84.96788	12.29300	12.30200	12.29300	0.00000	6.74432	6.95151	941.91519	NaN	11.17314	0.01029	0.01029	84.96598	12.29600	C01485		83.96140		HMDB02036	83.96142
1039	88.07652	88.08024	88.07652	5.00500	5.12000	5.00500	0.00000	7.03028	6.65466	936.79937	NaN	9.33570	0.00865	0.00865	88.07776	5.04333		HMDB01080	87.06841	C00048	HMDB00119	87.06841
591	215.08257	215.09039	215.08257	5.79400	6.12100	5.79400	0.00000	7.41935	6.22178	916.49979	NaN	10.17451	0.00797	0.00797	215.08517	5.90300			214.07760		HMDB04822	214.07761
840	145.04094	145.03801	145.04094	0.17800	0.36400	0.17800	0.00000	6.64398	6.98478	910.84939	NaN	10.56697	0.01011	0.01011	145.03996	0.24000	C07833		144.03419	C07833		144.03420
867	134.07253	134.07015	134.07253	12.30500	12.31300	12.30500	0.00000	7.08407	6.53626	907.01962	NaN	9.46882	0.01069	0.01069	134.07173	12.30767			133.06400	C10901		133.06400
610	206.11726	206.11841	206.11726	18.01500	17.76420	18.01500	0.00000	7.59253	6.02503	905.76242	NaN	9.39499	0.01091	0.01091	206.11765	17.93140			205.11028	C10869		205.11028
706	185.13133	185.13213	185.13133	33.79100	33.60000	33.79100	0.00000	6.53070	7.08591	905.33360	NaN	9.81694	0.01051	0.01051	185.13160	33.72733	C17235		184.12520	C09633		184.12520

958	112.07331	112.07269	112.07331	9.77300	9.39400	9.77300	0.00000	7.05342	6.56098	904.33428	NaN	9.28315	0.00936	0.00936	112.07310	9.64667	C19548		111.06840			111.06841
136	725.08588	725.08417	725.08588	6.33600	6.58000	6.33600	0.00000	6.52582	7.08786	904.01005	NaN	7.26970	0.00883	0.00883	725.08531	6.41733			724.06483			724.06483
928	117.01617	117.01772	117.01617	4.08700	4.13100	4.08700	0.00000	6.69654	6.90992	900.75531	NaN	10.25870	0.00987	0.00987	117.01668	4.10167	C00122	HMDB00134	116.01096	C01384	HMDB00176	116.01096
832	146.07219	146.07369	146.07219	19.15700	19.07100	19.15700	0.00000	6.68801	6.91285	898.23159	NaN	9.30784	0.01033	0.01033	146.07269	19.12833			145.07388	C03656	HMDB12131	145.07388
124	822.01807	822.01398	822.01807	0.97900	0.98700	0.97900	0.00000	6.73029	6.86952	897.75820	NaN	9.76030	0.01139	0.01139	822.01670	0.98167	C00894	HMDB02307	821.12578	C00894	HMDB02307	821.12579
1000	98.98530	98.98713	98.98530	9.95000	9.84100	9.95000	0.00000	6.89845	6.68906	892.25913	NaN	10.18160	0.00971	0.00971	98.98591	9.91367	C12893		97.97701	C12554		97.97700
543	234.94627	234.94933	234.94627	11.05650	11.08900	11.05650	0.00000	7.00694	6.57002	887.56149	NaN	8.30275	0.00923	0.00923	234.94729	11.06733			233.95416	C03575		233.95420
1057	84.96086	84.96234	84.96086	9.84400	10.15900	9.84400	0.00000	6.79838	6.77621	886.51184	NaN	9.96165	0.00975	0.00975	84.96136	9.94900	C02271		83.95340	C02390		83.95336
191	546.05896	546.06482	546.05896	6.73600	6.78000	6.73600	0.00000	6.50298	7.07070	886.10763	NaN	7.94871	0.01009	0.01009	546.06091	6.75067	C13143		545.01100	C13143		545.01096
408	310.11231	310.10492	310.11231	4.27500	4.23700	4.27500	0.00000	6.66762	6.90235	884.46723	NaN	9.30790	0.00842	0.00842	310.10984	4.26233	C10713		309.10011	C10713		309.10010
666	197.99312	197.99492	197.99312	0.19000	0.18700	0.19000	0.00000	6.69729	6.85426	876.35876	NaN	7.96113	0.00995	0.00995	197.99372	0.18900	C05659	HMDB04096	196.99550	C05335	HMDB03966	196.99550
273	437.09808	437.10074	437.09808	9.78500	9.84100	9.78500	0.00000	7.08296	6.46201	873.48145	NaN	9.86901	0.00966	0.00966	437.09897	9.80367	C10067		436.10056	C10093		436.10056
170	586.08588	586.08350	586.08588	4.44000	4.40200	4.44000	0.00000	6.50600	7.03772	872.93463	NaN	8.02153	0.00991	0.00991	586.08508	4.42733	C11375		585.17200	C07482		585.21040
846	144.07181	144.07967	144.07181	4.09900	4.08400	4.09900	0.00000	6.68776	6.83656	864.50858	NaN	10.50739	0.01187	0.01187	144.07443	4.09400			143.06948			143.07350
289	422.03531	422.03565	422.03531	7.86600	7.87500	7.86600	0.00000	6.75703	6.76105	861.81598	NaN	10.07389	0.01029	0.01029	422.03542	7.86900	C07758		421.03779	C07758		421.03780
1056	84.96136	84.95879	84.96136	11.18600	11.05400	11.18600	0.00000	6.91055	6.60121	859.09571	NaN	9.91437	0.00900	0.00900	84.96050	11.14200	C02390		83.95336	C02271		83.95340
803	158.00391	158.00272	158.00391	13.24700	13.56100	13.24700	0.00000	6.27774	7.21552	851.18436	NaN	8.94765	0.01133	0.01133	158.00351	13.35167	C14407		156.99310	C14456		156.99310
1036	88.50945	88.51018	88.50945	9.78500	9.84100	9.78500	0.00000	6.84079	6.61777	836.54215	NaN	11.50936	0.00974	0.00974	88.50969	9.80367						
839	145.04419	145.04259	145.04419	13.97600	14.36200	13.97600	0.00000	6.56643	6.89048	835.85245	NaN	9.06832	0.00963	0.00963	145.04366	14.10467	C07833		144.03420	C07833		144.03419
730	182.98453	182.98462	182.98453	12.56400	12.56100	12.56400	0.00000	6.80726	6.54482	793.16923	NaN	9.43132	0.00883	0.00883	182.98456	12.56300	C07598		181.97080	C07719		181.97075
119	850.04822	850.04572	850.04822	3.18000	3.26000	3.18000	0.00000	7.14004	6.20990	792.32312	NaN	10.27587	0.01057	0.01057	850.04738	3.20667	C04739		849.10070			849.10072
789	163.94356	163.94426	163.94356	0.17800	0.57500	0.17800	0.00000	6.82226	6.49911	781.08446	NaN	10.39144	0.00968	0.00968	163.94379	0.31033	C01152	HMDB00479	162.97016	C18445		162.89950
640	201.10172	201.10277	201.10172	22.50000	22.19100	22.50000	0.00000	6.97944	6.31081	769.02633	NaN	10.37133	0.00985	0.00985	201.10207	22.39700	C06537		200.09496			200.09496
503	253.19377	253.18938	253.19377	7.77200	7.63900	7.77200	0.00000	6.76704	6.50030	760.26634	NaN	11.02063	0.01055	0.01055	253.19231	7.72767			252.18378			252.17255
583	218.97923	218.98261	218.97923	7.52450	7.30950	7.52450	0.00000	6.76170	6.48099	750.95604	NaN	9.97574	0.00923	0.00923	218.98036	7.45283	C18670		217.96550	C16199		217.98850
1093	81.03031	81.03940	81.03031	11.49200	11.48900	11.49200	0.00000	6.53129	6.70380	748.10448	NaN	11.43663	0.01139	0.01139	81.03334	11.49100	C00396		80.03740		HMDB03361	80.03745
256	456.98764	456.99081	456.98764	6.05300	5.79100	6.05300	0.00000	6.32137	6.82180	714.50012	NaN	9.65952	0.00990	0.00990	456.98870	5.96567	C17877		456.00870	C18002		456.00874
387	330.60980	330.60864	330.60980	23.50100	23.76900	23.50100	0.00000	7.09329	6.03740	710.05689	NaN	9.76046	0.00994	0.00994	330.60942	23.59033						
532	242.11986	242.12006	242.11986	4.40500	4.30800	4.40500	0.00000	6.77647	6.32706	700.47953	NaN	8.85863	0.00991	0.00991	242.11992	4.37267	C02168		241.11030	C10731		241.11030
243	461.23013	461.22769	461.23013	14.98900	14.89200	14.98900	0.00000	6.49371	6.59725	696.08992	NaN	10.47902	0.01044	0.01044	461.22932	14.95667	C10715		460.20972	C10831		460.20972
907	122.96470	122.96377	122.96470	22.68900	22.32100	22.68900	0.00000	6.43405	6.64926	693.43438	NaN	10.20841	0.00968	0.00968	122.96439	22.56633		HMDB12216	121.97128	C08270	HMDB12251	121.97129
295	415.92996	415.92514	415.92996	4.48700	4.56700	4.48700	0.00000	6.66772	6.40919	691.21803	NaN	10.43207	0.00874	0.00874	415.92836	4.51367	C11754		415.06600	C11754		415.06605
829	147.03526	147.03497	147.03526	19.28600	19.03600	19.28600	0.00000	7.22483	5.84486	688.72497	NaN	8.53788	0.00938	0.00938	147.03517	19.20267	C08369		146.02240	C08383		146.02239
981	101.06207	101.06284	101.06207	36.38100	36.28400	36.38100	0.00000	6.14976	6.91089	685.62030	NaN	9.42579	0.00997	0.00997	101.06232	36.34867	C12518		100.05243		HMDB01862	100.05243
340	363.15631	363.16055	363.15631	4.47500	4.31900	4.47500	0.00000	6.27414	6.77570	681.92592	NaN	11.44007	0.01175	0.01175	363.15773	4.42300			362.14779	C17362		362.14380
498	257.24478	257.24051	257.24478	0.20200	0.17500	0.20200	0.00000	6.38926	6.63037	671.70071	NaN	9.75250	0.00836	0.00836	257.24336	0.19300	C00249	HMDB00220	256.24020			256.24022
729	182.98444	182.98544	182.98444	13.81200	13.77300	13.81200	0.00000	6.44792	6.52550	656.36082	NaN	10.04854	0.00883	0.00883	182.98477	13.79900	C07598		181.97080	C07719		181.97075
857	138.09357	138.10001	138.09357	13.31700	13.44400	13.31700	0.00000	6.10814	6.86219	655.34745	NaN	10.66585	0.01057	0.01057	138.09571	13.35933	C00483	HMDB00306	137.08410	C01183		137.08410
778	168.07143	168.07787	168.07143	3.76900	3.73100	3.76900	0.00000	6.20777	6.75211	651.93180	NaN	10.62653	0.00970	0.00970	168.07357	3.75633			167.06948	C16444		167.06948
516	247.09445	247.09503	247.09445	4.33400	4.36600	4.33400	0.00000	6.34637	6.60096	647.85263	NaN	10.20910	0.01088	0.01088	247.09465	4.34467		HMDB00497	246.08519		HMDB11160	246.08519
584	218.13480	218.13748	218.13480	7.10100	7.12100	7.10100	0.00000	6.63722	6.26605	633.73933	NaN	8.82243	0.00865	0.00865	218.13569	7.10767	C03017	HMDB00824	217.13139			217.13139
348	358.20065	358.20361	358.20065	7.57200	7.67500	7.57200	0.00000	6.72464	6.14179	622.17028	NaN	9.30390	0.00898	0.00898	358.20164	7.60633	C07251		357.19400	C09558		357.19400
432	292.94785	292.94632	292.94785	3.84000	4.04900	3.84000	0.00000	6.40567	6.45809	621.34048	NaN	9.18556	0.01123	0.01123	292.94734	3.90967	C11009		291.96140	C11019		291.96142
497	257.24551	257.24252	257.24551	3.79300	3.43600	3.79300	0.00000	6.46180	6.37364	612.60664	NaN	9.69168	0.01007	0.01007	257.24452	3.67400	C00249	HMDB00220	256.24020			256.24022
172	578.91950	578.91608	578.91950	3.81600	3.73100	3.81600	0.00000	6.50865	6.28066	598.63652	NaN	9.61657	0.00906	0.00906	578.91836	3.78767	C03034		578.05500	C06017		578.05500
255	456.98767	456.99057	456.98767	6.66500	6.59200	6.66500	0.00000	6.38694	6.38189	592.53871	NaN	10.00537	0.01034	0.01034	456.98864	6.64067	C17877		456.00870	C18002		456.00874
506	251.94537	251.94992	251.94537	5.47600	5.37900	5.47600	0.00000	6.49114	6.26857	589.84300	NaN	8.77927	0.01113	0.01113	251.94689	5.44367	C11686		251.02280	C11696		251.02283
511	248.11791	248.12425	248.11791	4.31100	4.27200	4.31100	0.00000	6.55562	6.20245	589.35827	NaN	9.08033	0.00997	0.00997	248.12002	4.29800			247.11095	C19552		247.11090
1054	84.95935	84.95989	84.95935	7.31300	7.68700	7.31300	0.00000	6.72027	6.00116	578.66070	NaN	11.59073	0.00867	0.00867	84.95953	7.43767	C02390		83.95336	C02271		83.95340
802	158.00406	158.00349	158.00406	7.86600	7.48600	7.86600	0.00000	6.17542	6.52905	573.77350	NaN	10.84559	0.00774	0.00774	158.00387	7.73933	C14407		156.99310	C14456		156.99310
426	295.97760	295.98624	295.97760	4.26300	4.47200	4.26300	0.00000	6.15051	6.55341	573.61606	NaN	10.15406	0.01020	0.01020	295.98048	4.33267	C07461		294.94883	C07461		294.94880
810	156.10300	156.09828	3.84000	3.44800	3.84000	0.00000	6.76315	5.90136	562.42236	NaN	12.14440	0.00875	0.00875	156.09985	3.70933	C06177		155.09460	C10129		155.09460
776	168.07512	168.08354	168.07512	6.79500	7.02700	6.79500	0.00000	6.49545	6.14508	555.72043	NaN	9.73585	0.00912	0.00912	168.07793	6.87233	C16396		167.06950	C16397		167.06950
949	113.06875	113.07076	113.06875	24.36100	24.41600	24.36100	0.00000	7.90626	4.72882	554.20834	NaN	9.82539	0.01071	0.01071	113.06942	24.37933			112.05243			112.05243
1097	80.24271	80.23932	80.24271	3.75700	3.74200	3.75700	0.00000	6.40473	6.22453	552.59731	NaN	10.55148	0.00947	0.00947	80.24158	3.75200	C00747	HMDB00926	79.04220			79.04220
777	168.07370	168.07846	168.07370	6.45300	6.15600	6.45300	0.00000	6.29482	6.29285	541.22372	NaN	10.34704	0.00957	0.00957	168.07529	6.35400			167.06948	C16444		167.06948
345	360.13428	360.13538	360.13428	3.75700	4.02500	3.75700	0.00000	6.18043	6.37681	533.05390	NaN	11.13546	0.00999	0.00999	360.13464	3.84633			359.12634			359.12634
244	461.21863	461.21903	461.21863	39.45400	39.23900	39.45400	0.00000	5.77089	6.78611	532.98700	NaN	10.90750	0.00975	0.00975	461.21876	39.38233	C10715		460.20972	C10831		460.20972
346	359.01895	359.02329	359.01895	6.93600	7.19175	6.93600	0.00000	6.44285	6.04131	513.92556	NaN	9.50916	0.00875	0.00875	359.02040	7.02125	C13678		358.01780	C13758		358.01782
704	185.13040	185.13353	185.13040	17.01400	17.12900	17.01400	0.00000	6.13992	6.34372	513.79195	NaN	8.80190	0.01011	0.01011	185.13145	17.05233	C17235		184.12520	C09633		184.12520
347	358.19946	358.20352	358.19946	6.81800	7.19200	6.81800	0.00000	6.36384	6.10282	509.44752	NaN	10.97955	0.01100	0.01100	358.20082	6.94267	C07251		357.19400	C09558		357.19400
663	198.10371	198.10599	198.10371	3.79300	3.76600	3.79300	0.00000	6.25327	6.21080	508.78870	NaN	8.71357	0.00900	0.00900	198.10447	3.78400	C14416		197.09530	C19187		197.09530
187	555.89069	555.88306	555.89069	7.39500	7.16900	7.39500	0.00000	6.53623	5.91197	504.76824	NaN	10.66510	0.01064	0.01064	555.88814	7.31967		HMDB11104	554.93066			554.93068
956	112.07391	112.07108	112.07391	0.41400	0.45800	0.41400	0.00000	6.64036	5.79734	502.12639	NaN	8.68744	0.01053	0.01053	112.07297	0.42867	C19548		111.06840			111.06841
1011	97.02765	97.02760	97.02765	6.71200	6.87400	6.71200	0.00000	5.94854	6.46426	495.91432	NaN	9.10188	0.00971	0.00971	97.02763	6.76600	C07090		96.02110	C14279		96.02110
775	168.07239	168.07040	168.07239	4.26300	4.40200	4.26300	0.00000	6.34868	6.05459	493.55388	NaN	11.26514	0.01070	0.01070	168.07173	4.30933			167.06948	C16444		167.06948
460	271.93451	271.93738	271.93451	3.85100	3.80100	3.85100	0.00000	6.33195	6.01076	478.83246	NaN	11.49387	0.01052	0.01052	271.93547	3.83433	C19007		271.01019	C19005		271.01020
1014	96.04842	96.04595	96.04842	7.56000	7.61600	7.56000	0.00000	6.07078	6.23608	470.32720	NaN	9.61246	0.01058	0.01058	96.04760	7.57867	C02502	HMDB13751	95.03712			95.03711
703	185.13075	185.13127	185.13075	18.81500	19.17700	18.81500	0.00000	6.39965	5.90110	468.89203	NaN	9.54934	0.00917	0.00917	185.13093	18.93567	C17235		184.12520	C09633		184.12520
558	227.98195	227.98064	227.98195	3.96900	3.87200	3.96900	0.00000	5.98536	6.21277	445.44078	NaN	10.49656	0.01127	0.01127	227.98151	3.93667	C01557		226.99047	C12469		226.99850
534	240.11612	240.11052	240.11612	4.08650	4.40200	4.08650	0.00000	6.15982	5.97225	430.96680	NaN	11.61039	0.00996	0.00996	240.11425	4.19167			239.10586	C06860	HMDB01510	239.10769
668	197.12271	197.13083	197.12271	3.92233	3.78933	3.92233	0.00000	6.09867	5.95072	413.51661	NaN	10.85282	0.01124	0.01124	197.12542	3.87800	C13688		196.12118	C13311		196.12120
1035	88.50816	88.50926	88.50816	4.20500	4.10700	4.20500	0.00000	6.08233	5.92844	405.60678	NaN	10.91294	0.00973	0.00973	88.50852	4.17233						
669	197.12129	197.12761	197.12129	4.48700	4.41350	4.48700	0.00000	5.91718	6.09334	405.55680	NaN	9.15576	0.00968	0.00968	197.12340	4.46250	C13688		196.12118	C13311		196.12120
101	922.01123	922.01019	922.01123	15.46000	15.59800	15.46000	0.00000	7.38911	4.61769	404.80117	NaN	8.86980	0.01031	0.01031	922.01088	15.50600			921.15707	C14120		921.15710

213	497.87427	497.87286	497.87427	4.29900	4.21300	4.29900	0.00000	6.07430	5.77638	374.40544	NaN	10.51239	0.00952	0.00952	497.87380	4.27033	C18861		496.93487	C18740		496.93490
771	171.10597	171.10861	171.10597	4.84000	4.60200	4.84000	0.00000	6.11788	5.65443	360.01813	NaN	12.26177	0.01050	0.01050	171.10685	4.76067	C11310		170.09700	C14280		170.09430
476	267.20606	267.20743	267.20606	4.34600	4.35500	4.34600	0.00000	5.90840	5.83715	355.23429	NaN	12.08526	0.00949	0.00949	267.20651	4.34900			266.19943	C04834		266.18820
212	497.87561	497.87524	497.87561	4.06333	3.77800	4.06333	0.00000	5.97776	5.69942	343.29450	NaN	11.41975	0.00978	0.00978	497.87549	3.96822	C18861		496.93487	C18740		496.93490
809	156.10294	156.10431	156.10294	4.45200	4.06000	4.45200	0.00000	6.07686	5.51523	328.99607	NaN	9.20466	0.00971	0.00971	156.10339	4.32133	C07939		155.09463			155.09463
732	182.98439	182.98354	182.98439	34.79200	35.18900	34.79200	0.00000	4.22235	7.35464	326.52091	NaN	10.00322	0.00927	0.00927	182.98411	34.92433	C07598		181.97080	C07719		181.97075
571	224.12549	224.13123	224.12549	6.41800	6.41500	6.41800	0.00000	6.31230	5.16251	310.25925	NaN	9.55195	0.00932	0.00932	224.12740	6.41700	C12058		223.12080	C13138		223.12080
764	173.10973	173.11264	173.10973	4.65200	4.68400	4.65200	0.00000	5.68343	5.78564	309.36908	NaN	10.12284	0.00896	0.00896	173.11070	4.66267		HMDB12488	172.10005			172.10005
509	249.19457	249.19432	249.19457	4.97000	5.00250	4.97000	0.00000	6.43107	4.98843	301.79537	NaN	9.97797	0.01099	0.01099	249.19448	4.98083			248.18886	C10171		248.18886
442	283.21088	283.20770	283.21088	4.36900	4.26000	4.36900	0.00000	5.39437	5.98361	295.59579	NaN	8.69690	0.01103	0.01103	283.20982	4.33267	C05918		282.19840	C05919		282.19840
242	461.22208	461.21848	461.22208	16.69600	16.87000	16.69600	0.00000	5.91766	5.16727	255.30639	NaN	10.25184	0.01095	0.01095	461.22088	16.75400	C10715		460.20972	C10831		460.20972
441	283.22650	283.22858	283.22650	6.17100	6.26200	6.17100	0.00000	5.67348	5.31922	243.80004	NaN	10.81694	0.00988	0.00988	283.22719	6.20133			282.21948			282.21948
886	130.01061	130.00971	130.01061	6.71200	6.83900	6.71200	0.00000	4.54820	5.76478	173.55385	NaN	9.58099	0.00901	0.00901	130.01031	6.75433	C06554		129.01740	C06560		129.01744
795	158.96130	158.96089	158.96069	30.56000	30.42100	30.43600	6.05376	7.01249	7.72559	1586.10292	425.71226	10.34945	0.01026	0.01026	158.96096	30.47233	C19212		157.97238	C19164		157.97240
951	113.07156	113.06876	113.06841	13.87700	13.93800	13.95300	6.13244	6.86696	6.78194	920.06925	460.55892	8.71270	0.00928	0.00928	113.06958	13.92267			112.05243			112.05243
984	101.07123	101.06580	101.06339	5.40100	4.94325	5.07600	6.15327	7.64530	7.52021	1964.02728	470.25200	8.31483	0.00957	0.00957	101.06681	5.14008	C08311		100.06366	C19296		100.06366
484	267.20758	267.20487	267.20749	2.85800	2.50600	2.50900	7.22283	7.83812	7.94685	2677.08399	1370.36781	11.87615	0.01095	0.01095	267.20665	2.62433			266.19943	C04834		266.18820
927	118.08660	118.08633	118.08606	9.85100	9.61700	9.60900	7.29943	8.16036	8.53840	4227.56670	1479.45194	10.79231	0.00952	0.00952	118.08633	9.69233			117.07897			117.07897
612	206.11992	206.11981	206.11856	11.68800	11.46600	11.37500	7.40537	8.08462	7.18134	2065.19793	1644.78874	10.61699	0.00902	0.00902	206.11943	11.50967	C10846		205.11030			205.11028
105	922.01080	922.00977	922.01044	13.50100	13.49100	13.36400	7.45571	8.43064	8.14569	3976.53614	1729.71437	10.50767	0.00989	0.00989	922.01034	13.45200			921.15707	C14120		921.15710
621	206.12083	206.11908	206.11876	3.17500	2.88300	2.82700	7.52383	8.12355	8.18685	3481.42758	1851.64119	8.38858	0.01036	0.01036	206.11956	2.96167	C10846		205.11030			205.11028
537	238.15610	238.15767	238.15781	0.17300	0.17500	0.16600	7.70176	7.29563	6.92292	1223.26381	2212.24076	9.28764	0.00977	0.00977	238.15719	0.17133			237.15175	C05314		237.15180
799	158.96114	158.96169	158.96138	9.62700	9.35800	9.30200	7.70657	8.38209	8.34181	4281.03879	2222.90839	10.86872	0.00855	0.00855	158.96140	9.42900	C19212		157.97238	C19164		157.97240
641	201.10400	201.10262	201.10214	20.94100	20.50800	20.67600	7.71983	7.00733	6.90197	1048.00883	2252.56503	10.77575	0.01083	0.01083	201.10292	20.70833	C06537		200.09500	C14759		200.09500
248	461.21814	461.21823	461.21976	9.28600	9.37000	9.29100	7.74318	8.31765	8.02259	3533.76230	2305.79589	7.76537	0.01054	0.01054	461.21871	9.31567	C10715		460.20972	C10831		460.20972
536	238.15749	238.15685	238.15311	8.02600	7.94600	7.86600	7.79055	6.27225	6.65386	641.01589	2417.65306	10.93428	0.01011	0.01011	238.15581	7.94600			237.15175	C05314		237.15180
349	358.20215	358.20459	358.19815	0.18500	0.42200	0.16600	7.79531	5.91656	6.67252	541.60768	2429.17884	9.35279	0.01053	0.01053	358.20163	0.25767	C07251		357.19400	C09558		357.19400
524	243.17931	243.17418	243.17442	12.33500	12.31300	12.31600	7.80111	7.67194	7.62937	2102.02837	2443.30648	9.92961	0.00868	0.00868	243.17597	12.32133	C08451		242.16710	C17716		242.16710
743	181.13419	181.13280	181.13261	10.05100	9.98200	10.09100	7.82118	7.83522	6.54877	1328.75273	2492.83312	11.13829	0.01105	0.01105	181.13320	10.04133	C11283		180.12626	C11120		180.12630
109	922.00952	922.01001	922.01080	12.95900	12.90200	12.91700	7.86583	8.62313	8.55186	5364.15427	2606.67592	9.02773	0.01200	0.01200	922.01011	12.92600			921.15707	C14120		921.15710
613	206.11919	206.11844	206.11598	12.53550	12.32500	12.26900	7.94408	7.75525	7.24229	1805.82139	2818.84164	10.81973	0.00980	0.00980	206.11787	12.37650			205.11028	C10869		205.11028
952	113.07034	113.07185	113.07154	9.01500	9.39400	9.33800	8.03735	7.89192	7.58156	2290.98819	3094.38776	9.93579	0.00839	0.00839	113.07124	9.24900			112.05243			112.05243
561	227.98387	227.98325	227.98496	0.17300	0.18700	0.19000	8.03825	7.59592	8.05409	2502.40381	3097.17221	9.99761	0.00979	0.00979	227.98402	0.18333	C01557		226.99047	C12469		226.99850
617	206.12087	206.11806	206.11900	8.07300	8.01600	8.16000	8.03844	7.19390	7.86219	1859.45822	3097.78844	11.46626	0.00940	0.00940	206.11931	8.08300	C10846		205.11030			205.11028
768	171.99944	171.99371	171.99191	0.17300	0.19900	0.20200	8.08892	7.08413	7.99900	1884.77014	3258.16801	11.03139	0.01099	0.01099	171.99502	0.19133	C13672		170.98445	C13058		170.98440
999	100.07672	100.07638	100.07610	9.28600	9.02900	8.97300	8.13977	8.91700	8.74998	6860.20258	3428.11057	10.93608	0.00951	0.00951	100.07640	9.09600		HMDB11749	99.06841	C11249		99.06841
115	922.01032	922.01007	922.01123	2.25700	1.92900	1.94400	8.22188	10.09931	10.17531	25268.28236	3721.48172	10.74788	0.01013	0.01013	922.01054	2.04333			921.15707	C14120		921.15710
620	206.11841	206.10994	206.11049	1.75100	1.65900	1.68533	8.25145	8.01759	7.99957	3006.65686	3833.17912	9.01723	0.01132	0.01132	206.11295	1.69844			205.11028	C10869		205.11028
712	185.13496	185.13205	185.12994	12.33500	12.32500	12.31600	8.33086	8.08785	8.35549	3720.72134	4149.98983	12.03276	0.01149	0.01149	185.13232	12.32533	C17235		184.12520	C09633		184.12520
994	100.07742	100.07652	100.07613	11.98200	11.90100	12.22200	8.33645	8.06947	7.91139	2952.56593	4173.24681	10.48752	0.01152	0.01152	100.07669	12.03500		HMDB11749	99.06841	C11249		99.06841
467	270.21951	270.21762	270.21683	12.33500	12.33700	12.32800	8.33749	7.66296	6.81123	1390.04944	4177.58324	9.72125	0.01039	0.01039	270.21799	12.33333			269.19909	C05763		269.19391
1015	96.04493	96.04432	96.04541	8.09700	8.16900	8.12500	8.35995	6.94877	6.65712	900.49530	4272.45985	9.75989	0.00998	0.00998	96.04489	8.13033	C02502	HMDB13751	95.03710			95.03711
468	270.22083	270.21863	270.21692	1.42100	1.74100	1.72000	8.37598	7.70154	7.36894	1872.88850	4341.52326	9.83140	0.00973	0.00973	270.21879	1.62733			269.19909	C05763		269.19391
998	100.07680	100.07704	100.07579	9.71000	9.29900	9.42000	8.41035	8.68080	8.54172	5493.16187	4493.32126	8.54342	0.01061	0.01061	100.07654	9.47633		HMDB11749	99.06841	C11249		99.06841
616	206.11917	206.11821	206.12041	13.08900	12.99600	13.25800	8.55528	7.95792	7.68432	2492.69490	5194.11176	11.06541	0.01205	0.01205	206.11926	13.11433	C10846		205.11030			205.11028
942	114.09160	114.09126	114.09098	13.46500	13.43200	13.40000	8.62839	8.68296	8.25393	4762.09419	5588.06535	10.05340	0.00824	0.00824	114.09128	13.43233			113.08406	C05853		113.08406
469	270.21851	270.21841	270.21973	0.78500	0.18700	0.54300	8.64276	7.37294	7.41087	1622.78903	5668.92842	9.95262	0.01126	0.01126	270.21888	0.50500			269.19909	C05763		269.19391
275	437.09689	437.09918	437.09790	18.79900	18.90700	18.87400	8.74901	9.08799	8.84481	7835.34934	6304.42136	9.22933	0.01087	0.01087	437.09799	18.86000	C10067		436.10056	C10093		436.10056
727	184.13341	184.13297	184.13348	10.35700	10.06500	10.36200	8.76243	9.11706	9.15635	9290.12586	6389.62087	9.05884	0.01091	0.01091	184.13329	10.26133	C12452		183.12590	C12453		183.12590
653	199.14517	199.14398	199.14441	39.90800	39.91000	39.91300	8.78567	8.09601	7.86497	2923.36226	6539.84406	8.53992	0.00869	0.00869	199.14452	39.91033	C06185		198.13680	C10858	HMDB06548	198.13683
724	184.13287	184.13332	184.13341	1.53900	1.76500	1.75600	8.86871	9.43256	9.01560	10138.38118	7106.11383	8.89146	0.00905	0.00905	184.13320	1.68667	C12452		183.12590	C12453		183.12590
1022	89.50727	89.50715	89.50760	14.86600	14.80900	15.10700	8.87423	8.67197	7.45325	3173.55604	7145.41561	9.74386	0.00907	0.00907	89.50734	14.92733						
699	186.15733	186.15642	186.15292	0.17300	0.17500	0.17800	8.92409	7.71281	7.85084	2396.63747	7510.77156	10.86885	0.01019	0.01019	186.15556	0.17533			185.15281	C16649		185.14158
623	206.11559	206.11716	206.11552	1.17400	1.15200	1.15500	8.94302	8.37278	8.34879	4276.05385	7654.26187	11.13209	0.00997	0.00997	206.11609	1.16033			205.11028	C10869		205.11028
112	922.01086	922.01025	922.00806	3.49300	3.41300	3.46300	8.94593	10.12990	9.29770	16544.31371	7676.58309	9.22981	0.01100	0.01100	922.00973	3.45633			921.15707	C14120		921.15710
716	184.13339	184.13330	184.13356	13.17100	12.91400	12.92900	8.97772	7.72754	7.11086	1667.70007	7924.51298	9.20277	0.01006	0.01006	184.13342	13.00467	C12452		183.12590	C12453		183.12590
691	186.95761	186.95705	186.95685	0.90300	0.88200	0.87300	8.99917	9.54062	9.57122	14128.05401	8096.34987	11.44268	0.00944	0.00944	186.95717	0.88600			185.93164	C14846		185.93160
880	130.96799	130.97681	130.97601	1.02100	1.07000	1.06100	9.03373	9.17639	9.07522	9189.41834	8381.02532	10.46816	0.00953	0.00953	130.97360	1.05067	C14867		129.95884	C14860		129.95880
854	141.95874	141.95873	141.95842	1.00900	1.03500	1.02600	9.04478	10.81164	10.63454	45391.98061	8474.16735	10.98184	0.01082	0.01082	141.95863	1.02333	C00169	HMDB01096	140.98270	C00169	HMDB01096	140.98271
695	186.15886	186.15794	186.15695	14.60700	14.62100	14.58900	9.14869	8.01644	7.09842	1914.92090	9402.11851	9.96930	0.01029	0.01029	186.15792	14.60567			185.15281	C16649		185.14158
224	480.30701	480.30701	480.30649	36.41150	36.30800	36.05200	9.22607	8.89991	8.60688	6332.14305	10158.57512	10.30349	0.01016	0.01016	480.30683	36.25717			479.30115			479.30115
485	267.20615	267.20709	267.20645	21.87200	21.86200	21.85300	9.24392	8.37795	8.13958	3861.30461	10341.52698	8.93303	0.01056	0.01056	267.20656	21.86233			266.19943	C04834		266.18820
294	419.08856	419.08829	419.08710	18.37500	18.38800	18.40300	9.26734	8.50369	8.73522	5538.38150	10586.55830	9.01478	0.01083	0.01083	419.08798	18.38867			418.08897	C06435		418.08900
739	182.98483	182.98447	182.98393	1.04400	1.03500	1.03800	9.36270	11.29483	11.21384	77214.06136	11645.76646	8.13098	0.00973	0.00973	182.98441	1.03900	C07598		181.97080	C07719		181.97075
647	199.98763	199.98801	199.98747	0.93900	0.81100	0.90800	9.36482	9.87703	9.89288	19632.75637	11670.52978	9.92830	0.00775	0.00775	199.98770	0.88600	C18905		198.97480	C19047		198.97477
608	207.11285	207.11160	207.11112	1.12700	1.15200	1.15500	9.43794	8.85499	8.70740	6510.66568	12555.80130	11.38451	0.00922	0.00922	207.11186	1.14467	C07499		206.10550	C12590		206.10550
690	186.95728	186.95644	186.95712	0.18500	0.17500	0.19000	9.48808	9.53289	9.56466	14027.49718	13201.47344	9.94517	0.00858	0.00858	186.95695	0.18333			185.93164	C14846		185.93160
1091	81.52153	81.52149	81.52152	0.17300	0.17500	0.19000	9.52813	9.75621	9.88219	18383.30642	13740.92579	9.52402	0.00931	0.00931	81.52151	0.17933						
117	922.00934	922.00977	922.01044	0.93900	0.92900	0.92000	9.54168	10.33580	10.50382	33517.04777	13928.35102	10.75746	0.00916	0.00916	922.00985	0.92933			921.15707	C14120		921.15710
781	167.01231	167.01277	167.01230	1.03300	1.08200	1.07300	9.61233	10.40519	10.33199	31843.59680	14947.89221	9.80177	0.01066	0.01066	167.01246	1.06267			166.00311	C17948		166.00310
929	116.97812	116.97693	116.97710	0.97400	0.88200	0.89600	9.65901	6.78109	7.04401	1004.80561	15662.19413	10.03547	0.00983	0.00983	116.97738	0.91733	C00122	HMDB00134	116.01096	C01384	HMDB00176	116.01096
1062	84.96035	84.96016	84.95989	1.03300	1.07000	1.07300	9.81596	10.19125	10.13123	25880.39991	18323.85146	8.79579	0.00990	0.00990	84.96013	1.05867	C02390		83.95336	C02271		83.95340
225	478.29077	478.29254	478.29108	33.89200	33.81200	33.79100	9.83788	9.11940	8.87179	8067.45568	18729.94706	8.87034	0.01083	0.01083	478.29146	33.83167			477.28550			477.28554
276	437.09830	437.09744	437.09726	14.70200	14.60900	14.61200	9.92162	9.42105	9.20191	11064.29084	20366.03783	12.43529	0.00818	0.00818	437.09767	14.64100	C10067		436.10056	C10093		436.10056
223	484.33997	484.33817	484.33786	39.02500	39.02700	39.03000	9.92963	9.37473	9.82352	14751.87313	20529.77244	10.52472	0.01150	0.01150	484.33866	39.02733			483.31960	C02592	HMDB00722	483.30185

915	121.05115	121.05086	121.05102	11.29900	11.28900	11.24500	10.05667	9.09444	9.59762	11453.28565	23310.84146	8.98078	0.00928	0.00928	121.05101	11.27767		HMDB01366	120.04359		HMDB01366	120.04360
917	121.05113	121.05078	121.05104	12.15900	11.87800	11.88100	10.09407	9.36304	9.91726	15369.71185	24199.12566	8.90619	0.00991	0.00991	121.05098	11.97267		HMDB01366	120.04359		HMDB01366	120.04360
357	354.28412	354.28330	354.28424	34.09200	34.10600	34.08500	10.19617	9.73992	10.13655	20707.14391	26800.30115	10.74686	0.00857	0.00857	354.28389	34.09433	C07055		353.25930			353.29298
372	344.22876	344.22778	344.22797	13.53600	13.51400	13.51700	10.25804	9.74528	9.41902	14503.51237	28510.91011	9.17940	0.00871	0.00871	344.22817	13.52233	C07879		343.22598	C07879		343.22600
1032	89.50736	89.50761	89.50740	0.96200	1.01100	1.00200	10.32640	11.81424	11.71864	128854.04827	30528.03646	10.25672	0.00814	0.00814	89.50746	0.99167						
323	388.25510	388.25565	388.25345	14.24200	14.23300	14.22400	10.49766	9.72053	9.46051	14625.40719	36230.44671	10.55860	0.00895	0.00895	388.25473	14.23300			387.24817			387.24817
728	184.13696	184.13138	184.12744	9.06200	9.15800	9.11450	10.51154	9.74552	9.36301	14104.72399	36736.89652	10.11003	0.01057	0.01057	184.13193	9.11150	C12452		183.12590	C12453		183.12590
252	457.30277	457.30338	457.30103	39.03700	39.05100	39.04200	10.51257	9.72290	9.89413	18187.92147	36775.01149	9.32693	0.01009	0.01009	457.30239	39.04333			456.29878			456.28755
314	399.24973	399.24957	399.24896	39.03700	39.05100	39.05400	10.79903	10.36453	10.76184	38684.07083	48973.39935	9.71581	0.00911	0.00911	399.24942	39.04733	C14446		398.24330	C14513		398.24334
1066	84.08128	84.08044	84.07974	39.90800	39.62800	39.70100	10.90508	10.07613	8.28059	9685.27094	54452.14092	8.71841	0.01031	0.01031	84.08049	39.74567			83.07350			83.07350
1031	89.50752	89.50762	89.50722	0.17300	0.17500	0.17800	10.94863	10.95816	11.05567	60289.55316	56875.97910	8.58707	0.01147	0.01147	89.50745	0.17533						
1044	86.09728	86.09712	86.09721	34.82200	34.73000	35.02700	10.99515	9.37635	8.65367	8225.61583	59584.19604	9.96779	0.01001	0.01001	86.09720	34.85967	C03219		85.08915	C01746		85.08910
1045	86.09731	86.09715	86.09702	35.56400	35.60100	35.68700	10.99674	9.74069	9.32917	13834.59389	59679.36934	11.09847	0.00857	0.00857	86.09716	35.61733	C03219		85.08915	C01746		85.08910
500	255.20714	255.20696	255.20664	14.97200	14.98600	14.97700	11.20832	10.96917	11.04262	60228.29274	73741.05428	9.95139	0.00816	0.00816	255.20691	14.97833	C17603		254.18820	C17606		254.18820
1092	81.52124	81.52158	81.52139	1.03300	1.05800	1.06100	11.21080	11.46347	11.46582	95286.65150	73924.55390	8.86964	0.00957	0.00957	81.52140	1.05067						
892	128.11185	128.11212	128.11153	0.95000	0.82300	0.76700	11.32970	10.43972	10.00315	27486.04993	83258.38499	10.73471	0.00959	0.00959	128.11183	0.84667			127.09971	C11519		127.09970
1077	83.05216	83.05320	83.04678	17.90400	17.60000	17.82600	11.38100	9.40150	9.07498	10282.92249	87640.69354	10.02786	0.01003	0.01003	83.05071	17.77667		HMDB13749	82.04186	C08389		82.05310
1048	86.09728	86.09714	86.09709	37.93000	37.80300	37.75900	11.49268	10.38884	9.84130	24712.61342	97995.64064	11.09628	0.00896	0.00896	86.09717	37.83067	C03219		85.08915	C01746		85.08910
889	128.11061	128.10956	128.10895	5.55350	5.70900	5.66450	11.53154	10.39039	9.79278	24139.03787	101878.57463	11.37342	0.01146	0.01146	128.10971	5.64233			127.09971	C11519		127.09970
1068	84.08072	84.08125	84.08074	1.62100	1.91800	1.86200	11.53721	8.92898	8.66756	6622.77588	102458.51557	10.93778	0.01006	0.01006	84.08091	1.80033			83.07350			83.07350
890	128.11267	128.11276	128.11238	0.17300	0.18700	0.17800	11.66526	10.43010	9.92455	26300.06966	116455.15401	11.85031	0.00910	0.00910	128.11261	0.17933			127.09971	C11519		127.09970
1046	86.09751	86.09717	86.09721	7.80200	7.56900	7.60700	11.67096	10.71261	9.45548	23957.64799	117120.91069	9.06912	0.01242	0.01242	86.09730	7.65933	C03219		85.08915	C01746		85.08910
700	186.15990	186.15999	186.15981	14.99600	14.99800	15.00100	11.69514	10.62175	10.15418	32466.49868	119987.52157	9.72075	0.01105	0.01105	186.15990	14.99833			185.15281	C16649		185.14158
1042	86.09753	86.09712	86.09716	12.60600	12.91400	12.94000	11.69940	10.20310	7.17100	5925.69640	120498.99251	9.84210	0.01133	0.01133	86.09727	12.82000	C03219		85.08915	C01746		85.08910
603	213.19649	213.19565	213.19635	14.99600	14.99800	15.00100	11.81641	10.79772	10.29772	38090.46539	135456.72158	9.78360	0.00852	0.00852	213.19616	14.99833			212.17763			212.17763
895	127.12339	127.12315	127.12352	26.92200	27.04200	26.79800	12.74002	8.23814	9.98882	9076.82257	341128.97688	10.18337	0.00954	0.00954	127.12336	26.92067	C07287		126.10450		HMDB06024	126.10447
896	127.12324	127.12304	127.12314	38.39000	38.00300	38.11200	12.74780	12.02074	11.24791	112907.24333	343794.74241	9.59484	0.01020	0.01020	127.12314	38.16833	C07287		126.10450		HMDB06024	126.10447
1051	86.09736	86.09716	86.09699	0.93900	0.92900	0.94300	12.77758	12.19286	11.46459	137135.22661	354186.20684	7.97622	0.01076	0.01076	86.09717	0.93700	C03219		85.08915	C01746		85.08910
1052	86.09741	86.09721	86.09715	0.52600	0.17500	0.17800	12.79888	12.55181	11.85611	199577.98441	361811.48307	9.28884	0.01087	0.01087	86.09725	0.29300	C03219		85.08915	C01746		85.08910
897	127.12336	127.12315	127.12315	38.96600	39.13300	38.96000	12.84674	12.07850	11.33577	121434.77807	379547.49672	9.68986	0.01104	0.01104	127.12322	39.01967	C07287		126.10450		HMDB06024	126.10447
900	127.12373	127.12351	127.12346	8.45000	8.49900	8.43100	15.67485	14.79629	14.61064	2430146.12401	6419496.61777	8.49716	0.00939	0.00939	127.12356	8.46000	C07287		126.10450		HMDB06024	126.10447

Appendix - C - Wild Type Cellobiose Non Polar Metabolites

id	MZ_blank	MZ_WTCb_NonPolar_Rep1	MZ_WTCb_NonPolar_Rep2	RT_blank	RT_WTCb_NonPolar_Rep1	RT_WTCb_NonPolar_Rep2	Int_blank	Int_WTCb_NonPolar_Rep1	Int_WTCb_NonPolar_Rep2	exp(mean.grp1)	exp(mean.grp2)	fold.mean	p.ttest	p.wilcox	mean_m/z	mean_rt	KEGG_ID	HMDB_ID_1	Match_mass	KEGG_ID_2	HMDB_ID_2	Match_mass_2
302	118.12277	118.12238	118.12277	3.42100	3.27200	3.42100	0.00000	7.69246	7.15790	1677.69627	NaN	10.94220	0.00927	0.00927	118.12264	3.37133	C00183	HMDB00883	117.079	C00431	HMDB03355	117.079
293	121.05108	121.05105	121.05094	4.59900	4.25000	4.29300	10.13943	8.54554	7.81161	3563.76987	25322.06036	9.89702	0.01062	0.01062	121.05102	4.38067		HMDB01366	120.043594		HMDB01366	120.043596
309	102.12760	102.12760	102.12822	33.68000	32.96500	33.12600	10.16170	8.00336	7.88514	2819.31422	25892.15049	11.14724	0.00966	0.00966	102.12791	33.25700	C08306		101.1204	C14691		101.1204
327	100.11165	100.11152	100.11165	7.56700	7.76000	7.56700	0.00000	7.30050	8.03603	2139.36587	NaN	8.47164	0.01148	0.01148	100.11161	7.63133			99.104799	C00571		99.1048
310	102.12780	102.12775	102.12780	16.07100	15.41500	16.07100	0.00000	8.36353	8.22918	4009.22911	NaN	9.36681	0.01113	0.01113	102.12779	15.85233	C08306		101.1204	C14691		101.1204
328	100.11026	100.11041	100.11126	1.61900	1.94100	1.58400	10.77013	8.19784	8.25804	3744.11755	47578.31620	10.55535	0.01044	0.01044	100.11064	1.71467			99.104799	C00571		99.1048
266	270.21777	270.21878	270.21777	2.73800	3.48400	2.73800	0.00000	7.05544	8.29412	2153.35711	NaN	10.01881	0.00829	0.00829	270.21811	2.98667			269.199094	C05763		269.193906
304	118.12193	118.12203	118.12144	3.13900	2.35350	2.41975	10.23772	8.66717	8.30318	4842.42256	27937.35389	11.24132	0.01010	0.01010	118.12180	2.63742	C00183	HMDB00883	117.079	C00431	HMDB03355	117.079
312	102.12802	102.12789	102.12786	12.92600	13.48400	13.17400	2.25092	8.30996	8.30496	4053.98937	9.49644	8.65404	0.00987	0.00987	102.12793	13.19467	C08306		101.1204	C14691		101.1204
272	202.21600	202.21614	202.21600	34.83400	35.16700	34.83400	0.00000	8.00644	8.32851	3524.42384	NaN	10.85759	0.01139	0.01139	202.21605	34.94500	C19325		201.1729			201.172866
329	100.11175	100.11118	100.11175	7.93200	8.56100	7.93200	0.00000	7.91700	8.34067	3390.83469	NaN	10.23844	0.01032	0.01032	100.11156	8.14167			99.104799	C00571		99.1048
313	102.12795	102.12743	102.12795	2.49100	2.56500	2.49100	0.00000	7.68084	8.39257	3092.40549	NaN	8.64268	0.01044	0.01044	102.12778	2.51567	C08306		101.1204	C14691		101.1204
314	102.12788	102.12795	102.12788	32.36000	32.60000	32.36000	0.00000	8.32290	8.48417	4462.83008	NaN	11.27630	0.01016	0.01016	102.12791	32.44000	C08306		101.1204	C14691		101.1204
343	69.07035	69.07034	69.07091	6.11900	7.14700	6.76600	9.13830	8.93520	8.49688	6099.95661	9304.88791	9.48559	0.01050	0.01050	69.07053	6.67733	C17530		68.0626	C16521		68.0626
315	102.12796	102.12786	102.12796	17.68500	17.73600	17.68500	0.00000	8.46658	8.50322	4841.10312	NaN	11.25272	0.01030	0.01030	102.12793	17.70200	C08306		101.1204	C14691		101.1204
316	102.12795	102.12788	102.12795	14.57500	14.60300	14.57500	0.00000	8.54876	8.55407	5174.08890	NaN	8.36089	0.00981	0.00981	102.12793	14.58433	C08306		101.1204	C14691		101.1204
317	102.12786	102.12816	102.12786	16.86000	16.11000	16.86000	0.00000	8.18200	8.55559	4310.43566	NaN	9.75087	0.00965	0.00965	102.12796	16.61000	C08306		101.1204	C14691		101.1204
296	121.05145	121.05103	121.05064	39.91000	39.91400	39.66300	11.24969	9.43126	8.61896	8309.10608	76856.31381	10.70676	0.00943	0.00943	121.05104	39.82900		HMDB01366	120.043594		HMDB01366	120.043596
318	102.12797	102.12791	102.12760	19.53400	19.60800	18.80400	6.74615	8.36197	8.67138	4997.41356	850.77949	10.38046	0.01030	0.01030	102.12783	19.31533	C08306		101.1204	C14691		101.1204
319	102.12781	102.12800	102.12781	37.83700	37.84100	37.83700	0.00000	8.04317	8.71034	4344.88819	NaN	9.89167	0.00786	0.00786	102.12787	37.83833	C08306		101.1204	C14691		101.1204
29	922.01093	922.00824	922.01001	6.31900	6.18100	5.63600	7.86967	6.83185	8.72838	2392.54701	2616.71167	11.60644	0.01162	0.01162	922.00973	6.04533			921.157073	C14120		921.1571
30	922.01074	922.01148	922.01038	2.42000	1.56400	2.38500	8.36540	8.51012	8.77132	5657.40726	4295.83374	10.87314	0.01024	0.01024	922.01086	2.12300			921.157073	C14120		921.1571
269	270.21829	270.21811	270.21829	4.57500	4.60300	4.57500	0.00000	8.68622	8.77504	6189.61272	NaN	11.11359	0.01161	0.01161	270.21823	4.58433			269.199094	C05763		269.193906
322	102.12793	102.12773	102.12780	26.60100	26.31000	27.30700	8.52636	8.52976	8.77962	5794.63980	5046.05229	8.41465	0.01080	0.01080	102.12782	26.73933	C08306		101.1204	C14691		101.1204
344	69.07015	69.07031	69.06996	2.05475	3.33100	2.45533	9.97758	7.13333	8.81130	2899.55627	21538.12258	9.89699	0.01049	0.01049	69.07014	2.61369	C17530		68.0626	C16521		68.0626
323	102.12816	102.12770	102.12756	30.34600	30.69200	30.16900	9.09843	8.86442	8.89441	7189.76960	8941.23767	11.34260	0.01020	0.01020	102.12781	30.40233	C08306		101.1204	C14691		101.1204
346	59.06101	59.06117	59.06101	17.13100	17.68900	17.13100	0.00000	9.12705	8.90390	8229.41953	NaN	10.95659	0.01118	0.01118	59.06106	17.31700	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419
324	102.12785	102.12784	102.12756	28.01400	28.23000	28.73300	8.17056	8.72822	8.93408	6844.14567	3535.32358	9.08901	0.01006	0.01006	102.12775	28.32567	C08306		101.1204	C14691		101.1204
347	59.06105	59.06126	59.06105	16.09500	15.76900	16.09500	0.00000	9.41412	8.94031	9674.19445	NaN	10.69792	0.01128	0.01128	59.06112	15.98633	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419
297	121.05103	121.05075	121.05103	25.38800	24.43800	25.38800	0.00000	8.46730	8.99896	6205.13612	NaN	8.74937	0.00937	0.00937	121.05094	25.07133		HMDB01366	120.043594		HMDB01366	120.043596
306	118.12296	118.12229	118.12296	39.89800	39.91400	39.89800	0.00000	8.88458	9.00423	7664.87519	NaN	9.17884	0.01024	0.01024	118.12273	39.90333	C00183	HMDB00883	117.079	C00431	HMDB03355	117.079
298	121.05075	121.05094	121.05087	1.08900	1.10500	1.10100	11.00842	8.79475	9.05402	7512.97435	60380.12156	9.91382	0.00896	0.00896	121.05085	1.09833		HMDB01366	120.043594		HMDB01366	120.043596
273	202.21645	202.21619	202.21645	23.76200	23.80200	23.76200	0.00000	9.21768	9.07666	9387.84409	NaN	9.08653	0.00978	0.00978	202.21636	23.77533	C19325		201.1729			201.172866
330	100.11172	100.11211	100.11172	21.18300	20.46800	21.18300	0.00000	9.53894	9.07910	11037.13864	NaN	7.22179	0.00814	0.00814	100.11185	20.94467			99.104799	C00571		99.1048
331	100.11235	100.11098	100.11235	9.18100	9.22000	9.18100	0.00000	8.43761	9.09334	6409.08717	NaN	11.44312	0.00875	0.00875	100.11189	9.19400			99.104799	C00571		99.1048
345	69.06948	69.07049	69.07091	1.07800	1.08100	1.07700	10.65830	9.11807	9.12349	9143.33635	42544.29272	9.55992	0.00933	0.00933	69.07005	1.07867	C17530		68.0626	C16521		68.0626
332	100.10996	100.11198	100.11118	39.89800	39.00700	39.91000	10.56385	8.68729	9.14919	7466.92846	38709.80857	10.18376	0.00875	0.00875	100.11104	39.60500			99.104799	C00571		99.1048
333	100.10974	100.11028	100.11066	1.07800	1.10500	1.12400	10.44302	9.49480	9.21231	11539.76843	34304.06940	11.24641	0.01130	0.01130	100.11023	1.10233			99.104799	C00571		99.1048
348	59.06117	59.06122	59.06117	15.75300	15.34500	15.75300	0.00000	9.67589	9.23161	12755.90011	NaN	8.77020	0.00884	0.00884	59.06118	15.61700	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419
262	302.24246	302.24289	302.24246	5.71800	5.76900	5.71800	0.00000	9.33274	9.26801	10942.07200	NaN	10.01598	0.00913	0.00913	302.24260	5.73500	C07171		301.240564	C08454		301.240565
274	202.21611	202.21632	202.21611	16.40100	16.62900	16.40100	0.00000	9.11659	9.30354	9997.22715	NaN	9.51710	0.01077	0.01077	202.21618	16.47700	C19325		201.1729			201.172866
349	59.06110	59.06126	59.06110	16.75400	16.11000	16.75400	0.00000	9.04887	9.39696	10126.57327	NaN	10.83849	0.01004	0.01004	59.06116	16.53933	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419
300	121.05089	121.05090	121.05130	21.08900	19.24350	20.18200	9.26767	7.71935	9.39719	5209.66516	10590.02179	10.31700	0.00933	0.00933	121.05103	20.17150		HMDB01366	120.043594		HMDB01366	120.043596
187	550.62805	550.62940	550.62805	25.50500	25.25000	25.50500	0.00000	9.67529	9.40193	13885.60659	NaN	9.06566	0.01014	0.01014	550.62850	25.42000			549.512067			
271	270.21854	270.20712	270.20636	1.07800	1.56400	1.57200	10.61128	8.99247	9.42128	9965.40086	40590.15382	9.74753	0.00837	0.00837	270.21067	1.40467			269.199094	C05763		269.193906
68	805.64008	805.64185	805.64008	22.69000	22.71800	22.69000	0.00000	9.44351	9.44647	12644.69119	NaN	10.29535	0.00849	0.00849	805.64067	22.69933			804.624379			804.624379
85	774.60669	774.60809	774.60669	21.63000	21.74000	21.63000	0.00000	9.52304	9.59447	14168.21110	NaN	10.67095	0.01227	0.01227	774.60716	21.66667			773.593455			773.593455
113	721.50549	721.50818	721.50543	32.67800	33.05900	32.92570	10.26669	8.79983	9.60251	9908.68671	28758.40321	9.55746	0.00996	0.00996	721.50637	32.88757		HMDB10571	720.494141		HMDB10585	720.494141
191	543.39954	543.40027	543.39954	12.24300	12.16500	12.24300	0.00000	9.66093	9.69666	15975.22602	NaN	11.04798	0.01108	0.01108	543.39978	12.21700			542.433492			542.43351
350	59.06105	59.06111	59.06105	15.34100	14.56700	15.34100	0.00000	9.90505	9.71506	18216.00484	NaN	8.74450	0.01023	0.01023	59.06107	15.08300	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419
279	179.03514	179.03461	179.03514	2.63200	3.07200	2.63200	0.00000	8.98708	9.73055	11600.61359	NaN	10.89250	0.01036	0.01036	179.03496	2.77867	C19495		178.026609			178.026609
103	740.54157	740.54334	740.54157	20.47600	20.53900	20.47600	0.00000	9.73115	9.73618	16876.26787	NaN	9.54888	0.01233	0.01233	740.54216	20.49700			739.551553			739.551553
214	473.26611	473.26700	473.26611	9.20400	9.20800	9.20400	0.00000	9.81213	9.74387	17641.35096	NaN	10.04656	0.01095	0.01095	473.26641	9.20933			472.258958		HMDB02522	472.249481
255	324.24316	324.24237	324.24316	7.68500	7.67700	7.68500	0.00000	9.62142	9.74557	16050.55558	NaN	9.73814	0.01043	0.01043	324.24290	7.68233	C09878		323.2097	C18699		323.2097
277	198.09732	198.09686	198.09732	1.40700	1.39900	1.40700	0.00000	9.63370	9.75854	16254.47030	NaN	10.63054	0.00840	0.00840	198.09717	1.40433			197.084064	C14462		197.095297
244	360.14981	360.15146	360.14981	1.31300	1.31700	1.31300	0.00000	9.80402	9.76572	17762.99007	NaN	10.67723	0.00933	0.00933	360.15036	1.31433			359.149264	C12650		359.1493
265	279.09277	279.09293	279.09277	6.37800	6.39300	6.37800	0.00000	9.66809	9.81816	17036.75119	NaN	8.18798	0.01048	0.01048	279.09282	6.38300			278.086052			278.086228
118	721.50708	721.50775	721.50812	31.14750	30.89200	30.62900	11.36560	9.21620	9.83183	13684.45229	86301.09057	10.92334	0.00968	0.00968	721.50765	30.88950		HMDB10571	720.494141		HMDB10585	720.494141
192	537.48975	537.48975	537.48975	22.01900	22.05800	22.01900	0.00000	9.72421	9.84803	17785.15444	NaN	12.18250	0.01025	0.01025	537.48975	22.03200		HMDB07041	536.444092		HMDB07125	536.444092
253	327.28967	327.28937	327.28967	22.44300	22.48200	22.44300	0.00000	9.72714	9.85297	17855.25642	NaN	11.18389	0.00985	0.00985	327.28957	22.45600			326.282081			326.282081
27	924.76862	924.76941	924.76862	25.61100	25.86300	25.61100	0.00000	9.83045	9.85538	18824.48105	NaN	9.83750	0.01231	0.01231	924.76888	25.69500		HMDB08618	923.734314		HMDB08810	923.734314
119	721.50586	721.50769	721.51117	28.78700	28.37100	28.68030	11.68039	9.94041	9.86660	20000.39303	118230.39221	8.11535	0.00905	0.00905	721.50824	28.58467		HMDB10571	720.494141		HMDB10585	720.494141
48	849.63123	849.63214	849.63123	20.46400	20.55100	20.46400	0.00000	9.34905	9.87527	14945.38237	NaN	9.80032	0.01072	0.01072	849.63153	20.49300			848.65059			848.65059
211	481.41031	481.41080	481.41031	10.74700	10.75100	10.74700	0.00000	9.83970	9.88825	19225.11777	NaN	7.57088	0.00908	0.00908	481.41047	10.74833			480.360333			480.360332
26	936.72607	936.72772	936.72607	23.64400	23.79000	23.64400	0.00000	9.89689	9.90639	19963.07473	NaN	8.85633	0.00939	0.00939	936.72662	23.69267						
60	819.64221	819.63934	819.64221	21.35900	21.46900	21.35900	0.00000	9.64999	9.90857	17663.90526	NaN	9.85291	0.00983	0.00983	819.64126	21.39567			818.640029			818.640029
188	550.62677	550.62824	550.62677	23.43200	23.49500	23.43200	0.00000	9.86280	9.91540	19714.29681	NaN	10.63343	0.01191	0.01191	550.62726	23.45300			549.512067			
351	59.06131	59.06116	59.06109	25.01100	26.34600	25.68200	10.64116	9.93138	9.91800	20428.53603	41821.04405	8.43359	0.00885	0.00885	59.06119	25.67967	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419
120	721.50794	721.50873	721.50794	27.33100	27.45300	27.33100	0.00000	9.74674	9.96546	19074.34317	NaN	10.89245	0.01131	0.01131	721.50820	27.37167		HMDB10571	720.494141		HMDB10585	720.494141
151	593.54840	593.55054	593.54840	23.58500	23.59000	23.58500	0.00000	9.93172	9.97337	21005.52818	NaN	9.83844	0.00904	0.00904	593.54911	23.58667			592.506675			592.506675
218	458.32362	458.32462	458.32312	11.69000	11.68200	11.69000	0.00000	10.02773	10.02479	22612.52940	NaN	10.02413	0.00910	0.00910	458.32362	11.68733			457.282797			457.243753
233	428.38229	428.38348	428.38229	12.12500	12.12900	12.12500	0.00000	10.11999	10.02749	23712.08582	NaN	9.60479	0.00806	0.00806	428.38269	12.12633			427.366159			427.366159
246	358.22675	358.22675	358.22745	7.04900	7.01800	7.04900	0.00000	9.91999	10.03390	21524.38077	NaN	10.69626	0.01045	0.01045	358.22721	7.03867			357.212636	C16546		357.2093
121	721.51038	721.51141	721.51038	26.14100	26.28700	26.14100	0.00000	9.86731	10.04024	21031.41178	NaN	11.77225	0.00915	0.00915	721.51072	26.18967		HMDB10571	720.494141		HMDB10585	720.494141
203	509.45575	509.45673	509.45673	18.66200	18.72500	18.66200	0.00000	9.92932	10.04290	21722.58690	NaN	9.87021	0.01078	0.01078	509.45640	18.68300			508.468942		HMDB07038	508.412781
282	130.15848	130.15877	130.15848	1.61900	1.61100	1.61900	0.00000	9.97966	10.05710	22435.10234	NaN	10.72640	0.00928	0.00928	130.15858	1.61633	C01757		129.15175	C01740		129.1518
122	721.50665	721.50964	721.50909	27.29600	26.91100	26.78900	10.80767	9.89282	10.05806	21492.04172	49398.34008	10.59061	0.01035	0.01035	721.50846	26.99867		HMDB10571	720.494141		HMDB10585	720.494141
123	721.50659	721.50818	721.50769	28.14400	27.68800	28.20300	11.49949	9.83916	10.06019	20945.40991	98665.70529	9.89896	0.01099	0.01099	721.50749	28.01167		HMDB10571	720.494141		HMDB10585	720.494141
41	863.64667	863.64551	863.64667	21.41800	21.46900	21.41800	0.00000	9.88055	10.06179	21400.48953	NaN	9.91145	0.01140	0.01140	863.64628	21.43500			862.66624			862.66624
236	414.32153	414.32175	414.32153	12.32700	12.36500	12.33700	0.00000	9.93574	10.06092	22077.81102	NaN	8.97003	0.01064	0.01064	414.32194	12.34633		HMDB13333	413.314117			413.314097
276	202.21664	202.21639	202.21596	37.49600	37.53500	37.51900	10.78055	10.02226	10.08174	23202.10582	48076.38534	10.68536	0.00686	0.00686	202.21633	37.51667	C19325		201.1729			201.172866
242	372.24453	372.24453	372.24442	7.67300	7.63000	7.67300	0.00000	9.91364	10.08391	21999.49427	NaN	8.83606	0.00947	0.00947	372.24412	7.65867			371.236135	C07108		371.224914
256	313.27362	313.27350	313.27362	20.46400	20.50400	20.46400	0.00000	9.99854	10.10010	23140.06260	NaN	11.22871	0.00992	0.00992	313.27358	20.47733			312.266431			312.266431
263	299.25760	299.25760	299.25800	20.98300	21.02200	20.98300	0.00000	10.06595	10.10265	23963.70523	NaN	10.09764	0.01040	0.01040	299.25786	20.99600			298.250781			298.250781
220	457.30380	457.30481	457.30380	10.99500	11.01000	10.99500	0.00000	10.01923	10.12209	23639.23076	NaN	10.69178	0.01035	0.01035	457.30414	11.00000			456.298781			456.287552
307	118.12255	118.12317	118.12270	37.44900	37.48800	37.46000	11.62625	10.06220	10.12708	24212.90030	111999.20985	9.78932	0.01083	0.01083	118.12281	37.46567	C00183	HMDB00883	117.079	C00431	HMDB03355	117.079
147	612.41504	612.41486	612.41504	11.41900	11.41100	11.41900	0.00000	9.96692	10.13159	23138.51201	NaN	9.75652	0.01030	0.01030	612.41498	11.41633	C10015		611.3683	C10242		611.368284
124	721.51306	721.51416	721.51306	21.34800	21.42200	21.34800	0.00000	9.95716	10.14019	23125.02867	NaN	10.77274	0.01010	0.01010	721.51343	21.37267		HMDB10571	720.494141		HMDB10585	720.494141
175	563.50226	563.50250	563.50226	32.07770	32.51700	32.07770	0.00000	9.89758	10.14421	22491.58033	NaN	9.66587	0.00887	0.00887	563.50234	32.22413			562.459725			562.459725
40	864.64319	864.64368	864.64319	22.46700	22.55300	22.46700	0.00000	10.22345	10.16420	26737.47309	NaN	8.67178	0.01157	0.01157	864.64335	22.49567			863.63333		HMDB08287	863.640364
43	861.74793	861.75049	861.74793	29.45100	29.63200	29.45100	0.00000	9.97435	10.16507	23616.72332	NaN	8.63056	0.00937	0.00937	861.74878	29.51133			860.783263			860.783263
207	500.30133	500.30170	500.30133	8.56800	8.57200	8.56800	0.00000	10.06237	10.17335	24781.68127	NaN	12.16463	0.01071	0.01071	500.30145	8.56933	C05465	HMDB00951	499.296728		HMDB00896	499.296728
221	457.27960	457.27960	457.27960	9.67500	9.67900	9.67500	0.00000	10.09991	10.20313	25630.05188	NaN	9.30491	0.01047	0.01047	457.27903	9.67633			456.287552		HMDB00907	456.254562
74	791.62231	791.62372	791.62231	22.04300	22.09400	22.04300	0.00000	10.15525	10.20837	26418.21314	NaN	9.86949	0.01043	0.01043	791.62278	22.06000			790.608729			790.608729
235	415.27374	415.27441	415.27374	10.59400	10.62200	10.59400	0.00000	10.16319	10.21931	26668.75797	NaN	8.63157	0.01090	0.01090	415.27397	10.60333			414.261754	C11171		414.2746

353	59.06098	59.06114	59.06098	12.65500	13.44900	12.65500	0.00000	10.12681	10.22000	26197.13653	NaN	10.29700	0.00826	0.00826	59.06103	12.91967	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419			
231	437.26071	437.26202	437.26071	8.58000	8.58400	8.58000	0.00000	10.06752	10.22128	25448.26137	NaN	9.08648	0.00867	0.00867	437.26115	8.58133		HMDB07855	436.258958			436.258958			
55	832.65509	832.65314	832.65509	22.34900	22.40000	22.34900	0.00000	10.12227	10.23883	26384.85000	NaN	8.91557	0.00848	0.00848	832.65444	22.36600			831.635274			831.635274			
204	505.39993	505.40018	505.39993	18.36800	18.43100	18.36800	0.00000	10.18179	10.25111	27349.46854	NaN	9.91982	0.00983	0.00983	505.40001	18.38900			504.381454			504.381454			
179	558.50678	558.50848	558.50678	21.53600	21.57500	21.53600	0.00000	10.28369	10.25300	28806.22384	NaN	8.97671	0.00955	0.00955	558.50735	21.54900	C07553		557.4318			557.34814			
208	497.35330	497.35523	497.35330	11.41900	11.44600	11.41900	0.00000	10.05157	10.25677	25697.97557	NaN	7.31547	0.00946	0.00946	497.35394	11.42800	C04102		496.3403	C11175		496.340004			
107	732.61676	732.61572	732.61676	24.09200	24.14300	24.09200	0.00000	10.17048	10.26531	27388.99271	NaN	8.26475	0.00980	0.00980	732.61641	24.10900		HMDB01348	731.606689			731.619243			
59	820.58191	820.58398	820.58191	19.99300	20.05600	19.99300	0.00000	10.14408	10.27620	27177.43576	NaN	8.20191	0.01080	0.01080	820.58260	20.01400			819.577764			819.577764			
62	816.65021	816.65332	816.65021	21.54800	21.58700	21.54800	0.00000	10.09754	10.28555	26676.66117	NaN	9.64574	0.01203	0.01203	816.65125	21.56100			815.640405			815.640405			
215	473.25330	473.25256	473.25330	9.68700	9.69100	9.68700	0.00000	10.18839	10.29297	28020.20769	NaN	8.93609	0.01037	0.01037	473.25305	9.68833			472.246103			472.246103			
87	766.72180	766.72315	766.72180	24.08000	24.14300	24.08000	0.00000	10.49899	10.30420	32912.10108	NaN	10.68576	0.01045	0.01045	766.72225	24.10100		HMDB08194	765.567261		HMDB08195	765.567261			
78	783.66187	783.66254	783.66187	16.24800	16.28700	16.24800	0.00000	10.35039	10.31889	30780.64006	NaN	9.23926	0.01016	0.01016	783.66209	16.26100			782.630138			782.590799			
100	747.57208	747.57294	747.57208	19.89900	19.91500	19.89900	0.00000	10.23069	10.32329	29056.34269	NaN	11.60629	0.00823	0.00823	747.57237	19.90433			746.582519			746.582519			
354	59.06116	59.06118	59.06116	9.46300	9.44400	9.46300	0.00000	10.33054	10.33065	30656.33276	NaN	10.16111	0.00986	0.00986	59.06117	9.45667	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419			
45	854.57550	854.57617	854.57550	21.17100	21.22200	21.17100	0.00000	10.29824	10.34497	30381.93627	NaN	10.49150	0.00963	0.00963	854.57572	21.18800			853.562155			853.562155			
34	878.77496	878.77753	878.77496	29.51000	29.63200	29.51000	0.00000	10.10386	10.34671	27592.01462	NaN	10.01848	0.01128	0.01128	878.77582	29.55067		HMDB13456	877.692444		HMDB09607	877.656067			
57	823.61755	823.61945	823.61755	22.03100	22.09400	22.03100	0.00000	10.28653	10.37384	30643.88708	NaN	9.64262	0.00944	0.00944	823.61819	22.05200			822.56216			822.56216			
264	286.24832	286.24823	286.24832	6.49500	6.48800	6.49500	0.00000	10.28069	10.40692	31064.02907	NaN	9.87634	0.01170	0.01170	286.24829	6.49267			285.245637			285.24565			
201	522.59735	522.59772	522.59699	21.28900	21.19900	21.17100	12.55638	10.32065	10.41590	31833.43652	2839014.44025	9.27501	0.00795	0.00795	522.59735	21.21967			521.480777						
228	445.23334	445.23456	445.23334	7.02500	7.01800	7.02500	0.00000	10.31576	10.42640	31922.90063	NaN	9.54401	0.01156	0.01156	445.23374	7.02267	C12959		444.226	C12959		444.226037			
357	59.06096	59.06112	59.06096	26.78900	26.86400	26.78900	0.00000	10.21688	10.44528	30825.03262	NaN	9.29944	0.01007	0.01007	59.06101	26.81400	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419			
258	337.14597	337.14606	337.14597	6.38900	6.39300	6.38900	0.00000	10.37580	10.46314	33505.59416	NaN	10.40018	0.00982	0.00982	337.14600	6.39033	C02590		336.1395			336.13953			
42	862.62891	862.62799	862.62891	19.81600	19.87900	19.81600	0.00000	10.30277	10.46562	32344.33830	NaN	8.54679	0.00949	0.00949	862.62860	19.83700			861.617744			861.617744			
197	523.47327	523.47217	523.47327	20.48800	20.50400	20.48800	0.00000	10.46384	10.47041	35140.97584	NaN	10.55016	0.00822	0.00822	523.47290	20.49333			522.537572			522.537572			
223	455.34915	455.35019	455.34915	12.33700	12.36500	12.33700	0.00000	10.36984	10.47596	33620.71965	NaN	10.62705	0.01106	0.01106	455.34950	12.34633			454.344682			454.344682			
217	468.30924	468.30991	468.30924	13.92700	13.96700	13.92700	0.00000	9.93645	10.47633	27075.71281	NaN	11.35553	0.00944	0.00944	468.30946	13.94033			467.301189			467.301189			
159	581.51410	581.51440	581.51410	19.44000	19.50200	19.44000	0.00000	10.41293	10.50711	34892.36099	NaN	10.50537	0.01051	0.01051	581.51420	19.46067			580.506652			580.506652			
257	313.27319	313.27280	313.27319	20.99400	21.03400	20.99400	0.00000	10.42714	10.51361	35255.31887	NaN	9.81534	0.00995	0.00995	313.27306	21.00733			312.266431			312.266431			
359	59.06138	59.06120	59.06118	27.99100	28.19500	28.06100	11.19110	10.25293	10.53972	32739.19361	72482.38137	8.62018	0.01059	0.01059	59.06125	28.08233	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419			
80	780.54968	780.55249	780.54968	19.19200	19.24300	19.19200	0.00000	10.45181	10.54154	36194.90716	NaN	11.65262	0.00916	0.00916	780.55062	19.20900		HMDB07984	779.546464		HMDB08015	779.546464			
261	308.18552	308.18594	308.18552	5.73000	5.72200	5.73000	0.00000	10.45380	10.54486	36291.12150	NaN	9.67350	0.01067	0.01067	308.18566	5.72733	C07219	HMDB05023	307.1685	C07219	HMDB05023	307.168462			
131	708.52765	708.52802	708.52765	19.13300	19.16100	19.13300	0.00000	10.45074	10.54876	36306.50865	NaN	11.57051	0.00943	0.00943	708.52777	19.14233			707.510074			707.510074			
54	833.65698	833.65735	833.65698	21.83100	21.88200	21.83100	0.00000	10.45564	10.56314	36658.18224	NaN	10.19566	0.01005	0.01005	833.65710	21.84800			832.655679			832.673332			
31	905.72723	905.72650	905.72723	24.09200	24.15500	24.09200	0.00000	10.76262	10.58568	43223.90940	NaN	10.10768	0.00994	0.00994	905.72699	24.11300			904.695477			904.69544			
360	59.06094	59.06121	59.06094	29.76900	29.05500	29.76900	0.00000	10.43051	10.60137	36899.01173	NaN	10.35076	0.01043	0.01043	59.06103	29.53100	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419			
154	591.53442	591.53613	591.53442	21.19500	21.25700	21.19500	0.00000	10.53562	10.60578	38975.84583	NaN	11.07112	0.00997	0.00997	591.53499	21.21567	C17566		590.5274	C17573		590.527411			
156	590.40283	590.40308	590.40283	11.46600	11.47000	11.46600	0.00000	10.47407	10.60905	37856.66731	NaN	9.60915	0.00947	0.00947	590.40291	11.46733			589.374354			589.470597			
93	760.59082	760.59283	760.59082	21.19500	21.22200	21.19500	0.00000	10.44325	10.61833	37450.91713	NaN	8.18023	0.00974	0.00974	760.59149	21.20400		HMDB07879	759.57782		HMDB07911	759.57782			
94	757.64825	757.64978	757.64850	24.76350	24.59100	24.52800	13.27193	10.56195	10.64002	40174.42879	580665.36178	10.76602	0.01116	0.01116	757.64884	24.62750		HMDB07702	756.663147		HMDB07814	756.663147			
252	330.21036	330.21060	330.21036	11.43000	11.45800	11.43000	0.00000	10.57397	10.65288	40677.24070	NaN	10.39836	0.01095	0.01095	330.21044	11.43933	C08687		329.1991	C12580		329.1991			
361	59.06078	59.06108	59.06078	30.38100	29.46700	30.38100	0.00000	10.28955	10.65980	35407.21582	NaN	8.88832	0.00891	0.00891	59.06088	30.07633	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419			
164	577.50598	577.50116	577.50598	35.17500	35.27350	35.17500	0.00000	10.33365	10.66400	36272.87056	NaN	9.22618	0.00961	0.00961	577.50437	35.20783		HMDB07075	576.475403		HMDB07076	576.475403			
19	986.66260	986.66229	986.66260	11.60700	11.62300	11.60700	0.00000	10.51401	10.66418	39699.42141	NaN	10.26757	0.01092	0.01092	986.66250	11.61233			985.843814			985.843856			
108	732.55444	732.56934	732.55444	22.26600	23.24800	22.26600	0.00000	13.69469	10.66433	194756.73540	NaN	11.94235	0.01178	0.01178	732.55941	22.59333		HMDB07872	731.546509		HMDB07873	731.546509			
247	358.24014	358.23984	358.24014	12.90300	12.94200	12.90300	0.00000	10.61442	10.67145	41895.63140	NaN	9.57115	0.01120	0.01120	358.24004	12.91600	C07360		357.2304	C08707		357.2304			
148	607.56537	607.56702	607.56537	22.51400	22.57700	22.51400	0.00000	10.53593	10.67198	40293.93955	NaN	8.49826	0.00874	0.00874	607.56592	22.53500		HMDB07080	606.522339		HMDB07416	606.522339			
38	874.70258	874.70111	874.70258	23.50300	23.57800	23.50300	0.00000	10.52271	10.70149	40623.44759	NaN	11.40489	0.01034	0.01034	874.70209	23.52800			873.718614			873.718614			
237	412.38870	412.38992	412.38870	14.63400	14.66200	14.63400	0.00000	10.60929	10.70274	42447.16474	NaN	10.73623	0.00809	0.00809	412.38911	14.64333		HMDB13314	411.371246			411.371244			
81	780.55383	780.55206	780.55383	19.61600	19.66700	19.61600	0.00000	10.60168	10.70616	42358.19195	NaN	9.85163	0.01071	0.01071	780.55324	19.63300		HMDB07984	779.546464		HMDB08015	779.546464			
364	59.06132	59.06118	59.06113	31.37100	31.50400	31.47700	11.97420	10.48629	10.70705	40015.16338	158609.24397	10.44537	0.01140	0.01140	59.06121	31.45067	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419			
17	992.78699	992.79102	992.78699	24.98700	25.07400	24.98700	0.00000	10.71138	10.71501	44944.90994	NaN	10.21952	0.00972	0.00972	992.78833	25.01600									
130	709.52771	709.52856	709.52771	19.74600	19.78500	19.74600	0.00000	10.65512	10.72071	43823.07250	NaN	11.42759	0.00892	0.00892	709.52800	19.75900			708.530479			708.530479			
169	565.51990	565.52014	565.51990	34.75100	35.00300	34.75100	0.00000	7.85511	10.74643	10946.45954	NaN	9.30636	0.01094	0.01094	565.51998	34.83500		HMDB07016	564.475403		HMDB07043	564.475403			
49	849.62720	849.62769	849.62720	20.97100	21.02200	20.97100	0.00000	10.67938	10.75527	45130.91413	NaN	10.13190	0.00926	0.00926	849.62736	20.98800			848.65059			848.65059			
161	579.53375	579.53577	579.53375	36.49400	36.56900	36.49400	0.00000	10.95831	10.76696	52189.25164	NaN	10.08626	0.00877	0.00877	579.53442	36.51900		HMDB07074	578.491028		HMDB07242	578.491028			
281	156.04211	156.04219	156.04211	1.33600	1.32900	1.33600	0.00000	10.77692	10.78471	48089.16056	NaN	9.99793	0.01010	0.01010	156.04214	1.33367	C01210		155.0347	C04122		155.0347			
212	480.33612	480.33597	480.33612	11.65400	11.65800	11.65400	0.00000	10.73992	10.79349	47415.45215	NaN	11.65863	0.00931	0.00931	480.33607	11.65533			479.337543			479.337543			
35	876.75903	876.75909	876.75903	28.36700	28.52500	28.36700	0.00000	10.49411	10.80223	42115.45938	NaN	10.51511	0.01049	0.01049	876.75905	28.43967		HMDB13450	875.676819		HMDB13457	875.676819			
150	595.53064	595.52991	595.53064	20.06400	20.13900	20.06400	0.00000	10.79874	10.82101	49507.25906	NaN	9.46362	0.01105	0.01105	595.53040	20.08900		HMDB07021	594.522339		HMDB07049	594.522339			
258	313.27341	313.27307	313.27341	22.50200	22.55300	22.50200	0.00000	10.71775	10.83399	47852.06492	NaN	11.53045	0.01074	0.01074	313.27330	22.51900			312.266431			312.266431			
39	869.58539	869.58771	869.58539	20.22900	20.28000	20.22900	0.00000	10.69653	10.85438	47832.19831	NaN	11.89829	0.01117	0.01117	869.58616	20.24600			868.566011			868.54651			
101	746.56860	746.56970	746.56860	22.43100	22.49400	22.43100	0.00000	10.73687	10.85516	48825.67565	NaN	9.97132	0.00988	0.00988	746.56897	22.45200			745.562112			745.562112			
248	348.31079	348.31043	348.31079	14.83400	14.86200	14.83400	0.00000	10.86881	10.86327	52367.33056	NaN	9.11283	0.00980	0.00980	348.31067	14.84333	C11695	HMDB04080	347.28244		HMDB13655	347.28244			
180	551.50458	551.50385	551.50458	23.35000	23.42500	23.35000	0.00000	10.87273	10.87914	52888.02862	NaN	10.71441	0.01018	0.01018	551.50433	23.37500			550.49611	C13864		550.4961			
25	942.63733	942.63562	942.63733	11.65400	11.67000	11.65400	0.00000	10.84282	10.88590	52279.36117	NaN	10.99086	0.01099	0.01099	942.63676	11.65933			941.499752						
36	876.64392	876.64307	876.64392	20.71130	20.76300	20.71130	0.00000	10.88285	10.95771	55286.17269	NaN	9.91733	0.01096	0.01096	876.64364	20.72853			875.640364			875.640364			
97	749.54810	749.54569	749.54810	20.62900	20.57450	20.62900	0.00000	10.54828	10.96030	46830.42641	NaN	9.70810	0.01193	0.01193	749.54716	20.61083		HMDB10573	748.525452		HMDB10574	748.525452			
259	313.27304	313.27399	313.27304	21.98400	22.02300	21.98400	0.00000	10.89572	10.98251	56337.27220	NaN	10.31281	0.01039	0.01039	313.27336	21.99700			312.266431			312.266431			
89	764.54724	764.54675	764.54724	20.91200	20.97500	20.91200	0.00000	10.77613	10.98327	53087.42720	NaN	8.72349	0.00929	0.00929	764.54708	20.93300		HMDB12356	763.536316		HMDB12376	763.536316			
224	454.29337	454.29321	454.29337	13.26800	13.28400	13.26800	0.00000	10.67456	10.98739	50562.87138	NaN	9.02254	0.00824	0.00824	454.29331	13.27333			453.285501			453.285503			
209	495.42676	495.42661	495.42676	11.40700	11.42300	11.40700	0.00000	10.89438	10.99150	56553.35644	NaN	9.26815	0.00819	0.00819	495.42671	11.41233			494.357133			494.357131			
249	344.22531	344.22534	344.22531	12.19600	12.22400	12.19600	0.00000	10.94184	11.00212	58219.70628	NaN	9.48498	0.00938	0.00938	344.22532	12.20533	C07879		343.225977	C07879		343.226			
254	327.28926	327.28928	327.28906	21.96000	22.01100	21.96000	0.00000	10.91608	11.02348	58091.77986	NaN	10.12459	0.00979	0.00979	327.28913	21.97700			326.282081			326.282081			
75	790.61231	790.60980	790.61231	21.85400	21.90500	21.85400	0.00000	10.92602	11.05607	59340.10581	NaN	9.43144	0.00839	0.00839	790.61147	21.87100			789.588324			789.588324			
24	950.74255	950.74408	950.74255	23.97400	24.04900	23.97400	0.00000	11.00859	11.06593	62147.36013	NaN	10.11693	0.00917	0.00917	950.74306	23.99900			949.749956						
234	426.36971	426.36997	426.36971	12.79700	12.81200	12.79700	0.00000	10.99399	11.06733	61738.20622	NaN	10.56300	0.01051	0.01051	426.36913	12.80200			425.350509		HMDB05065	425.350494			
205	502.34866	502.34943	502.34866	11.61900	11.61100	11.61900	0.00000	10.90654	11.07157	59222.38469	NaN	8.57391	0.00985	0.00985	502.34892	11.61633			501.385181	C06999	HMDB05030	501.287909			
238	412.38931	412.38940	412.38931	14.31600	14.33200	14.31600	0.00000	10.95106	11.07504	60660.54920	NaN	10.70080	0.00834	0.00834	412.38934	14.32133		HMDB13314	411.371246			411.371244			
176	563.50372	563.50305	563.50372	23.78600	24.42600	23.78600	0.00000	12.65133	11.08756	142834.78588	NaN	10.20240	0.01083	0.01083	563.50350	23.99933			562.459725			562.459725			
243	364.18283	364.18240	364.18283	6.40100	6.39300	6.40100	0.00000	11.01550	11.09917	63407.42909	NaN	10.00539	0.00925	0.00925	364.18269	6.39833			363.179422			363.179422			
181	551.50372	551.50391	551.50372	22.45500	22.49400	22.45500	0.00000	11.01072	11.10038	63294.38011	NaN	10.86694	0.00981	0.00981	551.50378	22.46800			550.496092	C13864		550.4961			
56	830.66089	830.65033	830.66089	21.76000	21.83480	21.76000	0.00000	10.93366	11.10723	61111.02915	NaN	8.89488	0.00983	0.00983	830.65737	21.78493			829.656014			829.656014			
196	524.36426	524.36389	524.36426	11.57200	11.57600	11.57200	0.00000	10.99334	11.10890	63014.34931	NaN	11.01398	0.01015	0.01015	524.36414	11.57333			523.363753		HMDB10384	523.363753			
365	59.06144	59.06113	59.06111	1.08900	1.09300	1.08900	12.91571	11.13626	11.11202	67787.81090	406650.11075	9.73830	0.00979	0.00979	59.06123	1.09033	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419			
142	654.33289	654.33197	654.33197	13.64500	13.66100	13.64500	0.00000	11.03118	11.12881	64860.84216	NaN	9.21235	0.00948	0.00948	654.33228	13.65033	C15681		653.321334	C15661		653.3213			
102	746.56647	746.56049	746.56647	20.59400	21.52800	20.59400	0.00000	13.23330	11.14281	196428.50543	NaN	10.90843	0.01066	0.01066	746.56447	20.90533			745.562112			745.562112			
23	963.73944	963.73834	963.73944	23.36200	23.43600	23.36200	0.00000	11.15523	11.14949	69728.33863	NaN	9.04083	0.00974	0.00974	963.73908	23.38667			962.736313			962.736313			
20	978.77374	978.77539	978.77374	24.63400	24.73200	24.63400	0.00000	11.19299	11.15641	71303.18867	NaN	8.96941	0.00997	0.00997	978.77429	24.66667			977.723741	C16157		977.723704			
170	565.51923	565.51990	565.51923	34.08000	34.34330	34.08000	0.00000	10.59734	11.16170	53078.14966	NaN	10.52263	0.01007	0.01007	565.51945	34.16777		HMDB07016	564.475403		HMDB07043	564.475403			
61	817.65076	817.65247	817.65076	22.46700	22.52900	22.46700	0.00000	11.10326	11.16207	68368.27508	NaN	9.59264	0.01029	0.01029	817.65133	22.48767			816.660769			816.624379			
32	898.61060	898.60980	898.61060	11.70100	11.70500	11.70100	0.00000	11.08049	11.16256	67610.84626	NaN	11.83674	0.01003	0.01003	898.61033	11.70233			897.645834			897.645834			
141	663.45331	663.45410	663.45477	20.71200	20.61000	20.59400	13.02022	11.06332	11.16434	67092.56060	451448.98433	8.44287	0.01059	0.01059	663.45406	20.63867			662.440721			662.415839			
182	523.47247	523.47192	523.47247	23.31500	23.37800	23.31500	0.00000	11.14050	11.18709	70530.06477	NaN	11.07903	0.00892	0.00892	523.47229	23.33600			522.537572			522.537572			
183	551.50342	551.50501	551.50342	23.60900	23.68400	23.60900	0.00000	11.27849	11.20046	76075.08072	NaN	10.38872	0.00893	0.00893	551.50395	23.63400			550.49611	C13864		550.4961			
155	591.52551	591.52997	591.52551	25.05800	25.14400	25.05800	0.00000	11.31317	11.20072	77415.59275	NaN	10.14092	0.01036	0.01036	591.52700	25.08667	C17566		590.5274	C17573		590.527411			
144	636.46008	636.46021	636.46008	19.06300	19.11400	19.06300	0.00000	11.06458	11.20406	68481.56190	NaN	9.10449	0.00922	0.00922	636.46012	19.08000			635.452561			635.452561			
171	565.51874	565.52002	565.51874	36.48300	36.54600	36.48300	0.00000	11.06428	11.22244	69103.21999	NaN	8.73316	0.01030	0.01030	565.51917	36.50400		HMDB07016	564.475403		HMDB07043	564.475403			
139	664.49121	664.49280	664.49121	19.75800	19.80900	19.75800	0.00000	11.14518	11.25511	73141.08844	NaN	8.00089	0.01030	0.01030	664.49174	19.77500			663.483905			663.483905			
110	722.54279	722.54456	722.54279	19.75800	19.80900	19.75800	0.00000	11.12123	11.25621	72310.23728	NaN	10.38716	0.00994	0.00994	722.54338	19.77500			721.525724			721.525724			
334	86.09720	86.09715	86.09720	26.81300	27.44100	26.81300	0.00000	10.05958	11.27243	42873.16095	NaN	10.74350	0.00968	0.00968	86.09718	27.02233	C03219		85.089149	C01746		85.0891			

104	736.55518	736.55731	736.55518	20.46400	20.49200	20.46400	0.00000	11.17641	11.27397	74996.08464	NaN	9.90071	0.01120	0.01120	736.55589	20.47333			735.541374			735.541374
335	86.09728	86.09726	86.09728	27.29600	28.24200	27.29600	0.00000	10.07959	11.28786	43639.64032	NaN	10.86208	0.01030	0.01030	86.09727	27.61133	C03219		85.089149	C01746		85.0891
53	834.59796	834.59827	834.59796	20.53500	20.61000	20.53500	0.00000	11.16104	11.29477	75199.89676	NaN	9.59332	0.00781	0.00781	834.59806	20.56000		HMDB08057	833.593414			833.593414
50	848.61304	848.61292	848.61304	21.12400	21.17500	21.12400	0.00000	11.22988	11.29707	77922.84874	NaN	10.90053	0.00940	0.00940	848.61300	21.14100			847.609064			847.609064
366	59.06137	59.06125	59.06096	36.50600	37.11100	37.06000	13.05987	11.23486	11.30191	78306.35337	469708.48089	11.01392	0.00972	0.00972	59.06119	36.89233	C00207	HMDB01659	58.0419	C00479	HMDB03366	58.0419
22	964.75800	964.75745	964.75800	24.31600	24.39000	24.31600	0.00000	11.31507	11.32413	82421.26512	NaN	9.86593	0.01186	0.01186	964.75781	24.34067			963.765564			963.765564
251	331.28418	331.28442	331.28418	14.83400	14.86200	14.83400	0.00000	11.21644	11.34182	79152.44426	NaN	9.77931	0.00960	0.00960	331.28426	14.84333			330.276992		HMDB11564	330.276992
167	572.52515	572.52521	572.52515	22.00700	22.03500	22.00700	0.00000	11.32607	11.38782	85557.46954	NaN	9.81045	0.00834	0.00834	572.52517	22.01633			571.475316			571.36379
225	454.29315	454.29318	454.29315	12.92600	12.95400	12.92600	0.00000	10.95551	11.40533	71712.31670	NaN	10.71938	0.01088	0.01088	454.29316	12.93533			453.285501			453.285503
46	854.58398	854.58447	854.58398	11.74800	11.75200	11.74800	0.00000	11.26956	11.43629	85214.55287	NaN	9.09965	0.01028	0.01028	854.58415	11.74933			853.583234			853.583234
326	102.12768	102.12790	102.12797	1.07800	1.42300	1.43100	10.90442	11.31081	11.43805	87066.36682	54416.35889	10.11148	0.00952	0.00952	102.12785	1.31067	C08306		101.1204	C14691		101.1204
92	761.58948	761.58899	761.58948	20.50000	20.52700	20.50000	0.00000	11.27462	11.43812	85508.54590	NaN	10.91278	0.01185	0.01185	761.58932	20.50900	C13875		760.5856			760.598166
229	444.37982	444.37997	444.37982	15.40000	15.42700	15.40000	0.00000	11.32028	11.45453	88203.63117	NaN	11.88424	0.00870	0.00870	444.37987	15.40900		HMDB13154	443.361084			443.303559
177	563.50366	563.50397	563.50366	20.13400	20.19700	20.13400	0.00000	11.45019	11.49981	96278.39484	NaN	10.94886	0.00925	0.00925	563.50376	20.15500			562.459725			562.459725
219	458.34784	458.34787	458.34784	12.26700	12.27100	12.26700	0.00000	11.44045	11.52397	96974.94080	NaN	10.40835	0.00925	0.00925	458.34785	12.26833			457.391965			457.391966
178	563.49512	563.48639	563.49512	34.16230	34.57830	34.16230	0.00000	11.22081	11.52686	87015.16179	NaN	9.86407	0.00857	0.00857	563.49221	34.30097			562.459725			562.459725
193	537.48822	537.48798	537.48822	21.00600	21.03400	21.00600	0.00000	11.48282	11.54260	99978.24744	NaN	9.22747	0.01039	0.01039	537.48814	21.01533		HMDB07041	536.444092		HMDB07125	536.444092
51	846.67059	846.66950	846.67059	22.63150	22.72950	22.63150	0.00000	11.44781	11.54935	98575.82860	NaN	9.46080	0.00989	0.00989	846.67023	22.66417			845.650924			845.687314
165	577.51990	577.51996	577.51990	20.67600	20.72700	20.67600	0.00000	11.50126	11.55537	101551.05593	NaN	11.22804	0.00913	0.00913	577.51992	20.69300		HMDB07075	576.475403		HMDB07076	576.475403
64	809.60181	809.60242	809.60181	21.54800	21.62300	21.54800	0.00000	11.54991	11.58096	105391.51644	NaN	11.56126	0.01067	0.01067	809.60201	21.57300			808.598169			808.598169
96	749.69354	749.69495	749.69354	24.09200	24.13100	24.09200	0.00000	11.79206	11.62297	121480.85679	NaN	11.04925	0.01135	0.01135	749.69401	24.10500	C10385		748.615832	C10385		748.6158
146	614.57233	614.57288	614.57233	23.30300	23.35400	23.30300	0.00000	11.54070	11.63150	107591.79929	NaN	6.63331	0.01037	0.01037	614.57251	23.32000						
63	810.55774	810.55811	810.55774	11.79600	11.80000	11.79600	0.00000	11.53277	11.65493	108428.98559	NaN	11.18462	0.01162	0.01162	810.55786	11.79733		HMDB12394	809.520691		HMDB12404	809.520691
199	523.47229	523.47308	523.47229	23.65600	23.71900	23.65600	0.00000	11.64236	11.67808	115869.24474	NaN	8.98812	0.00802	0.00802	523.47255	23.67700			522.537572			522.537572
172	565.52002	565.52045	565.52002	22.00700	22.04700	22.00700	0.00000	11.44326	11.68360	105179.96214	NaN	10.96238	0.01117	0.01117	565.52016	22.02033		HMDB07016	564.475403		HMDB07043	564.475403
132	706.53650	706.52893	706.53650	19.72200	19.73800	19.72200	0.00000	11.58541	11.69333	113479.01462	NaN	8.83937	0.00856	0.00856	706.53398	19.72733			705.530814			705.530814
260	313.27356	313.27362	313.27356	21.53600	21.56400	21.53600	0.00000	11.66329	11.71264	119129.64124	NaN	9.72701	0.01060	0.01060	313.27358	21.54533			312.266431			312.266431
37	876.64465	876.64459	876.64465	20.35800	20.40900	20.35800	0.00000	11.59820	11.75335	117685.87210	NaN	11.08573	0.00785	0.00785	876.64463	20.37500			875.640364			875.640364
95	753.54059	753.53980	753.54059	19.36900	19.42000	19.36900	0.00000	11.68226	11.76946	123729.97170	NaN	9.65781	0.00905	0.00905	753.54032	19.38600			752.535569			752.535569
88	766.53229	766.53204	766.53229	11.84300	11.84700	11.84300	0.00000	11.74245	11.83467	131736.76495	NaN	10.94773	0.00997	0.00997	766.53221	11.84433			765.530814			765.530814
340	79.02187	79.02167	79.02187	1.45400	1.45800	1.45400	0.00000	11.73635	11.85195	132475.12838	NaN	10.38256	0.00963	0.00963	79.02180	1.45533	C11143	HMDB02151	78.013939	C11143	HMDB02151	78.013937
160	580.53839	580.53992	580.53839	24.77500	24.87300	24.77500	0.00000	11.81809	11.85582	138268.95321	NaN	12.79826	0.00802	0.00802	580.53890	24.80767			579.559027		HMDB10398	579.426392
216	473.26584	473.26569	473.26584	8.56800	8.58400	8.56800	0.00000	11.83720	11.85974	139870.12692	NaN	11.16638	0.01146	0.01146	473.26579	8.57333			472.258958		HMDB02522	472.249481
232	429.29016	429.28967	429.29016	11.44200	11.47000	11.44200	0.00000	11.76367	11.90315	137779.66122	NaN	11.29042	0.00997	0.00997	429.29000	11.45133			428.277372			428.277372
206	502.37421	502.37488	502.37421	12.20800	12.20000	12.20800	0.00000	11.89548	11.95558	151074.58003	NaN	10.60691	0.01189	0.01189	502.37443	12.20533			501.385181	C06999	HMDB05030	501.287909
222	457.32169	457.32105	457.32169	12.91400	12.96600	12.91400	0.00000	11.86806	11.01422	153451.59229	NaN	9.95330	0.01083	0.01083	457.32147	12.93133			456.305092			456.305091
111	722.50629	722.50592	722.50629	11.89000	11.90600	11.89000	0.00000	11.89548	11.95558	151074.58003	NaN	10.98690	0.00923	0.00923	722.50617	11.89533			721.504603		HMDB09215	721.504639
341	74.09730	74.09701	74.09730	1.38400	1.38800	1.38400	0.00000	11.93272	11.03151	159869.68270	NaN	11.11941	0.00998	0.00998	74.09720	1.38533			73.089149	C05985		73.089149
84	775.60346	775.60547	775.60346	21.04100	21.08100	21.04100	0.00000	11.90773	11.03740	158350.31110	NaN	9.92661	0.01031	0.01031	775.60413	21.05433			774.613819			774.613819
189	550.62927	550.62964	550.62872	22.38400	22.23500	22.20700	14.45180	12.06563	12.04616	172110.45088	1889461.82981	9.44655	0.01017	0.01017	550.62921	22.27533			549.512067			549.512067
213	476.37396	476.37326	476.37396	15.96300	15.96500	15.95300	0.00000	12.04086	12.04785	170136.04005	NaN	9.94429	0.01020	0.01020	476.37373	15.95833			475.369531	C13142		475.314517
152	593.55096	593.55206	593.55096	25.27000	25.40300	25.27000	0.00000	11.95765	12.06149	164320.15657	NaN	11.16301	0.01070	0.01070	593.55133	25.31433			592.506675			592.506675
109	732.55585	732.55475	732.55585	21.87800	21.92900	21.87800	0.00000	11.15031	12.12131	113075.48022	NaN	10.01350	0.00748	0.00748	732.55548	21.89500		HMDB07872	731.546509		HMDB07873	731.546509
44	860.68518	860.68610	860.68518	23.11400	23.15400	23.11400	0.00000	11.99914	12.13042	173647.43238	NaN	10.45896	0.00895	0.00895	860.68549	23.12733			859.666574			859.666574
230	443.30579	443.30615	443.30579	12.20800	12.24700	12.20800	0.00000	12.02898	12.13082	176292.76988	NaN	7.98012	0.01035	0.01035	443.30591	12.22100			442.308292			442.308292
82	779.61224	779.61298	779.61224	22.57230	22.63500	22.57230	0.00000	11.94049	12.14183	169593.17064	NaN	9.74334	0.00882	0.00882	779.61249	22.59320	C02970		778.6029			778.602898
143	650.47626	650.47687	650.47626	19.68700	19.73800	19.68700	0.00000	12.04148	12.15456	179515.33993	NaN	10.94732	0.00956	0.00956	650.47646	19.70400			649.4683		HMDB08823	649.468262
127	720.56183	720.56091	720.56183	20.39400	20.39800	20.39400	0.00000	11.82264	12.16048	161386.81999	NaN	10.23567	0.01047	0.01047	720.56152	20.39533		HMDB07935	719.546509		HMDB07967	719.546509
136	678.47982	678.47974	678.47982	11.94900	11.95300	11.94900	0.00000	12.06469	12.16168	182259.85006	NaN	9.34988	0.00935	0.00935	678.47982	11.95033			677.463124			677.499513
190	546.40118	546.40051	546.40118	12.13700	12.12900	12.13700	0.00000	12.11165	12.16781	187097.42279	NaN	8.87748	0.01045	0.01045	546.40096	12.13433		HMDB10393	545.348145		HMDB10394	545.359145
145	634.45355	634.45367	634.45355	11.99600	12.01200	11.99600	0.00000	12.15616	12.20233	194705.04989	NaN	9.56225	0.00965	0.00965	634.45359	12.00133			633.436955			633.436955
168	566.52374	566.52423	566.52374	24.38600	24.46100	24.38600	0.00000	12.23243	12.23426	205529.91752	NaN	12.08935	0.01111	0.01111	566.52391	24.41100		HMDB04950	565.543377		HMDB11763	565.543377
149	600.55634	600.55707	600.55634	22.89100	22.94200	22.89100	0.00000	12.15434	12.25709	199927.82409	NaN	8.91263	0.00949	0.00949	600.55658	22.90800			599.458345			599.458318
157	590.42706	590.42719	590.42706	12.06600	12.08200	12.06600	0.00000	12.18005	12.26243	203056.27047	NaN	10.56607	0.01011	0.01011	590.42710	12.07133			589.374354			589.470597
137	678.50818	678.50757	678.50818	20.46400	20.53900	20.46400	0.00000	12.16818	12.29678	205351.70856	NaN	9.91668	0.00911	0.00911	678.50798	20.48900		HMDB07866	677.499573		HMDB08890	677.499573
200	523.47363	523.47339	523.47363	19.36900	19.43200	19.36900	0.00000	12.24218	12.33499	217201.87445	NaN	10.06131	0.00885	0.00885	523.47355	19.39000			522.537572			522.537572
72	793.62689	793.62726	793.62689	23.13800	23.24800	23.13800	0.00000	12.24514	12.33450	218561.73756	NaN	8.41059	0.01031	0.01031	793.62701	23.17467			792.624379			792.624379
183	551.50433	551.50413	551.50433	21.52400	21.56400	21.52400	0.00000	11.99004	12.36637	194503.50386	NaN	11.06180	0.01134	0.01134	551.50437	21.53733			550.49611	C13864		550.4961
69	803.63654	803.63794	803.63654	21.98350	22.04700	21.98350	0.00000	12.32274	12.42064	236023.72115	NaN	12.32358	0.00921	0.00921	803.63700	22.00467			802.645119			802.645119
71	794.56763	794.56824	794.56763	19.81600	19.87900	19.81600	0.00000	12.34729	12.44487	241850.93090	NaN	9.79548	0.00942	0.00942	794.56783	19.83700			793.562114			793.562114
280	176.11375	176.10977	176.11375	1.38400	1.38800	1.38400	0.00000	12.36526	12.44759	244366.77435	NaN	9.67577	0.00949	0.00949	176.11243	1.38533	C17249		175.1031			175.103085
67	806.64026	806.64014	806.64026	23.49100	23.60100	23.49100	0.00000	12.41190	12.46159	251889.08217	NaN	8.64518	0.00938	0.00938	806.64022	23.52767			805.634893			805.634926
166	577.51727	577.51721	577.51727	24.77500	24.86150	24.77500	0.00000	12.17889	12.50789	229438.10094	NaN	10.61160	0.00938	0.00938	577.51725	24.80383		HMDB07075	576.475403		HMDB07076	576.475403
21	977.75537	977.75586	977.75537	23.69100	23.76600	23.69100	0.00000	12.47962	12.54139	271171.66018	NaN	9.48380	0.01098	0.01098	977.75553	23.71600			976.751963			976.751963
240	391.28479	391.28470	391.28500	16.02400	15.98100	15.96500	12.55373	12.52280	12.57428	281683.18274	283148.30946	10.57968	0.01013	0.01013	391.28483	15.99000		HMDB00328	390.277008		HMDB00460	390.277008
73	792.62463	792.62524	792.62463	23.42100	23.36570	23.42100	0.00000	13.03537	12.58526	365974.39453	NaN	11.03505	0.00944	0.00944	792.62484	23.40257			791.603974			791.603974
336	86.09741	86.09747	86.09741	4.52800	4.23800	4.52800	0.00000	12.28775	12.59442	252985.29330	NaN	9.41848	0.00916	0.00916	86.09743	4.43133	C03219		85.089149	C01746		85.0891
337	86.09747	86.09735	86.09739	9.68700	9.93900	9.91100	13.90609	12.41113	12.61070	271281.60471	1094805.01419	12.04850	0.01023	0.01023	86.09740	9.84567	C03219		85.089149	C01746		85.0891
194	537.48871	537.48932	537.48871	23.91500	23.81300	23.91500	0.00000	12.54558	12.61259	290420.41429	NaN	10.00663	0.00911	0.00911	537.48891	23.88100		HMDB07041	536.444092		HMDB07125	536.444092
283	127.12354	127.12348	127.12354	3.98700	3.30700	3.98700	0.00000	13.50560	12.63727	475173.36792	NaN	11.11056	0.01160	0.01160	127.12352	3.76033	C07287		126.1045		HMDB06024	126.104465
47	850.62982	850.62982	850.62982	21.99500	22.05800	21.99500	0.00000	12.56800	12.64282	298167.49723	NaN	8.77939	0.01103	0.01103	850.62982	22.01600			849.624714			849.624714
86	767.55634	767.55689	767.55634	19.95800	20.02100	19.95800	0.00000	12.55527	12.64304	296308.24438	NaN	10.95727	0.00926	0.00926	767.55652	19.97900			766.551219			766.551219
134	695.35986	695.36084	695.35986	13.64500	13.66100	13.64500	0.00000	12.54285	12.64708	295068.05800	NaN	9.60515	0.00983	0.00983	695.36019	13.65033	C08692		694.346546	C08681		694.3465
158	586.54144	586.54193	586.54144	22.49000	22.52900	22.49000	0.00000	12.55082	12.65598	297569.36738	NaN	9.92150	0.00971	0.00971	586.54161	22.50300						
65	808.58600	808.58637	808.58600	20.67600	20.73900	20.67600	0.00000	12.63804	12.70930	319230.59588	NaN	11.06068	0.01136	0.01136	808.58612	20.69700		HMDB07989	807.57782		HMDB07990	807.57782
241	376.34291	376.34296	376.34291	16.29500	16.32200	16.29500	0.00000	12.72213	12.83223	354044.39355	NaN	10.16103	0.00920	0.00920	376.34259	16.30400		HMDB13626	375.313721		HMDB13626	375.313721
77	789.62158	789.62128	789.62158	21.51250	21.55200	21.51250	0.00000	12.79569	12.83796	368362.35375	NaN	8.30498	0.00944	0.00944	789.62148	21.52567			788.629469			788.629469
239	410.37451	410.37491	410.37451	13.70400	13.71900	13.70400	0.00000	12.74151	12.86552	363493.58869	NaN	8.95595	0.00934	0.00934	410.37464	13.70900			409.391966			409.391979
76	790.63825	790.63696	790.63825	23.11400	23.24800	23.11400	0.00000	12.81506	12.89560	382824.13590	NaN	8.93554	0.00996	0.00996	790.63782	23.15867		HMDB07886	789.624756		HMDB07977	789.624756
153	593.55225	593.55231	593.55225	22.05400	22.08200	22.05400	0.00000	12.77283	12.94487	384173.72590	NaN	8.89094	0.00786	0.00786	593.55227	22.06333			592.506675			592.506675
202	520.38678	520.38568	520.38678	9.68700	9.69100	9.68700	0.00000	12.89532	12.96981	413561.95936	NaN	10.75629	0.00893	0.00893	520.38641	9.68833			519.368875			519.368843
70	795.58612	795.58722	795.58612	21.10000	21.16300	21.10000	0.00000	12.90764	12.98916	420164.10907	NaN	9.64939	0.01060	0.01060	795.58649	21.12100			794.582519			794.582519
33	890.66119	890.66126	890.66119	20.95900	21.02200	20.95900	0.00000	12.89431	13.02057	423979.40492	NaN	9.29184	0.01002	0.01002	890.66121	20.98000			889.656014			889.656014
308	118.10165	118.08695	118.08711	1.37200	1.38800	1.38400	10.71491	12.95664	13.05517	445034.56354	45022.33108	9.63233	0.01061	0.01061	118.09190	1.38133	C00183	HMDB00883	117.079	C00431	HMDB03355	117.079
66	808.58429	808.58435	808.58429	20.33500	20.38600	20.33500	0.00000	12.91485	13.05730	436339.11333	NaN	10.15668	0.00915	0.00915	808.58431	20.35200		HMDB07989	807.577764		HMDB07990	807.577764
245	359.31622	359.31619	359.31622	16.29500	16.32200	16.29500	0.00000	12.96642	13.07507	451686.49264	NaN	10.63710	0.01061	0.01061	359.31621	16.30400		HMDB11131	358.308319		HMDB11535	358.308319
105	734.57861	734.57929	734.57861	21.03000	21.05700	21.03000	0.00000	13.00306	13.09776	465288.62282	NaN	9.26976	0.00957	0.00957	734.57884	21.03900			733.562155			733.562155
83	776.62561	776.62585	776.62561	22.54900	22.63500	22.54900	0.00000	12.88555	13.10467	440253.78360	NaN	11.59364	0.00986	0.00986	776.62569	22.57767		HMDB07944	775.609131		HMDB08264	775.609131
90	764.59442	764.59320	764.59442	21.80700	21.89330	21.80700	0.00000	12.97626	13.10787	461418.46170	NaN	9.36444	0.00929	0.00929	764.59401	21.83577			763.572674			763.572674
284	127.12374	127.12392	127.12374	14.55200	15.19200	14.55200	0.00000	13.60319	13.21696	666685.97503	NaN	9.71687	0.00884	0.00884	127.12380	14.76533	C07287		126.1045		HMDB06024	126.104465
98	748.58752	748.58655	748.58752	23.58500	23.57800	23.58500	0.00000	13.18777	13.22646	544224.24472	NaN	9.82060	0.00943	0.00943	748.58720	23.58267		HMDB07937	747.57782		HMDB08033	747.57782
162	579.53656	579.53717	579.53656	24.94000	25.02600	24.94000	0.00000	13.06479	13.25169	518262.41395	NaN	9.70170	0.01052	0.01052	579.53676	24.96867		HMDB07074	578.491028		HMDB07242	578.491028
285	127.12396	127.12391	127.12396	18.21500	18.24200	18.21500	0.00000	13.74791	13.30027	747202.09464	NaN	9.62714	0.00966	0.00966	127.12394	18.22400	C07287		126.1045		HMDB06024	126.104465
125	721.50855	721.51611	721.51556	20.72400	20.61000	20.59400	15.66671	13.18769	13.30795	566830.33468	6367424.57631	10.13858	0.01100	0.01100	721.51341	20.64267		HMDB10571	720.494141		HMDB10585	720.494141
140	664.49304	664.49353	664.49304	20.37000	20.42100	20.37000	0.00000	13.39655	13.45923	678668.98104	NaN	8.49045	0.01017	0.01017	664.49321	20.38700			663.483905			663.483905
18	991.76990	991.77081	991.76990	24.00900	24.07200	24.00900	0.00000	13.44315	13.50088	709286.34896	NaN	10.24915	0.00963	0.00963	991.77020	24.03000			990.861513			990.861513
173	565.52051	565.52112	565.52051	24.56300	24.65000	24.56300	0.00000	13.46709	13.53519	730248.81709	NaN	10.20941	0.00942	0.00942	565.52071	24.59200		HMDB07016	564.475403		HMDB07043	564.475403
195	537.48956	537.48975	537.48956	19.94600	20.00900	19.94600	0.00000	13.45392	13.54057	727406.76049	NaN	8.28695	0.00933	0.00933	537.48962	19.96700		HMDB07041	536.444092		HMDB07125	536.444092
227	449.33807	449.33868	449.33881	16.02400	15.99300	15.96500	13.75153	13.50744	13.56947	758012.36069	938020.09915	9.76213	0.00915	0.00915	449.33852	15.99400			448.335256			448.335256
79	781.57324	781.57282	781.57324	20.52300	20.58600	20.52300	0.00000	13.55366	13.64874	807100.76232	NaN	10.20123	0.01105	0.01105	781.57310	20.54400			780.566869			780.566869

99	748.59546	748.59509	748.59546	21.51300	21.54000	21.51300	0.00000	13.63705	13.67558	852828.74431	NaN	8.69724	0.01115	0.01115	748.59534	21.52200		HMDB07937	747.57782		HMDB08033	747.57782
52	836.61456	836.61438	836.61456	21.44200	21.50500	21.44200	0.00000	13.58946	13.70868	846675.89029	NaN	10.24231	0.01189	0.01189	836.61450	21.46300		HMDB08055	835.609064		HMDB08056	835.609064
91	762.61176	762.61133	762.61176	21.99500	22.05800	21.99500	0.00000	13.69667	13.79249	931529.77796	NaN	9.76609	0.00693	0.00693	762.61161	22.01600			761.593455			761.593455
126	721.56010	721.56079	721.55981	21.96000	22.62400	22.63100	12.53890	13.95939	13.90360	1122980.19518	278980.00654	8.95408	0.01112	0.01112	721.54224	22.40500			720.530479			720.530479
163	579.53711	579.53729	579.53711	21.58300	21.65800	21.58300	0.00000	13.83934	13.96287	1089367.76161	NaN	10.79322	0.00956	0.00956	579.53717	21.60800		HMDB07074	578.491028		HMDB07242	578.491028
58	822.60004	822.60034	822.60004	20.93550	20.98700	20.93550	0.00000	13.83598	13.96337	1087808.90330	NaN	10.60512	0.00977	0.00977	822.60014	20.95267			821.593414			821.593414
184	551.50537	551.50531	551.50537	24.26900	24.35500	24.26900	0.00000	13.89782	13.97047	1125956.04083	NaN	9.92774	0.01116	0.01116	551.50535	24.29767			550.49611	C13864		550.4961
226	452.32455	452.32352	452.32455	9.67500	9.69100	9.67500	0.00000	13.89457	13.97389	1126056.75867	NaN	9.78475	0.00959	0.00959	452.32421	9.68033			451.319878	C05150		451.3199
185	551.50592	551.50617	551.50592	24.03300	24.09600	24.03300	0.00000	13.89617	13.99445	1138601.57093	NaN	9.77231	0.00876	0.00876	551.50600	24.05400			550.49611	C13864		550.4961
138	678.50958	678.50989	678.50958	20.95900	20.99800	20.95900	0.00000	14.06067	14.13348	1325199.84496	NaN	9.21203	0.00982	0.00982	678.50969	20.97200		HMDB07866	677.499573		HMDB08890	677.499573
286	127.12396	127.13243	127.12396	31.19400	32.02300	31.19400	0.00000	14.28543	14.16699	1507872.44450	NaN	8.26820	0.01112	0.01112	127.12679	31.47033	C07287		126.1045		HMDB06024	126.104465
129	718.54004	718.54132	718.54004	22.63100	22.62400	22.63100	0.00000	14.08987	14.38725	1526612.64548	NaN	10.47501	0.01065	0.01065	718.54047	22.62867	C13877		717.5309		HMDB07936	717.530884
106	734.57306	734.57233	734.57306	23.06700	23.22450	23.06700	0.00000	14.49915	14.42362	1907661.06341	NaN	10.21652	0.01096	0.01096	734.57282	23.11950			733.562155			733.562155
210	493.35077	493.34973	493.35077	9.68700	9.69100	9.68700	0.00000	14.38610	14.47836	1852836.13423	NaN	10.92583	0.00914	0.00914	493.35042	9.68833			492.325297			492.32528
339	86.09738	86.09733	86.09720	39.91000	39.91400	39.91000	15.97745	14.44426	14.48399	1912890.31971	8687999.33958	10.84367	0.01108	0.01108	86.09730	39.91133	C03219		85.089149	C01746		85.0891
287	127.12366	127.12358	127.12357	2.11400	2.13000	2.13700	16.31284	14.54417	14.65305	2188241.26655	12149969.90504	9.88474	0.01019	0.01019	127.12360	2.12700	C07287		126.1045		HMDB06024	126.104465
288	127.12375	127.12349	127.12339	1.54900	1.48200	1.51300	16.36392	14.62781	14.66415	2294403.68459	12786712.36267	11.77107	0.01042	0.01042	127.12354	1.51467	C07287		126.1045		HMDB06024	126.104465
289	127.12364	127.12352	127.12352	1.07800	1.09300	1.10100	16.32701	14.55188	14.69807	2246699.02176	12323336.86594	8.94459	0.01163	0.01163	127.12356	1.09067	C07287		126.1045		HMDB06024	126.104465
128	720.55597	720.55615	720.55597	22.71400	22.76500	22.71400	0.00000	14.75514	14.94394	2812385.32097	NaN	9.47782	0.01238	0.01238	720.55603	22.73100		HMDB07935	719.546509		HMDB07967	719.546509
174	565.52020	565.52130	565.52020	21.05300	21.11600	21.05300	0.00000	14.90572	14.98911	3101549.40954	NaN	9.59927	0.01076	0.01076	565.52057	21.07400		HMDB07016	564.475403		HMDB07043	564.475403
133	706.54163	706.54144	706.54163	22.12500	22.15300	22.12500	0.00000	15.00631	15.01974	3311867.33720	NaN	10.09170	0.01075	0.01075	706.54157	22.13433		HMDB07869	705.530884		HMDB07934	705.530884
290	127.12412	127.12405	127.12412	36.71800	36.02700	36.71800	0.00000	14.42309	15.18033	2681026.04584	NaN	12.28302	0.00820	0.00820	127.12410	36.48767	C07287		126.1045		HMDB06024	126.104465
135	692.52466	692.52557	692.52466	21.59500	21.65800	21.59500	0.00000	15.15306	15.27386	4046892.38468	NaN	10.42465	0.01037	0.01037	692.52496	21.61600			691.515205			691.515205
186	551.50543	551.50562	551.50543	20.53500	20.58600	20.53500	0.00000	15.22148	15.33298	4313377.10249	NaN	10.31504	0.01016	0.01016	551.50549	20.55200			550.49611	C13864		550.4961

Appendix - D - Wild Type Avicel Polar Metabolites

ID	MZ_blank	MZ_WTAv_Polar_Rep1	MZ_WTAv_Polar_Rep2	RT_blank	RT_WTAv_Polar_Rep1	RT_WTAv_Polar_Rep2	Int_blank	Int_WTAv_Polar_Rep1	Int_WTAv_Polar_Rep2	exp(mean.grp1)	exp(mean.grp2)	fold.mean	p.ttest	p.wilcox	mean_m/z	mean_rt	KEGG_ID_1	HMDB_ID_1	Match_mass_1	KEGG_ID_2	HMDB_ID_2	Match_mass_2
571	157.03607	157.03615	157.03607	2.08300	2.06800	2.08300	0.00000	15.46013	15.25799	4681174.53856	NaN	9.69898	0.01117	0.01117	157.03610	2.07800	C07931		156.03419	C14715		156.03420
644	127.12373	127.12353	127.12328	8.45000	8.44900	8.49900	15.59402	14.82121	14.49690	2324588.38613	5921038.16242	8.94294	0.00785	0.00785	127.12351	8.46600	C07287		126.10450		HMDB06024	126.10447
680	118.08718	118.08729	118.08712	1.51500	1.43200	1.43500	7.20715	14.51623	14.44546	1945143.64476	1349.04662	11.47020	0.00864	0.00864	118.08720	1.46067	C00183	HMDB00883	117.07900	C00431	HMDB03355	117.07900
748	98.98499	98.98515	98.98499	1.57700	1.58500	1.57700	0.00000	14.57746	14.37216	1933432.46313	NaN	10.75870	0.00819	0.00819	98.98504	1.57967	C12893		97.97701	C12554		97.97700
458	196.96178	196.96210	196.96178	1.56500	1.57300	1.56500	0.00000	13.81123	13.59172	892224.71621	NaN	10.81657	0.00922	0.00922	196.96188	1.56767	C19183		195.95090	C19300		195.97160
332	247.12940	247.12981	247.12940	9.13500	9.10800	9.13500	0.00000	13.52645	13.60976	780824.97705	NaN	9.78067	0.01099	0.01099	247.12953	9.12600	C19972		246.12160			246.12157
318	261.14551	261.14572	261.14551	12.09000	12.07500	12.09000	0.00000	13.22243	13.28550	570326.44112	NaN	10.53514	0.01016	0.01016	261.14558	12.08500			260.13722			260.13722
233	348.07132	348.07126	348.07132	2.56600	2.55000	2.56600	0.00000	13.28972	13.18804	561786.64803	NaN	8.58842	0.01159	0.01159	348.07130	2.56067			347.06310	C00020	HMDB00045	347.06310
523	182.08150	182.08147	182.08150	4.44900	4.29300	4.44900	0.00000	13.23193	13.20295	549870.08930	NaN	11.23110	0.01057	0.01057	182.08149	4.39700			181.07389	C01624		181.07389
821	81.01847	81.01857	81.01847	2.14200	2.12700	2.14200	0.00000	13.14748	13.04564	487263.83726	NaN	9.63996	0.00878	0.00878	81.01850	2.13700	C06753		80.00290	C19160		80.00290
329	249.10898	249.10910	249.10898	2.00100	1.99700	2.00100	0.00000	12.95888	12.97416	427845.86466	NaN	10.01435	0.01014	0.01014	249.10902	1.99967			248.10084			248.10084
284	279.10202	279.10193	279.10202	9.41800	9.39100	9.41800	0.00000	12.91063	13.02141	427630.41453	NaN	10.44827	0.00933	0.00933	279.10199	9.40900			278.09428			278.09429
758	90.97750	90.97752	90.97750	1.27100	1.26700	1.27100	0.00000	12.83122	12.69499	349096.56594	NaN	9.08737	0.01061	0.01061	90.97751	1.26967	C06613		89.98720	C16348		89.98720
819	81.52124	81.52171	81.52156	1.03300	1.06700	1.07000	11.12997	12.75912	12.73493	343527.20952	68184.49028	9.64966	0.01081	0.01081	81.52150	1.05667						
579	148.06117	148.06125	148.06117	1.44700	1.44400	1.44700	0.00000	12.69493	12.62273	314528.84249	NaN	9.71771	0.01086	0.01086	148.06120	1.44600	C00025	HMDB00148	147.05320	C00217	HMDB03339	147.05320
380	226.95190	226.95218	226.95190	1.24700	1.24400	1.24700	0.00000	12.57082	12.50841	279180.82452	NaN	10.50648	0.01184	0.01184	226.95200	1.24600	C12835		225.94360	C12958		225.94358
576	151.03534	151.03546	151.03534	1.05900	1.04300	1.05900	0.00000	12.60903	12.37737	266518.89447	NaN	10.29929	0.00976	0.00976	151.03538	1.05367	C02137	HMDB01587	150.03169		HMDB01973	150.03169
317	261.14508	261.14520	261.14508	11.66600	11.61600	11.66600	0.00000	12.51406	12.44372	262731.39041	NaN	9.15623	0.01024	0.01024	261.14512	11.64933			260.13722			260.13722
363	235.16623	235.16660	235.16623	1.44700	1.43200	1.44700	0.00000	12.43010	12.51359	260888.09985	NaN	8.94107	0.00852	0.00852	235.16635	1.44200			234.16197			234.16197
789	86.09741	86.09730	86.09720	0.52600	0.17200	0.17600	12.71805	12.84759	12.09561	260823.06306	333717.69259	9.76641	0.01002	0.01002	86.09730	0.29133	C03219		85.08915	C01746		85.08910
386	223.09668	223.09654	223.09668	30.12700	30.11200	30.12700	0.00000	12.30777	12.55480	250516.87171	NaN	11.09984	0.01025	0.01025	223.09663	30.12200			222.08919			222.08919
643	127.12329	127.12344	127.12329	7.80500	7.61300	7.80500	0.00000	11.94065	12.63314	216836.23121	NaN	9.56495	0.01001	0.01001	127.12334	7.74100	C07287		126.10450		HMDB06024	126.10447
533	176.10535	176.10750	176.10535	1.44700	1.44400	1.44700	0.00000	12.32350	12.20678	212169.46653	NaN	8.75565	0.01090	0.01090	176.10606	1.44600			175.09971	C00327	HMDB00904	175.09570
788	86.09736	86.09720	86.09718	0.93900	0.79600	0.94100	12.69675	12.52985	11.80853	192758.05435	326684.50070	8.80114	0.01157	0.01157	86.09725	0.89200	C03219		85.08915	C01746		85.08910
336	244.19154	244.19113	244.19154	25.11200	25.13200	25.11200	0.00000	11.91617	12.20100	172574.42300	NaN	10.29121	0.01055	0.01055	244.19141	25.11867		HMDB13286	243.18344	C07673		243.19870
568	158.96193	158.96445	158.96442	1.65700	1.26700	1.27100	8.71659	12.09869	11.92529	164718.25453	6103.34119	10.48416	0.00852	0.00852	158.96360	1.39833	C19212		157.97238	C19164		157.97240
538	173.02115	173.02126	173.02115	1.62400	1.64400	1.62400	0.00000	12.03808	11.86494	155051.02641	NaN	10.30724	0.00902	0.00902	173.02118	1.63067	C03189	HMDB00126	172.01367	C02979	HMDB02520	172.01367
716	110.00779	110.00822	110.00779	1.05900	1.05500	1.05900	0.00000	11.92461	11.87502	147239.26937	NaN	9.80059	0.00958	0.00958	110.00794	1.05767	C00519	HMDB00965	109.01970	C00519	HMDB00965	109.01975
755	94.04569	94.04582	94.04569	1.07000	1.04300	1.07000	0.00000	11.93595	11.80238	142794.59151	NaN	11.50598	0.01073	0.01073	94.04573	1.06100	C00292	HMDB03012	93.05780	C14447		93.05780
551	166.08644	166.08646	166.08644	9.07600	9.02600	9.07600	0.00000	11.74634	11.90389	136641.85093	NaN	9.24240	0.00919	0.00919	166.08645	9.05933			165.07898	C02765	HMDB01943	165.07898
267	295.12964	295.12958	295.12964	12.62000	12.58100	12.62000	0.00000	11.75374	11.88468	135837.38387	NaN	9.77055	0.00947	0.00947	295.12962	12.60700	C11045	HMDB01894	294.12160		HMDB00594	294.12158
193	444.13745	444.13715	444.13745	10.10100	10.07400	10.10100	0.00000	11.78449	11.82939	134180.13250	NaN	10.01853	0.01045	0.01045	444.13735	10.09200			443.12885	C18886		443.12480
549	167.01231	167.01294	167.01294	1.03300	1.06700	1.07000	9.53150	11.76817	11.68922	124081.56109	13787.22438	9.68302	0.00942	0.00942	167.01273	1.05667			166.00311	C17948		166.00310
616	134.04564	134.04562	134.04564	1.48300	1.50300	1.48300	0.00000	11.70473	11.65172	117974.61700	NaN	9.59798	0.01110	0.01110	134.04563	1.48967	C00049	HMDB00191	133.03751	C03440		133.03751
239	334.14047	334.14029	334.14047	14.68000	14.65300	14.68000	0.00000	11.58845	11.73143	115837.12197	NaN	11.71892	0.00825	0.00825	334.14041	14.67100			333.13247			333.13247
367	231.17011	231.17056	231.17011	1.97700	1.95000	1.97700	0.00000	11.53631	11.75170	114005.99807	NaN	10.08873	0.00890	0.00890	231.17026	1.96800			230.16304			230.16304
573	156.06729	156.07195	156.06729	1.40000	1.40800	1.40000	0.00000	11.69019	11.57589	112762.89187	NaN	9.25789	0.00978	0.00978	156.06884	1.40267			155.05824	C17517		155.05824
172	478.06274	478.06302	478.06274	2.02400	2.00900	2.02400	0.00000	11.60896	11.60090	109636.95495	NaN	9.61691	0.00854	0.00854	478.06284	2.01900	C00513		477.05500			477.05496
223	362.92667	362.92703	362.92667	1.24700	1.24400	1.24700	0.00000	11.62109	11.46800	103212.61189	NaN	9.54408	0.00949	0.00949	362.92679	1.24600	C07552		361.87572	C07552		361.87570
529	179.01706	179.01689	179.01706	2.07100	2.06800	2.07100	0.00000	11.56139	11.51426	102521.44282	NaN	11.21025	0.00858	0.00858	179.01700	2.07000	C11582		178.00650			178.00645
268	294.93893	294.93955	294.93893	1.24700	1.24400	1.24700	0.00000	11.58591	11.47976	102010.57203	NaN	10.92956	0.01006	0.01006	294.93914	1.24600			293.99057			293.99057
346	242.92546	242.92557	242.92546	1.24700	1.24400	1.24700	0.00000	11.57131	11.44538	99542.63843	NaN	10.92190	0.00928	0.00928	242.92550	1.24600	C18251		241.89404	C18242		241.89400
797	84.96035	84.96046	84.96024	1.03300	1.06700	1.07000	9.73513	11.54121	11.46183	98865.91410	16901.04852	7.42665	0.01015	0.01015	84.96035	1.05667	C02390		83.95336	C02271		83.95340
251	311.12418	311.12399	311.12418	12.00800	11.98100	12.00800	0.00000	11.48139	11.51883	98726.55243	NaN	10.20905	0.00839	0.00839	311.12412	11.99900		HMDB11741	310.11649			310.11649
391	218.94339	218.94367	218.94339	1.50600	1.50300	1.50600	0.00000	11.54042	11.42643	97092.98920	NaN	9.08157	0.00896	0.00896	218.94348	1.50500	C06989		217.92240			217.92236
200	430.91437	430.91428	430.91437	1.23500	1.24400	1.23500	0.00000	11.53724	11.39414	95386.22951	NaN	10.44723	0.01051	0.01051	430.91434	1.23800	C13706		429.97763			429.97769
647	125.98637	125.98631	125.98637	1.07000	1.06700	1.07000	0.00000	11.49144	11.43605	95201.17520	NaN	9.55018	0.01025	0.01025	125.98635	1.06900	C18872		124.98690	C00245	HMDB00251	125.01466
733	101.00361	101.00366	101.00361	2.08300	2.11500	2.08300	0.00000	11.59838	11.29287	93491.29081	NaN	9.64849	0.00904	0.00904	101.00363	2.09367	C18588		99.99370	C18675		99.99365
133	922.01068	922.00977	922.01086	1.53900	1.62000	1.62400	9.37977	11.61927	11.23279	91676.87075	11846.26551	10.73827	0.00864	0.00864	922.01044	1.59433			921.15707	C14120		921.15710
155	621.24176	621.24182	621.24176	10.57200	10.52100	10.57200	0.00000	11.33751	11.44346	88475.67848	NaN	8.99287	0.00919	0.00919	621.24178	10.55500	C20138		620.25010			620.21051
159	593.08893	593.09033	593.08893	2.07100	2.03200	2.07100	0.00000	11.40442	11.30421	85333.03262	NaN	9.80342	0.00972	0.00972	593.08940	2.05800			592.07005			592.14275
550	166.08608	166.08643	166.08608	13.12600	13.11100	13.12600	0.00000	11.25303	11.39336	82718.15637	NaN	10.58518	0.01051	0.01051	166.08619	13.12100			165.07898	C02765	HMDB01943	165.07898
287	277.13956	277.14002	277.13956	9.12300	9.09600	9.12300	0.00000	11.26846	11.34629	81419.90058	NaN	8.91483	0.01028	0.01028	277.13971	9.11400	C00449	HMDB00279	276.13210	C00449	HMDB00279	276.13214
275	286.11337	286.11359	286.11337	1.90600	1.89100	1.90600	0.00000	11.21923	11.37931	80762.62450	NaN	9.88408	0.00879	0.00879	286.11344	1.90100	C07195		285.10730	C07372		285.10350
531	177.05443	177.05441	177.05443	30.11500	30.11200	30.11500	0.00000	11.16205	11.42477	80290.63227	NaN	9.81169	0.00968	0.00968	177.05442	30.11400	C01173		176.04730	C03081		176.04730
593	142.94829	142.94875	142.94829	1.38800	1.38500	1.38800	0.00000	11.29389	11.21713	77304.67385	NaN	9.72359	0.01050	0.01050	142.94844	1.38700	C13558		141.94080	C13199		141.93130
772	89.50736	89.50734	89.50731	0.96200	0.97300	0.96500	10.24557	11.28403	11.22503	77228.63482	28157.60793	11.93505	0.00958	0.00958	89.50733	0.96667						
313	263.12357	263.12415	263.12357	2.13000	2.11500	2.13000	0.00000	11.20307	11.10789	69945.90669	NaN	10.49682	0.00896	0.00896	263.12376	2.12500			262.11649	C01683		262.11650
672	121.05033	121.05082	121.05033	0.17600	0.17200	0.17600	0.00000	10.68505	11.51867	66294.09593	NaN	10.22085	0.00912	0.00912	121.05049	0.17467	C01796		120.04230	C02022		120.04230
264	298.09705	298.09753	298.09705	11.54900	11.53400	11.54900	0.00000	11.00182	11.20127	66273.19243	NaN	8.62890	0.01009	0.01009	298.09721	11.54400	C00170	HMDB01173	297.08956	C00170	HMDB01173	297.08957
167	498.90146	498.90195	498.90146	1.24700	1.23200	1.24700	0.00000	11.14444	11.05453	66137.30178	NaN	9.94054	0.01043	0.01043	498.90162	1.24200			497.89119			498.04675
727	102.03448	102.03476	102.03448	1.07000	1.05500	1.07000	0.00000	11.11320	11.05895	65812.98596	NaN	13.06860	0.01182	0.01182	102.03457	1.06500			101.04768	C02948		101.04768
588	144.98793	144.98787	144.98793	2.13000	2.12700	2.13000	0.00000	11.20332	10.93170	64055.76530	NaN	8.15690	0.01185	0.01185	144.98791	2.12900	C18424		143.97431	C18399		143.97430
160	591.08569	591.08624	591.08569	34.53000	34.51500	34.53000	0.00000	11.02933	11.00423	60887.41341	NaN	9.79530	0.00720	0.00720	591.08588	34.52500			590.06432	C04630		590.10260
162	566.88971	566.88947	566.88971	1.23500	1.24400	1.23500	0.00000	11.06990	10.95197	60532.52448	NaN	8.92015	0.01053	0.01053	566.88963	1.23800			565.89537	C00029	HMDB00286	566.05499
689	114.98775	114.98807	114.98775	1.04700	1.03200	1.04700	0.00000	11.02016	10.91479	57957.93726	NaN	10.38896	0.00867	0.00867	114.98785	1.04200	C03248		113.99530	C00975	HMDB02050	113.99531
544	170.04273	170.04289	170.04273	1.41200	1.42000	1.41200	0.00000	10.90951	10.91843	54938.41821	NaN	9.91271	0.00993	0.00993	170.04278	1.41467	C03340		169.03750	C11465		169.03750
771	89.50752	89.50749	89.50723	0.17300	0.17200	0.17600	10.86780	10.86865	10.94594	54572.95159	52459.69627	10.43545	0.01071	0.01071	89.50742	0.17367						

671	121.05069	121.05098	121.05069	39.91100	39.90700	39.91100	0.00000	10.87161	10.94123	54525.47587	NaN	9.89125	0.01137	0.01137	121.05079	39.90967		HMDB01366	120.04359		HMDB01366	120.04360
327	255.20714	255.20700	255.20685	14.97200	14.98300	14.97500	11.12749	10.80554	10.97614	53682.36569	68015.23897	9.53674	0.00916	0.00916	255.20700	14.97667	C17603		254.18820	C17606		254.18820
809	83.04298	83.04514	83.04298	0.88200	0.92600	0.88200	0.00000	10.92332	10.85495	53590.95621	NaN	8.68945	0.00961	0.00961	83.04370	0.89667		HMDB13749	82.04186	C08389		82.05310
606	138.05806	138.05678	138.05806	2.49500	2.46800	2.49500	0.00000	11.53377	10.18285	51964.06437	NaN	10.21053	0.01056	0.01056	138.05763	2.48600			137.04882	C15533		137.04880
679	118.08613	118.08192	118.08613	1.97700	1.96200	1.97700	0.00000	10.79941	10.91238	51838.96762	NaN	9.80998	0.00825	0.00825	118.08473	1.97200			117.07897			117.07897
206	415.21158	415.21130	415.21158	32.85800	32.86700	32.85800	0.00000	10.67819	11.02499	51616.24570	NaN	9.65710	0.01056	0.01056	415.21149	32.86100	C10658		414.20420	C12512		414.20420
721	106.95055	106.95090	106.95055	1.28200	1.27900	1.28200	0.00000	10.88992	10.73504	49636.33379	NaN	9.24748	0.00976	0.00976	106.95067	1.28100	C18765		105.94340	C19207		105.94181
277	281.11322	281.11325	281.11322	10.88900	10.86200	10.88900	0.00000	10.68355	10.88439	48241.14635	NaN	10.17358	0.01188	0.01188	281.11323	10.88000			280.10592		HMDB00706	280.10592
370	230.17529	230.17534	230.17529	22.93400	22.94200	22.93400	0.00000	10.62103	10.89338	46967.16106	NaN	10.43176	0.01018	0.01018	230.17531	22.93667		HMDB13267	229.16780	C11707		229.14670
627	130.08609	130.08650	130.08609	2.09500	2.06800	2.09500	0.00000	10.75375	10.70057	45577.15512	NaN	8.18271	0.00982	0.00982	130.08623	2.08600			129.07898	C03969		129.07898
217	378.90024	378.90064	378.90024	1.24700	1.24400	1.24700	0.00000	10.80191	10.63687	45224.36525	NaN	10.68150	0.01081	0.01081	378.90037	1.24600	C18124		377.87063	C13718		377.87060
640	128.10875	128.10907	128.10875	5.07300	5.40000	5.07300	0.00000	11.12435	10.30650	45045.47249	NaN	11.43146	0.01017	0.01017	128.10886	5.18200			127.09971	C11519		127.09970
605	138.05663	138.05751	138.05663	3.00100	2.70400	3.00100	0.00000	11.49417	9.87167	43604.69062	NaN	11.69150	0.01167	0.01167	138.05692	2.90200			137.04882	C15533		137.04880
201	428.03638	428.03702	428.03638	2.78900	2.78600	2.78900	0.00000	10.78972	10.54969	43032.09512	NaN	7.58889	0.00798	0.00798	428.03659	2.78800	C00008	HMDB01341	427.02940	C00054	HMDB00061	427.02940
152	695.13196	695.13208	695.13196	2.56600	2.52700	2.56600	0.00000	10.71693	10.61933	42964.40095	NaN	8.05009	0.00920	0.00920	695.13200	2.55300			694.13805			694.13813
521	182.98483	182.98441	182.98421	1.04400	1.02000	1.02300	9.28187	10.69434	10.62848	42676.76803	10741.50073	10.99700	0.01141	0.01141	182.98448	1.02900	C07598		181.97080	C07719		181.97075
405	213.19649	213.19638	213.19576	14.99600	14.99500	14.99800	11.73558	10.94846	10.33723	41891.81203	124938.83330	8.75204	0.00799	0.00799	213.19621	14.99633			212.17763			212.17763
253	309.14438	309.14484	309.14438	11.65500	11.62800	11.65500	0.00000	10.55124	10.72073	41605.32239	NaN	11.45334	0.00896	0.00896	309.14453	11.64600			308.14123			308.14123
190	446.88806	446.88852	446.88806	1.23500	1.24400	1.23500	0.00000	10.72928	10.53080	41358.66967	NaN	10.16677	0.01178	0.01178	446.88821	1.23800			445.96131			445.96131
759	90.52552	90.52615	90.52552	1.03500	1.03200	1.03500	0.00000	10.84659	10.36531	40374.46513	NaN	10.34446	0.00893	0.00893	90.52573	1.03400						
556	160.99495	160.99356	160.99495	1.04700	1.04300	1.04700	0.00000	10.66558	10.54304	40308.04766	NaN	10.23357	0.00952	0.00952	160.99449	1.04567	C18300		159.98470	C19165		159.98470
552	165.05421	165.05458	165.05421	4.44900	4.30500	4.44900	0.00000	10.59815	10.59761	40049.81936	NaN	11.27982	0.00979	0.00979	165.05434	4.40100	C00166	HMDB00205	164.04730	C00811		164.04730
334	245.09566	245.09586	245.09566	15.22200	15.20700	15.22200	0.00000	10.55232	10.64137	40008.32556	NaN	9.17283	0.00928	0.00928	245.09572	15.21700	C00120	HMDB00030	244.08817	C00120	HMDB00030	244.08817
628	130.05023	130.04985	130.05023	3.22500	3.21000	3.22500	0.00000	10.58653	10.60636	39992.42433	NaN	9.85370	0.01003	0.01003	130.05011	3.22000	C01879	HMDB00267	129.04259	C02237	HMDB00805	129.04259
252	310.91284	310.91306	310.91284	1.24700	1.24400	1.24700	0.00000	10.65132	10.50315	39231.29197	NaN	9.04793	0.01119	0.01119	310.91291	1.24600			309.92993	C01151	HMDB11688	309.98547
534	174.93771	174.93771	174.93771	1.28200	1.27900	1.28200	0.00000	10.63538	10.49848	38829.23020	NaN	10.48157	0.00853	0.00853	174.93771	1.28100			173.91193		HMDB00250	173.91193
617	133.06137	133.06125	133.06137	1.44700	1.46700	1.44700	0.00000	10.67492	10.43742	38413.68776	NaN	8.62865	0.01056	0.01056	133.06133	1.45367	C00152	HMDB00168	132.05350	C01043		132.05350
611	136.07526	136.07533	136.07526	4.44900	4.30500	4.44900	0.00000	10.55381	10.52666	37806.31251	NaN	10.71537	0.01073	0.01073	136.07528	4.40100	C02505	HMDB10715	135.06840	C07565		135.06840
389	220.18243	220.18247	220.18243	11.46600	11.46300	11.46600	0.00000	10.78743	10.28342	37625.09169	NaN	10.52173	0.00864	0.00864	220.18244	11.46500	C16362		219.16231	C09961		219.16231
639	128.10867	128.10880	128.10867	4.74400	4.63400	4.74400	0.00000	11.00001	10.06766	37565.23706	NaN	10.47293	0.01100	0.01100	128.10871	4.70733			127.09971	C11519		127.09970
591	143.08159	143.08192	143.08159	1.63600	1.62000	1.63600	0.00000	10.43486	10.61087	37155.44929	NaN	10.03541	0.00983	0.00983	143.08170	1.63067	C06231		142.07420	C06231		142.07420
522	182.08144	182.08217	182.08144	10.57200	10.53300	10.57200	0.00000	10.50991	10.51217	36718.64011	NaN	10.60255	0.00965	0.00965	182.08168	10.55900			181.07389	C01624		181.07389
489	186.15990	186.15947	186.15927	14.99600	14.99500	14.99800	11.61432	10.77238	10.24420	36617.73198	110670.77943	9.84592	0.00997	0.00997	186.15955	14.99633			185.15281	C16649		185.14158
228	353.18216	353.18228	353.18216	13.12600	13.11100	13.12600	0.00000	10.40792	10.59633	36392.61471	NaN	7.93534	0.00894	0.00894	353.18220	13.12100			352.17869			352.17869
618	132.99822	132.99806	132.99822	1.04700	1.04300	1.04700	0.00000	10.54050	10.45731	36275.64938	NaN	8.93688	0.01016	0.01016	132.99816	1.04567			132.00585	C03981		132.00585
687	116.04435	116.04302	116.04435	1.56500	1.55000	1.56500	0.00000	10.50806	10.48690	36224.01158	NaN	10.04327	0.00879	0.00879	116.04391	1.56000			115.02694	C01596		115.02690
128	922.00934	922.01013	922.00952	0.93900	0.91400	0.91700	9.46085	10.64777	10.33967	36088.10596	12846.84810	8.67655	0.00862	0.00862	922.00966	0.92333			921.15707	C14120		921.15710
352	240.92516	240.92560	240.92516	1.45900	1.47900	1.45900	0.00000	10.54663	10.43672	36014.33415	NaN	8.68994	0.00947	0.00947	240.92530	1.46567	C14310		239.92600	C14335		239.92601
470	191.03182	191.03223	191.03182	1.55300	1.55000	1.55300	0.00000	10.52947	10.43214	35625.01292	NaN	11.83502	0.01131	0.01131	191.03195	1.55200			190.02416	C04110		190.02660
785	86.09751	86.09728	86.09706	7.80200	7.35400	7.53400	11.59013	10.82974	10.11666	35355.10988	108026.75398	7.41044	0.00934	0.00934	86.09729	7.56333	C03219		85.08915	C01746		85.08910
208	399.24973	399.25031	399.24973	39.03700	39.04800	39.06300	10.71821	10.16887	10.64932	33159.80041	45170.73281	11.00880	0.00975	0.00975	399.24992	39.04933	C14446		398.24330	C14513		398.24334
381	226.18024	226.18005	226.18024	25.11200	25.13200	25.11200	0.00000	10.17914	10.63445	33083.68923	NaN	11.94271	0.00960	0.00960	226.18018	25.11867	C14186		225.15900	C18768		225.15900
131	922.01032	922.01068	922.01032	4.22600	3.98700	4.22600	0.00000	10.06028	10.74472	32941.92313	NaN	10.43478	0.01159	0.01159	922.01044	4.14633			921.15707	C14120		921.15710
637	128.11185	128.11162	128.11159	0.95000	0.70200	0.89400	11.24888	10.84260	9.94828	32710.17713	76793.57186	10.72332	0.00920	0.00920	128.11168	0.84867			127.09971	C11519		127.09970
626	130.96799	130.96516	130.96564	1.02100	1.05500	1.07000	8.95290	10.42063	10.34733	32337.33459	7730.25889	9.03279	0.00715	0.00715	130.96626	1.04867	C14860		129.95880	C14867		129.95884
125	922.00922	922.00958	922.00922	1.93000	1.93800	1.93000	0.00000	10.50917	10.16222	30813.05529	NaN	10.76302	0.00871	0.00871	922.00934	1.93267			921.15707	C14120		921.15710
688	116.05261	116.05340	116.05261	34.53000	34.50300	34.53000	0.00000	10.10259	10.55991	30676.45348	NaN	12.41316	0.01072	0.01072	116.05287	34.52100			115.02694	C01596		115.02690
636	128.11061	128.10959	128.10878	5.55350	5.96500	5.72100	11.45071	10.76893	9.82570	29652.85467	93967.94862	9.33216	0.00992	0.00992	128.10966	5.74650			127.09971	C11519		127.09970
165	514.87579	514.87573	514.87579	1.24700	1.24400	1.24700	0.00000	10.37190	10.18638	29118.73501	NaN	11.58367	0.00949	0.00949	514.87577	1.24600			514.04166			514.04173
778	88.04015	88.04009	88.04015	1.45900	1.47900	1.45900	0.00000	10.41161	10.09874	28429.26376	NaN	9.35997	0.00968	0.00968	88.04013	1.46567			87.03203	C06748		87.03203
463	193.14604	193.14697	193.14604	11.46600	11.47500	11.46600	0.00000	10.36290	10.11069	27911.47171	NaN	9.72438	0.00961	0.00961	193.14635	11.46900	C07142		192.12630			192.12626
163	541.32593	541.32599	541.32593	32.87000	32.86700	32.87000	0.00000	10.55820	9.89954	27691.20166	NaN	9.95750	0.01042	0.01042	541.32595	32.86900	C17766		540.30870			540.34268
673	120.08073	120.08060	120.08073	13.15000	13.11100	13.15000	0.00000	10.22999	10.22169	27607.42798	NaN	10.66190	0.01100	0.01100	120.08068	13.13700			119.05824	C00188	HMDB00167	119.05824
384	224.07639	224.07698	224.07639	7.45200	7.34200	7.45200	0.00000	10.30304	10.13899	27474.53378	NaN	9.72464	0.01134	0.01134	224.07658	7.41533			223.06333	C14499		223.06333
580	147.11273	147.11290	147.11273	1.10600	1.10200	1.10600	0.00000	10.25734	10.17210	27302.16082	NaN	10.26852	0.00755	0.00755	147.11279	1.10467	C00047	HMDB00182	146.10550	C00739	HMDB03405	146.10550
784	86.09760	86.09737	86.09720	17.93900	17.69100	17.81200	11.39485	10.58538	9.79182	26598.12153	88863.04280	9.63171	0.01023	0.01023	86.09739	17.81400	C03219		85.08915	C01746		85.08910
722	105.04235	105.04287	105.04235	1.17600	1.18500	1.17600	0.00000	10.43198	9.93234	26427.48628	NaN	9.97636	0.01057	0.01057	105.04252	1.17900	C02221		104.03740	C02234		104.03740
199	432.23767	432.23810	432.23767	32.87000	32.86700	32.87000	0.00000	10.08265	10.27868	26387.93835	NaN	10.03516	0.01028	0.01028	432.23781	32.86900			431.22810			431.22810
423	205.09731	205.09683	205.09731	11.64300	11.59200	11.64300	0.00000	10.09785	10.25957	26336.34068	NaN	9.54951	0.01042	0.01042	205.09715	11.62600	C00078	HMDB00929	204.08987	C00525	HMDB13609	204.08987
601	141.95874	141.95902	141.95863	1.00900	1.02000	1.02300	8.96395	10.20280	10.14978	26272.68977	7816.16866	11.06058	0.00936	0.00936	141.95880	1.01733	C00169	HMDB01096	140.98270	C00169	HMDB01096	140.98271
509	184.13287	184.13318	184.13294	1.53900	1.59700	1.60000	8.78788	10.46021	9.88784	26213.37976	6554.34120	9.01365	0.00937	0.00937	184.13300	1.57867	C12452		183.12590	C12453		183.12590
315	262.90707	262.90778	262.90707	1.43500	1.43200	1.43500	0.00000	10.25084	10.08884	26103.83923	NaN	10.40686	0.00933	0.00933	262.90731	1.43400	C19129		261.80803	C19122		261.80800
173	473.26434	473.26382	473.26434	32.85800	32.86700	32.85800	0.00000	10.20464	10.12587	25984.41333	NaN	9.40389	0.01029	0.01029	473.26417	32.86100			472.25896		HMDB02522	472.24948
319	261.03671	261.03708	261.03671	1.55300	1.55000	1.55300	0.00000	10.20638	10.09510	25610.03463	NaN	9.64815	0.00945	0.00945	261.03684	1.55200			260.02894	C00085	HMDB00124	260.02970
149	718.83759	718.83948	718.83759	1.24700	1.23200	1.24700	0.00000	10.29927	9.99767	25551.96168	NaN	8.43887	0.00954	0.00954	718.83822	1.24200						
545	169.04491	169.04567	169.04491	1.03500	1.02000	1.03500	0.00000	10.56118	9.68046	24855.10644	NaN	9.01046	0.01156	0.01156	169.04516	1.03000			168.04224	C01839		168.04224
670	121.05090	121.05090	121.05102	38.79000	38.63600	38.49800	10.42665	10.13922	10.10135	24841.80668	33747.11141	10.33122	0.00954	0.00954	121.05094	38.64133		HMDB01366	120.04359		HMDB01366	120.04360
207	412.16443	412.16553	412.16443	10.46600	10.42700	10.46600	0.00000	9.97842	10.23449	24500.67056	NaN	11.51797	0.00732	0.00732	412.16480	10.45300	C15038		411.15829	C15038		411.15830
459	195.00276	195.00227	195.00276	1.57700	1.59700	1.57700	0.00000	10.12977	10.06969	24336.40734	NaN	10.35211	0.00928	0.00928	195.00260	1.58367	C12836		193.99820	C13342		193.99820
130	922.01044	922.01044	922.01044	4.82600	4.58700	4.82600	0.00000	9.53603	10.66031	24298.52747	NaN	9.13695	0.01096	0.01096	922.01044	4.74633			921.15707	C14120		921.15710
590	144.00131	143.99681	143.99677	1.02100	1.05500	1.07000	9.48946	10.31111	9.88325	24274.39979	13219.60095	9.52877	0.01122	0.01122	143.99830	1.04867	C18316		143.02186	C18232		143.02190
394	217.08171	217.08212	217.08171	1.70600	1.70300	1.70600	0.00000	10.11892	10.06571	24156.56521	NaN	8.56881	0.01227	0.01227	217.08185	1.70500	C17359		216.07460			216.07462
366	233.11330	233.11337	233.11330	3.88400	3.78700	3.88400	0.00000	10.08125	10.08586	23945.89781	NaN	9.55623	0.00960	0.00960	233.11332	3.85167	C01410		232.10590	C03415		232.10590

546	168.12270	168.12383	168.12270	8.71100	8.69600	8.71100	0.00000	10.00056	10.07170	22836.88087	NaN	11.21061	0.01108	0.01108	168.12307	8.70600	C10916		167.10590	C11006		167.10586
230	351.20593	351.20593	351.20593	8.48800	8.40200	8.48800	0.00000	10.34123	9.72298	22745.09345	NaN	8.59229	0.00881	0.00881	351.20593	8.45933			350.19943			350.19943
696	114.09120	114.09159	114.09120	1.80000	1.79700	1.80000	0.00000	10.44545	9.56365	22126.87028	NaN	9.98703	0.01183	0.01183	114.09133	1.79900			113.08406	C05853		113.08406
250	311.12424	311.12354	311.12424	9.80600	9.76800	9.80600	0.00000	9.95516	10.04697	22049.83543	NaN	10.56003	0.00920	0.00920	311.12400	9.79333		HMDB11741	310.11649			310.11649
697	114.09161	114.09151	114.09161	12.07900	12.06300	12.07900	0.00000	9.87576	10.11058	21876.54094	NaN	9.73934	0.00938	0.00938	114.09157	12.07367			113.08406	C05853		113.08406
385	223.98985	223.99069	223.98985	1.08200	1.06700	1.08200	0.00000	10.07417	9.85004	21207.43883	NaN	10.98612	0.01054	0.01054	223.99013	1.07700			223.00362	C04327		223.00680
323	258.89948	258.89874	258.89948	1.25900	1.25500	1.25900	0.00000	10.03895	9.87721	21122.19284	NaN	10.19556	0.00880	0.00880	258.89923	1.25767		HMDB12282	257.90955		HMDB12282	257.90956
754	96.98956	96.98928	96.98956	1.07000	1.05500	1.07000	0.00000	10.20257	9.69762	20954.11407	NaN	10.79769	0.00839	0.00839	96.98947	1.06500	C11145		95.98810	C11261		95.98812
669	121.05100	121.05102	121.05108	10.71000	10.29700	10.33600	9.85664	9.82644	10.05075	20714.64770	19084.70619	11.07801	0.00858	0.00858	121.05103	10.44767		HMDB01366	120.04359		HMDB01366	120.04360
274	288.92197	288.92166	288.92197	1.16500	1.16100	1.16500	0.00000	9.97528	9.84958	20179.64097	NaN	8.88432	0.01034	0.01034	288.92187	1.16367	C18450		287.88620	C18456		287.88618
774	89.00025	88.99907	89.00025	1.07000	1.05500	1.07000	0.00000	9.95639	9.86156	20110.05688	NaN	8.64999	0.01041	0.01041	88.99986	1.06500	C19233		88.00798	C19208		88.00800
655	122.92428	122.92486	122.92428	1.30600	1.30300	1.30600	0.00000	9.96838	9.79204	19539.77093	NaN	9.87504	0.01037	0.01037	122.92447	1.30500	C14870		121.93670	C15220		121.93673
781	86.09689	86.09734	86.09689	13.38500	13.42900	13.38500	0.00000	10.61121	9.14439	19492.73666	NaN	11.48258	0.00967	0.00967	86.09704	13.39967	C03219		85.08915	C01746		85.08910
235	345.03424	345.03485	345.03424	1.65900	1.66700	1.65900	0.00000	9.93087	9.80815	19331.94483	NaN	10.32470	0.00945	0.00945	345.03444	1.66167	C11719		344.03860			344.03863
808	83.04708	83.05550	83.04708	39.48700	39.44800	39.48700	0.00000	10.20329	9.53097	19285.89545	NaN	11.65163	0.01018	0.01018	83.04989	39.47400		HMDB13749	82.04186	C08389		82.05310
140	838.83960	838.83691	838.83960	1.23500	1.23200	1.23500	0.00000	9.93603	9.77773	19089.28805	NaN	9.54033	0.00940	0.00940	838.83871	1.23400			837.70577			837.70577
667	121.05113	121.05097	121.05096	12.15900	11.84000	11.85500	10.01324	9.80071	9.88227	18797.71594	22320.12182	9.28795	0.00992	0.00992	121.05102	11.95133		HMDB01366	120.04359		HMDB01366	120.04360
246	325.04330	325.04343	325.04330	2.75400	2.76200	2.75400	0.00000	9.79698	9.82778	18258.42101	NaN	9.11972	0.00889	0.00889	325.04335	2.75667	C00105	HMDB00288	324.03586	C01168	HMDB01271	324.03586
498	185.04462	185.04048	185.04462	1.07000	1.06700	1.07000	0.00000	10.11882	9.49898	18194.91445	NaN	11.28251	0.00850	0.00850	185.04324	1.06900	C20125		184.03470			184.03467
665	121.05099	121.05090	121.05099	12.92600	12.87600	12.92600	0.00000	9.81975	9.78220	18051.28956	NaN	8.99548	0.00938	0.00938	121.05096	12.90933		HMDB01366	120.04359		HMDB01366	120.04360
266	295.12894	295.12866	295.12894	12.16100	12.13400	12.16100	0.00000	9.66612	9.92794	17980.27499	NaN	10.99966	0.01010	0.01010	295.12885	12.15200			294.12157			294.12157
202	424.89600	424.89529	424.89600	1.16500	1.16100	1.16500	0.00000	9.84758	9.74058	17927.29287	NaN	10.28554	0.01235	0.01235	424.89576	1.16367		HMDB01372	424.03714			424.03714
236	344.22876	344.22855	344.22794	13.53600	13.52300	13.51500	10.17721	9.94054	9.63951	17854.80683	26297.10659	10.90179	0.00973	0.00973	344.22841	13.52467	C07879		343.22598	C07879		343.22600
803	84.07663	84.07938	84.07663	1.04700	0.99600	1.04700	0.00000	9.79372	9.77754	17776.44463	NaN	10.05161	0.01086	0.01086	84.07755	1.03000			83.07350			83.07350
780	86.09707	86.09728	86.09707	14.77500	14.92400	14.77500	0.00000	10.53003	9.03945	17760.60397	NaN	9.35853	0.01125	0.01125	86.09714	14.82467	C03219		85.08915	C01746		85.08910
326	256.17578	256.17621	256.17578	11.66300	11.66300	11.66600	0.00000	9.70559	9.84013	17550.91500	NaN	10.05670	0.01232	0.01232	256.17592	11.66500	C07180		255.17350			255.17355
213	388.25510	388.25427	388.25394	14.24200	14.24100	14.23300	10.41683	9.91793	9.61692	17455.76839	33417.23976	10.48975	0.00975	0.00975	388.25444	14.23867			387.24817			387.24817
622	132.10156	132.10138	132.10156	3.59000	3.52800	3.59000	0.00000	9.76270	9.75551	17311.08421	NaN	8.77727	0.01086	0.01086	132.10150	3.56933	C00123	HMDB00687	131.09460	C00407	HMDB00172	131.09460
666	121.05111	121.05090	121.05090	12.52400	12.68700	12.32600	10.06240	9.69555	9.81503	17245.18970	23444.67468	9.83547	0.00984	0.00984	121.05097	12.51233		HMDB01366	120.04359		HMDB01366	120.04360
227	354.28412	354.28510	354.28400	34.09200	34.09100	34.08300	10.11534	9.51888	9.99025	17232.64613	24719.32229	9.57468	0.01132	0.01132	354.28440	34.08867			353.29298			353.29298
520	182.98503	182.98479	182.98503	0.17600	0.17200	0.17600	0.00000	9.69488	9.80767	17176.14394	NaN	10.43854	0.00931	0.00931	182.98495	0.17467	C07598		181.97080	C07719		181.97075
292	272.94458	272.94467	272.94458	1.16500	1.16100	1.16500	0.00000	9.75494	9.73323	17053.09414	NaN	10.59351	0.00982	0.00982	272.94461	1.16367	C14189		271.95620	C14737		271.95620
723	102.12820	102.12771	102.12820	2.47100	2.53900	2.47100	0.00000	9.69976	9.78087	16988.92705	NaN	10.06180	0.00936	0.00936	102.12803	2.49367	C08306		101.12040	C14691		101.12040
184	457.30277	457.30353	457.30478	39.03700	39.03600	39.03900	10.43175	9.68428	9.79260	16957.03616	33919.52039	10.13250	0.01103	0.01103	457.30369	39.03733			456.29878			456.28755
668	121.05106	121.05091	121.05089	9.13300	9.30800	9.32400	9.66271	9.56838	9.89971	16882.64998	15720.35222	10.37901	0.00970	0.00970	121.05095	9.25500		HMDB01366	120.04359		HMDB01366	120.04360
232	350.17560	350.17481	350.17560	34.53000	34.49200	34.53000	0.00000	9.51444	9.89413	16387.71167	NaN	9.03795	0.01092	0.01092	350.17533	34.51733	C18411		349.16779	C18411		349.16780
464	192.97325	192.97313	192.97325	1.04700	1.05500	1.04700	0.00000	9.75365	9.64737	16325.97697	NaN	10.03602	0.01095	0.01095	192.97321	1.04967	C18315		191.97449	C18302		191.97450
372	229.11829	229.11841	229.11829	11.91400	11.88700	11.91400	0.00000	9.60625	9.77741	16184.84726	NaN	10.46251	0.00966	0.00966	229.11833	11.90500	C13733		228.11100			228.11101
331	247.12877	247.12892	247.12877	9.61800	9.60300	9.61800	0.00000	9.64778	9.68803	15802.21033	NaN	9.69729	0.00804	0.00804	247.12882	9.61300		HMDB11166	246.12157		HMDB11172	246.12157
263	300.20215	300.20160	300.20215	12.67900	12.66400	12.67900	0.00000	9.64989	9.67251	15696.60899	NaN	10.47348	0.00911	0.00911	300.20197	12.67400			299.18853	C11819		299.18853
664	121.05103	121.05102	121.05103	8.98200	8.93200	8.98200	0.00000	9.53621	9.75883	15483.37376	NaN	10.62276	0.01160	0.01160	121.05102	8.96533		HMDB01366	120.04359		HMDB01366	120.04360
807	83.05695	83.05496	83.05129	7.99100	8.13100	8.22900	10.20318	9.78302	9.50019	15392.05045	26988.84764	10.69853	0.01072	0.01072	83.05440	8.11700		HMDB13749	82.04186	C08389		82.05310
779	86.09739	86.09728	86.09696	10.39300	10.30900	10.34800	11.50138	10.57028	8.67193	15079.64921	98852.44881	10.72012	0.01059	0.01059	86.09721	10.35000	C03219		85.08915	C01746		85.08910
422	205.11748	205.11803	205.11748	5.13200	4.95200	5.13200	0.00000	9.61802	9.61682	15024.20273	NaN	8.57438	0.01182	0.01182	205.11766	5.07200	C03955		204.11100	C04210		204.11100
747	98.98449	98.98434	98.98449	2.35400	2.33900	2.35400	0.00000	9.69258	9.52703	14910.30012	NaN	9.63898	0.01204	0.01204	98.98444	2.34900	C00009	HMDB02142	97.97690	C00009	HMDB02142	97.97690
286	277.13889	277.13968	277.13889	7.85200	7.80100	7.85200	0.00000	9.46946	9.74627	14881.34045	NaN	10.27087	0.01046	0.01046	277.13915	7.83500	C00449	HMDB00279	276.13210	C00449	HMDB00279	276.13214
783	86.09728	86.09737	86.09728	34.82200	34.85700	34.83600	10.91432	9.82394	9.38237	14811.36463	54957.62668	8.44924	0.01145	0.01145	86.09731	34.83833	C03219		85.08915	C01746		85.08910
424	204.95601	204.95786	204.95601	1.18800	1.17300	1.18800	0.00000	9.60297	9.56448	14526.40528	NaN	10.02114	0.01065	0.01065	204.95662	1.18300			203.97854			203.97854
270	291.11853	291.11945	291.11853	8.13400	8.10800	8.13400	0.00000	9.39941	9.76119	14476.79341	NaN	8.38125	0.01154	0.01154	291.11884	8.12533		HMDB12267	290.11139	C04421		290.11140
532	176.97826	176.97275	176.97826	1.05900	1.05500	1.05900	0.00000	9.56801	9.56959	14311.19769	NaN	10.51011	0.01078	0.01078	176.97642	1.05767	C14099		175.95514	C13964		175.95510
238	340.93146	340.93167	340.93146	1.17600	1.16100	1.17600	0.00000	9.65968	9.47725	14306.41731	NaN	9.93534	0.00871	0.00871	340.93153	1.17100	C11044		339.87830	C14372		339.87830
382	224.16315	224.16356	224.16315	33.77700	33.77300	33.77700	0.00000	9.71937	9.40396	14209.47468	NaN	9.32830	0.00960	0.00960	224.16328	33.77567	C10868		223.15720			223.15723
540	171.99228	171.99289	171.99228	1.05900	1.05500	1.05900	0.00000	9.59041	9.49299	13928.61404	NaN	9.63678	0.01114	0.01114	171.99248	1.05767	C13672		170.98445	C13058		170.98440
456	199.14427	199.14388	199.14427	1.67100	1.65600	1.67100	0.00000	9.78150	9.29398	13873.50515	NaN	9.23142	0.00720	0.00720	199.14414	1.66600	C06185		198.13680	C10858	HMDB06548	198.13683
473	190.07059	190.07134	190.07059	4.16700	4.08100	4.16700	0.00000	9.47886	9.55847	13611.38990	NaN	11.07000	0.01108	0.01108	190.07084	4.13833	C00624	HMDB01138	189.06370	C03871		189.06370
278	281.08127	281.08026	281.08127	34.10600	34.06800	34.10600	0.00000	9.12840	9.90114	13558.49169	NaN	11.66312	0.01066	0.01066	281.08093	34.09333			280.07354			280.07356
256	308.18478	308.18524	308.18478	30.11500	30.10000	30.11500	0.00000	9.42871	9.59600	13525.75350	NaN	9.78526	0.01239	0.01239	308.18494	30.11000	C07219	HMDB05023	307.16850	C07219	HMDB05023	307.16846
409	207.13727	207.13712	207.13727	33.78900	33.76200	33.78900	0.00000	9.24290	9.76732	13428.11492	NaN	9.62463	0.01035	0.01035	207.13722	33.78000	C01588	HMDB01925	206.13068	C01588	HMDB01925	206.13068
211	395.18652	395.18631	395.18652	9.67700	9.66200	9.67700	0.00000	9.47728	9.52636	13384.03370	NaN	10.97052	0.00819	0.00819	395.18645	9.67200			394.17917			394.18524
508	184.13329	184.13303	184.13329	0.85900	0.85500	0.85900	0.00000	9.62109	9.35583	13206.42616	NaN	11.84751	0.00862	0.00862	184.13320	0.85767	C12452		183.12590	C12453		183.12590
110	971.29486	971.29498	971.29486	3.82500	3.66900	3.82500	0.00000	9.49168	9.43163	12857.09971	NaN	7.78514	0.01164	0.01164	971.29490	3.77300	C11502		970.28820			970.28824
169	484.33997	484.34067	484.33847	39.02500	39.03600	39.03900	9.84880	9.24023	9.67049	12776.45083	18935.68504	10.44229	0.01030	0.01030	484.33970	39.03333			483.31960	C02592	HMDB00722	483.30185
507	184.13272	184.13361	184.13272	0.17600	0.17200	0.17600	0.00000	9.52353	9.28923	12165.75312	NaN	11.45687	0.01152	0.01152	184.13302	0.17467	C12452		183.12590	C12453		183.12590
663	121.05092	121.05087	121.05092	36.43800	36.48100	36.43800	0.00000	9.41596	9.37646	12042.59700	NaN	10.25876	0.01012	0.01012	121.05090	36.45233		HMDB01366	120.04359		HMDB01366	120.04360
654	122.96469	122.96468	122.96469	0.92900	0.93800	0.92900	0.00000	9.44002	9.35173	12038.56222	NaN	12.15328	0.00950	0.00950	122.96469	0.93200		HMDB12216	121.97128	C08270	HMDB12251	121.97129
469	191.06621	191.06664	191.06621	3.08400	3.05700	3.08400	0.00000	9.42292	9.36707	12028.02857	NaN	9.23453	0.01073	0.01073	191.06635	3.07500			190.05897		HMDB11185	190.05897
662	121.05100	121.05113	121.05100	14.82200	14.78300	14.82200	0.00000	9.42280	9.32547	11779.70946	NaN	8.54801	0.00833	0.00833	121.05105	14.80900		HMDB01366	120.04359		HMDB01366	120.04360
502	184.13696	184.13759	184.13643	9.06200	9.10800	9.17100	10.43071	9.92575	8.81631	11743.21541	33884.36496	11.17980	0.00879	0.00879	184.13699	9.11367			183.12593	C10865		183.12593
504	184.13312	184.13306	184.13312	10.41800	10.38000	10.41800	0.00000	9.65601	9.00177	11258.64844	NaN	9.61039	0.01239	0.01239	184.13310	10.40533	C12452		183.12590	C12453		183.12590
661	121.05119	121.05097	121.05119	15.41000	15.67800	15.41000	0.00000	9.38115	9.26218	11177.62248	NaN	7.20859	0.01009	0.01009	121.05112	15.49933		HMDB01366	120.04359		HMDB01366	120.04360
471	190.98042	190.97966	190.98042	1.05900	1.03200	1.05900	0.00000	9.52335	9.10632	11101.45931	NaN	10.02712	0.01062	0.01062	190.98017	1.05000	C15042		189.96294			189.96294
506	184.13339	184.13408	184.13345	13.17100	12.95800	12.99700	8.89689	9.45556	9.16966	11076.80806	7309.19362	10.01785	0.01072	0.01072	184.13364	13.04200	C12452		183.12590	C12453		183.12590
396	214.08966	214.08878	214.08966	28.71400	28.68700	28.71400	0.00000	8.95847	9.65442	11008.75858	NaN	10.14675	0.00858	0.00858	214.08937	28.70500	C12865		213.07900	C13697		213.07900

192	445.82596	445.82697	445.82596	1.56500	1.58500	1.56500	0.00000	9.35793	9.24161	10935.49017	NaN	10.46795	0.01080	0.01080	445.82629	1.57167						
607	137.03961	137.03876	137.03961	3.33100	3.28000	3.33100	0.00000	9.29226	9.28063	10790.73716	NaN	9.63860	0.01013	0.01013	137.03933	3.31400			136.03715			136.03715
574	155.15421	155.15358	155.15421	11.09000	11.03900	11.09000	0.00000	9.19099	9.34735	10605.92612	NaN	10.59950	0.00923	0.00923	155.15400	11.07300	C00843		154.13580	C01411		154.13580
261	302.24408	302.24396	302.24408	25.11200	25.13200	25.11200	0.00000	9.27113	9.24742	10501.48698	NaN	10.29521	0.00854	0.00854	302.24404	25.11867	C07171		301.24056	C08454		301.24057
678	118.08582	118.08627	118.08582	9.14700	9.10800	9.14700	0.00000	8.96363	9.55172	10484.72367	NaN	8.39600	0.01038	0.01038	118.08597	9.13400			117.07897			117.07897
528	180.03957	180.03870	180.03957	30.12700	30.08800	30.12700	0.00000	8.95450	9.55951	10477.69327	NaN	11.01705	0.00994	0.00994	180.03928	30.11400	C00745	HMDB01934	179.02523	C03727		179.02520
660	121.05105	121.05109	121.05108	17.04400	16.93800	17.12900	9.97607	9.31651	9.17707	10371.23533	21505.65251	9.33954	0.01001	0.01001	121.05107	17.03700		HMDB01366	120.04359		HMDB01366	120.04360
383	224.09242	224.09238	224.09242	12.85600	12.82900	12.85600	0.00000	8.99099	9.44389	10071.26006	NaN	9.07588	0.01042	0.01042	224.09241	12.84700	C14433		223.08450	C18953		223.08450
483	186.95761	186.95670	186.95784	0.90300	0.85500	0.85900	8.91834	9.43030	8.99470	10021.65570	7467.68779	11.49972	0.01188	0.01188	186.95738	0.87233			185.93164	C14846		185.93160
801	84.08072	84.08050	84.08077	1.62100	1.95000	1.96500	11.45639	9.36340	9.06122	10019.70477	94502.85854	11.37729	0.01140	0.01140	84.08066	1.84533			83.07350			83.07350
364	234.10872	234.10980	234.10872	9.46500	9.42600	9.46500	0.00000	9.05876	9.34884	9934.81869	NaN	11.94303	0.01097	0.01097	234.10908	9.45200			233.10117			233.10117
355	239.14954	239.15093	239.14954	11.66600	11.66300	11.66600	0.00000	9.10501	9.29772	9910.66899	NaN	8.77352	0.01152	0.01152	239.15000	11.66500	C11155		238.14298	C11079		238.14300
194	439.30759	439.30682	439.30759	37.48500	37.49400	37.48500	0.00000	9.22257	9.17723	9896.09580	NaN	10.05804	0.00845	0.00845	439.30733	37.48800			438.29814			438.29811
345	243.13469	243.13619	243.13469	14.48000	14.47700	14.48000	0.00000	9.17652	9.20481	9805.15809	NaN	10.01970	0.01000	0.01000	243.13519	14.47900			242.12666			242.12666
151	710.85059	710.85248	710.85059	1.22400	1.22000	1.22400	0.00000	9.24280	9.08618	9551.81275	NaN	9.36284	0.01044	0.01044	710.85122	1.22267						
659	121.05106	121.05115	121.05106	17.49400	17.36100	17.49400	0.00000	9.29814	9.02736	9535.26074	NaN	8.83020	0.00918	0.00918	121.05109	17.44967		HMDB01366	120.04359		HMDB01366	120.04360
658	121.05129	121.05104	121.05113	19.35200	18.92700	19.17800	10.21540	9.34547	8.97495	9511.03050	27320.82440	9.38703	0.00994	0.00994	121.05115	19.15233		HMDB01366	120.04359		HMDB01366	120.04360
166	499.95767	499.95950	499.95767	2.55400	2.52700	2.55400	0.00000	9.35875	8.92536	9339.95205	NaN	9.36412	0.01066	0.01066	499.95828	2.54500						
657	121.05109	121.05112	121.05109	18.07100	18.24400	18.07100	0.00000	9.30005	8.94980	9181.29874	NaN	9.16635	0.00757	0.00757	121.05110	18.12867		HMDB01366	120.04359		HMDB01366	120.04360
530	178.13367	178.13388	178.13367	11.23100	11.19200	11.23100	0.00000	9.15681	9.08831	9159.58342	NaN	10.42081	0.00891	0.00891	178.13374	11.21800			177.12660	C07432		177.11540
368	231.13428	231.13405	231.13428	10.23000	10.21500	10.23000	0.00000	8.92691	9.27978	8985.26223	NaN	9.62142	0.01106	0.01106	231.13420	10.22500			230.13067			230.13067
505	184.13341	184.13345	184.13300	10.35700	10.68600	10.72500	8.68160	9.12713	9.07804	8978.49882	5893.48220	10.27575	0.01003	0.01003	184.13329	10.58933	C12452		183.12590	C12453		183.12590
816	81.52113	81.52114	81.52129	12.84100	12.97000	12.99700	8.30484	9.19674	8.99088	8900.06858	4043.38012	10.70749	0.00999	0.00999	81.52119	12.93600						
720	107.07053	107.07033	107.07053	2.73100	2.70400	2.73100	0.00000	9.09783	9.06756	8801.62864	NaN	10.16025	0.00820	0.00820	107.07047	2.72200	C14743		106.06299	C14689		106.06300
455	199.14433	199.14401	199.14433	10.74800	10.85100	10.74800	0.00000	9.27351	8.87102	8710.34496	NaN	8.93887	0.00825	0.00825	199.14423	10.78233	C06185		198.13680	C10858	HMDB06548	198.13683
482	186.95728	186.95712	186.95660	0.18500	0.18400	0.17600	9.40726	9.48278	8.64714	8646.92769	12176.41082	11.03550	0.00921	0.00921	186.95700	0.18167			185.93164	C14846		185.93160
139	843.23901	843.23554	843.23901	11.39600	11.40400	11.39600	0.00000	9.00689	9.12258	8644.97953	NaN	11.94516	0.00978	0.00978	843.23785	11.39867			842.19056			842.19056
191	446.83371	446.83450	446.83371	1.64700	1.64400	1.64700	0.00000	9.23529	8.89224	8636.56891	NaN	7.83443	0.00926	0.00926	446.83397	1.64600			445.96131			445.96131
260	304.15262	304.15027	304.15262	5.96800	5.75300	5.96800	0.00000	9.14646	8.96798	8580.28207	NaN	11.63570	0.00877	0.00877	304.15184	5.89633			303.14304			303.14304
537	173.09270	173.09108	173.09270	10.86600	10.83900	10.86600	0.00000	8.93897	9.15748	8503.41056	NaN	12.31705	0.00869	0.00869	173.09216	10.85700			172.08479	C01507	HMDB11632	172.08479
258	305.13376	305.13495	305.13376	10.13600	10.08500	10.13600	0.00000	8.89300	9.19515	8468.18425	NaN	10.07782	0.00858	0.00858	305.13416	10.11900	C15485		304.12705	C15485		304.12710
535	174.07549	174.07629	174.07549	13.69100	13.65300	13.69100	0.00000	8.83877	9.24850	8464.49006	NaN	9.04060	0.00966	0.00966	174.07576	13.67833	C01250		173.06880	C12121		173.06880
746	98.98486	98.98430	98.98486	2.74200	2.75100	2.74200	0.00000	9.05898	9.00829	8380.27409	NaN	10.72372	0.01026	0.01026	98.98468	2.74500	C00009	HMDB02142	97.97690	C00009	HMDB02142	97.97690
744	100.07655	100.07690	100.07655	12.98500	12.98200	12.98500	0.00000	9.24927	8.78858	8257.88978	NaN	8.83459	0.00894	0.00894	100.07667	12.98400		HMDB11749	99.06841	C11249		99.06841
293	270.99783	270.99948	270.99783	1.61200	1.62000	1.61200	0.00000	9.05330	8.97160	8204.59526	NaN	9.60751	0.01004	0.01004	270.99838	1.61467		HMDB06343	270.01187		HMDB06343	270.01188
766	89.50778	89.50764	89.50748	33.42100	33.57300	33.58800	9.99332	9.21555	8.80887	8202.60815	21879.73159	8.71180	0.01111	0.01111	89.50763	33.52733						
501	184.13251	184.13333	184.13251	3.41300	3.43300	3.41300	0.00000	9.25995	8.76278	8195.71177	NaN	11.36743	0.00838	0.00838	184.13278	3.41967	C12452		183.12590	C12453		183.12590
583	146.95873	146.96492	146.95873	1.01200	1.02000	1.01200	0.00000	9.12268	8.89485	8174.38909	NaN	9.47580	0.01133	0.01133	146.96079	1.01467	C14400		145.94570	C14402		145.94568
171	478.29077	478.29102	478.29504	33.89200	33.85600	33.83600	9.75705	9.17864	8.80916	8053.83821	17275.61177	11.27599	0.00991	0.00991	478.29228	33.86133			477.28550			477.28554
767	89.50735	89.50729	89.50743	32.00800	32.01900	32.37600	9.99633	9.10091	8.83443	7845.27171	21945.83223	12.36700	0.01037	0.01037	89.50736	32.13433						
124	922.00934	922.01160	922.00934	11.84300	11.82800	11.84300	0.00000	7.90763	9.97762	7651.22859	NaN	9.32397	0.00959	0.00959	922.01009	11.83800			921.15707	C14120		921.15710
569	158.15268	158.14987	158.15268	27.44300	27.43900	27.44300	0.00000	8.66722	9.21484	7639.03285	NaN	10.70567	0.00888	0.00888	158.15174	27.44167	C07724		157.13275	C07674		157.13270
147	752.83545	752.83521	752.83545	1.27100	1.26700	1.27100	0.00000	9.08265	8.76183	7496.87497	NaN	10.31681	0.01071	0.01071	752.83537	1.26967						
817	81.52100	81.52113	81.52100	10.68900	10.39200	10.68900	0.00000	8.58851	9.24615	7460.11380	NaN	10.56836	0.01036	0.01036	81.52104	10.59000						
222	363.15451	363.15558	363.15451	4.42600	4.29300	4.42600	0.00000	8.86966	8.96067	7444.02317	NaN	10.64220	0.00856	0.00856	363.15487	4.38167			362.14779	C17362		362.14380
365	233.12328	233.12378	233.12328	4.75600	4.49300	4.75600	0.00000	8.91961	8.90784	7433.30590	NaN	11.34388	0.01005	0.01005	233.12344	4.66833			232.11332	C17232		232.11330
467	192.02721	192.02258	192.02721	1.07000	1.06700	1.07000	0.00000	9.07673	8.74373	7407.35847	NaN	7.62468	0.00993	0.00993	192.02567	1.06900			191.02186	C17938		191.02190
567	158.96179	158.96077	158.96130	10.65200	10.39200	10.43000	6.84823	8.94423	8.86071	7350.09765	942.20773	10.82571	0.00941	0.00941	158.96129	10.49133	C19212		157.97238	C19164		157.97240
408	208.03853	208.03893	208.03853	1.05900	1.04300	1.05900	0.00000	8.93580	8.82513	7190.13199	NaN	10.56135	0.01004	0.01004	208.03866	1.05367	C11628		207.03300	C11723		207.03300
623	132.00282	132.00322	132.00282	1.22400	1.23200	1.22400	0.00000	9.07674	8.68411	7189.87383	NaN	10.66375	0.01089	0.01089	132.00296	1.22667		HMDB01131	131.02184		HMDB01131	131.02185
135	887.33844	887.34345	887.33844	9.68900	9.67300	9.68900	0.00000	8.80977	8.95048	7187.67216	NaN	8.17361	0.01217	0.01217	887.34011	9.68367		HMDB12920	886.29572			886.27429
234	347.24039	347.24237	347.24039	34.68300	34.66800	34.68300	0.00000	8.71730	9.02937	7139.06388	NaN	9.97111	0.01186	0.01186	347.24105	34.67800			346.23551			346.23551
768	89.50720	89.50707	89.50720	13.00900	12.88700	13.00900	0.00000	8.85668	8.88679	7127.61312	NaN	10.47691	0.00918	0.00918	89.50716	12.96833						
503	184.13350	184.13342	184.13338	12.47600	12.36900	12.26700	8.46567	8.81032	8.92708	7106.05020	4748.90968	11.50041	0.01164	0.01164	184.13343	12.37067	C12452		183.12590	C12453		183.12590
621	132.10114	132.10120	132.10114	3.17800	3.13900	3.17800	0.00000	8.75225	8.98050	7089.56346	NaN	8.25174	0.01171	0.01171	132.10116	3.16500	C00123	HMDB00687	131.09460	C00407	HMDB00172	131.09460
198	437.09830	437.09876	437.09833	14.70200	14.66500	14.64500	9.84080	8.83202	8.88617	7038.11686	18784.66403	11.17614	0.01080	0.01080	437.09846	14.67067	C10067		436.10056	C10093		436.10056
120	922.01080	922.01086	922.01080	9.91200	10.29700	9.91200	0.00000	8.22669	9.45261	6902.59779	NaN	10.28864	0.00923	0.00923	922.01082	10.04033			921.15707	C14120		921.15710
765	89.50750	89.50736	89.50750	31.61100	31.39500	31.61100	0.00000	8.92123	8.74185	6846.82517	NaN	8.90563	0.01105	0.01105	89.50745	31.53900						
259	304.95664	304.96014	304.95664	1.09400	1.04367	1.09400	0.00000	8.82581	8.83400	6835.60512	NaN	10.16724	0.01021	0.01021	304.95781	1.07722	C14282		303.95787	C14282		303.95790
255	308.92407	308.92896	308.92407	2.21200	2.22100	2.21200	0.00000	8.84631	8.80152	6794.79818	NaN	9.48453	0.00883	0.00883	308.92570	2.21500	C18707		307.96210	C18707		307.96212
742	100.07613	100.07638	100.07613	10.44200	10.41500	10.44200	0.00000	9.07073	8.55309	6713.74980	NaN	10.15632	0.01287	0.01287	100.07622	10.43300	C11118		99.06840	C18796		99.06840
452	199.14287	199.14415	199.14287	2.27100	2.26800	2.27100	0.00000	9.40082	8.21715	6694.12598	NaN	11.46212	0.00962	0.00962	199.14330	2.27000	C06185		198.13680	C10858	HMDB06548	198.13683
174	468.01715	468.01880	468.01715	2.53000	2.50300	2.53000	0.00000	8.98134	8.62362	6650.69576	NaN	9.90217	0.00953	0.00953	468.01770	2.52100	C00458	HMDB00998	466.98961	C00458	HMDB00998	466.98960
371	229.15340	229.15503	229.15340	11.00700	10.96800	11.00700	0.00000	8.77687	8.82012	6624.24592	NaN	9.55130	0.01042	0.01042	229.15394	10.99400		HMDB11174	228.14739		HMDB11175	228.14739
769	89.50726	89.50758	89.50726	13.27900	13.37000	13.27900	0.00000	8.63012	8.96167	6607.07236	NaN	10.15541	0.01064	0.01064	89.50737	13.30933						
743	100.07587	100.07658	100.07587	10.70100	11.02700	10.70100	0.00000	9.01566	8.56942	6584.93191	NaN	9.22573	0.01069	0.01069	100.07611	10.80967	C11118		99.06840	C18796		99.06840
656	121.05112	121.05090	121.05112	20.39100	20.75200	20.39100	0.00000	9.25488	8.32168	6556.95953	NaN	10.18098	0.00974	0.00974	121.05104	20.51133		HMDB01366	120.04359		HMDB01366	120.04360
330	247.12883	247.12795	247.12883	10.78300	10.74500	10.78300	0.00000	8.64536	8.91599	6507.24959	NaN	9.44128	0.01034	0.01034	247.12854	10.77033		HMDB11166	246.12157		HMDB11172	246.12157
649	124.03725	124.03652	124.03725	1.14100	1.12600	1.14100	0.00000	8.91479	8.64351	6497.33142	NaN	10.03200	0.00924	0.00924	124.03701	1.13600	C00253	HMDB01488	123.03200	C06813		123.03200
221	364.06470	364.06592	364.06470	4.04900	3.99900	4.04900	0.00000	8.72510	8.83246	6494.94289	NaN	9.82396	0.01023	0.01023	364.06510	4.03233			363.05800			363.05800
454	199.14444	199.14484	199.14444	12.98500	12.95800	12.98500	0.00000	9.21882	8.32069	6436.61061	NaN	8.37957	0.00854	0.00854	199.14457	12.97600	C06185		198.13680	C10858	HMDB06548	198.13683
245	326.88681	326.88669	326.88681	1.25900	1.25500	1.25900	0.00000	8.87292	8.65856	6410.78442	NaN	10.33164	0.01076	0.01076	326.88677	1.25767			325.92647	C14967		325.92650
427	204.08733	204.08687	204.08733	1.69400	1.70300	1.69400	0.00000	8.72748	8.80123	6401.90918	NaN	8.84937	0.01129	0.01129	204.08717	1.69700			203.07937	C12986		203.07940

390	220.10790	220.10835	220.10790	9.54700	9.48500	9.54700	0.00000	8.64816	8.80142	6153.56958	NaN	8.09346	0.01064	0.01064	220.10805	9.52633	C03417		219.09680			219.09675
694	114.09160	114.09114	114.08239	13.46500	12.98200	13.32700	8.54756	9.32296	8.12288	6142.08540	5154.16553	10.04776	0.01063	0.01063	114.08838	13.25800			113.08406	C05853		113.08406
324	258.16284	258.16467	258.16284	1.83600	1.79700	1.83600	0.00000	8.63011	8.78236	6040.44843	NaN	9.73391	0.00900	0.00900	258.16345	1.82300	C05759		257.15752		HMDB13161	257.16272
564	158.96133	158.96225	158.96133	10.71300	10.67400	10.71300	0.00000	8.93547	8.46221	5995.97348	NaN	10.40365	0.01034	0.01034	158.96164	10.70000	C19212		157.97238	C19164		157.97240
474	189.03932	189.03966	189.03932	7.46300	7.33000	7.46300	0.00000	8.46586	8.88050	5844.05117	NaN	10.45478	0.00892	0.00892	189.03943	7.41867			188.03209			188.03209
566	158.96133	158.96147	158.96133	12.99700	12.95800	12.99700	0.00000	8.81228	8.53407	5844.02006	NaN	12.50000	0.01190	0.01190	158.96138	12.98400	C19212		157.97238	C19164		157.97240
541	171.14832	171.14681	171.14832	19.77800	19.74000	19.77800	0.00000	8.36789	8.97745	5841.05820	NaN	11.15677	0.01153	0.01153	171.14781	19.76533			170.14191	C03092		170.13070
210	395.67908	395.67883	395.67908	10.32400	10.29700	10.32400	0.00000	8.38744	8.95527	5833.40615	NaN	8.98137	0.00946	0.00946	395.67900	10.31500						
713	111.02190	111.02192	111.02190	39.91100	39.90700	39.91100	0.00000	8.39999	8.93029	5797.26378	NaN	9.21856	0.01079	0.01079	111.02190	39.90967	C18676		110.01350			110.01346
555	161.04436	161.04497	161.04436	7.46300	7.33000	7.46300	0.00000	8.42396	8.88571	5737.83192	NaN	9.78546	0.01174	0.01174	161.04456	7.41867	C00846	HMDB00398	160.03715	C00322	HMDB00225	160.03715
170	480.30701	480.30753	480.30554	36.41150	36.38700	36.08400	9.14525	8.66658	8.62513	5686.49818	9369.78623	11.02893	0.01049	0.01049	480.30669	36.29417			479.30115			479.30115
123	922.01025	922.01123	922.01025	11.25400	11.19200	11.25400	0.00000	7.47020	9.80353	5635.61125	NaN	8.63780	0.00946	0.00946	922.01058	11.23333			921.15707	C14120		921.15710
285	277.13910	277.13773	277.13910	3.53100	3.50400	3.53100	0.00000	8.62300	8.60260	5501.62923	NaN	9.25021	0.00881	0.00881	277.13864	3.52200	C00449	HMDB00279	276.13210	C06386		276.12950
421	206.11984	206.11942	206.11984	2.33000	2.40900	2.33000	0.00000	8.90007	8.30516	5445.90219	NaN	9.00850	0.01124	0.01124	206.11970	2.35633	C10846		205.11030			205.11028
362	236.21234	236.21332	236.21164	17.78600	17.83200	17.88300	9.80389	8.83661	8.31396	5299.06392	18104.05904	10.90312	0.01053	0.01053	236.21243	17.83367	C07401		235.16850	C07401		235.16846
777	88.51063	88.51031	88.51063	1.01200	1.00800	1.01200	0.00000	8.54999	8.58312	5252.99449	NaN	10.09580	0.00791	0.00791	88.51052	1.01067						
121	922.00952	922.01141	922.00952	13.89200	13.98200	13.89200	0.00000	7.66939	9.45804	5238.09821	NaN	10.27869	0.00820	0.00820	922.01015	13.92200			921.15707	C14120		921.15710
620	132.10136	132.10150	132.10136	12.09000	12.08700	12.09000	0.00000	8.52702	8.59076	5212.88839	NaN	9.07203	0.01062	0.01062	132.10141	12.08900	C00123	HMDB00687	131.09460	C00407	HMDB00172	131.09460
410	207.11285	207.11314	207.10410	1.12700	1.16100	1.14100	9.35711	8.63327	8.47514	5188.52684	11580.87356	10.60971	0.00967	0.00967	207.11003	1.14300	C07499		206.10550	C12590		206.10550
243	328.15094	328.14972	328.15094	11.13700	11.12100	11.13700	0.00000	8.50998	8.59330	5175.23267	NaN	10.11348	0.00935	0.00935	328.15053	11.13167			327.14304			327.14304
244	327.05017	327.05057	327.05017	1.25900	1.25500	1.25900	0.00000	8.47889	8.57603	5051.61079	NaN	11.41510	0.01049	0.01049	327.05030	1.25767			326.04262			326.04262
154	676.88196	676.88434	676.88196	2.83600	2.78600	2.83600	0.00000	8.63853	8.40851	5031.73158	NaN	10.17342	0.00964	0.00964	676.88275	2.81933						
497	185.13069	185.13081	185.13069	4.65000	4.55200	4.65000	0.00000	8.74892	8.26213	4942.00230	NaN	11.19258	0.00994	0.00994	185.13073	4.61733	C17235		184.12520	C09633		184.12520
220	372.54596	372.54593	372.54596	7.89900	8.11900	7.89900	0.00000	8.48514	8.52054	4928.73002	NaN	9.84729	0.01017	0.01017	372.54595	7.97233			371.38426			371.38395
406	209.13759	209.13857	209.13759	11.97300	11.96900	11.97300	0.00000	8.30642	8.67797	4876.55123	NaN	10.53853	0.01099	0.01099	209.13791	11.97167	C14514		208.12520	C14585		208.12520
265	295.12796	295.12952	295.12796	13.71500	13.67600	13.71500	0.00000	8.44444	8.53407	4862.24615	NaN	11.14848	0.01178	0.01178	295.12848	13.70200			294.12157			294.12157
122	922.01080	922.01263	922.01056	13.50100	13.44100	13.44400	7.37488	7.47508	9.48946	4828.39621	1595.40622	10.51324	0.01150	0.01150	922.01133	13.46200			921.15707	C14120		921.15710
565	158.96086	158.96108	158.96086	10.06500	9.83800	10.06500	0.00000	8.47072	8.46474	4758.71603	NaN	10.49668	0.00888	0.00888	158.96093	9.98933	C19212		157.97238	C19164		157.97240
237	341.14664	341.14722	341.14664	9.93600	9.92100	9.93600	0.00000	8.41297	8.46043	4613.30353	NaN	10.90954	0.01042	0.01042	341.14683	9.93100			340.13695	C04698		340.13690
248	316.15207	316.15088	316.15207	10.87800	10.86200	10.87800	0.00000	8.28032	8.58905	4604.01012	NaN	10.42523	0.00990	0.00990	316.15167	10.87267			315.14304			315.14304
205	419.08856	419.08582	419.08655	18.37500	18.42100	18.40100	9.18651	8.23840	8.57637	4480.02892	9764.53754	7.51310	0.01117	0.01117	419.08698	18.39900			418.08897	C06435		418.08900
219	373.17288	373.17355	373.17288	9.81800	9.79100	9.81800	0.00000	8.27052	8.54237	4475.81125	NaN	10.02891	0.01071	0.01071	373.17311	9.80900			372.16450			372.16450
249	311.12521	311.12531	311.12521	11.14800	11.14500	11.14800	0.00000	8.33482	8.45896	4433.24912	NaN	11.43688	0.01005	0.01005	311.12524	11.14700			310.11649			310.11649
146	775.10004	775.09863	775.10004	2.62500	2.68000	2.62500	0.00000	8.32867	8.45435	4409.46805	NaN	9.82847	0.01041	0.01041	775.09957	2.64333			774.21591			774.21599
118	922.00952	922.00891	922.00952	6.82800	6.43600	6.82800	0.00000	7.66879	9.09948	4377.06732	NaN	11.63808	0.00941	0.00941	922.00932	6.69733			921.15707	C14120		921.15710
404	213.19646	213.19571	213.19515	14.59600	14.60600	14.59800	9.34622	8.77511	7.98627	4362.03204	11455.40866	9.22540	0.01088	0.01088	213.19577	14.60000			212.17763			212.17763
800	84.08077	84.08085	84.08077	2.23600	2.22100	2.23600	0.00000	8.46630	8.29160	4354.44232	NaN	10.45228	0.00913	0.00913	84.08080	2.23100			83.07350			83.07350
439	199.98778	199.98673	199.98778	12.99700	12.98200	12.99700	0.00000	8.58451	8.16485	4335.88184	NaN	9.09171	0.00973	0.00973	199.98743	12.99200	C18905		198.97480	C19047		198.97477
592	143.03482	143.03401	143.03482	7.45200	7.33000	7.45200	0.00000	8.14241	8.60514	4331.95910	NaN	10.86648	0.01022	0.01022	143.03455	7.41133		HMDB02349	142.02661		HMDB02432	142.02661
142	816.56146	816.57025	816.56146	38.39200	38.55300	38.39200	0.00000	9.13250	7.60852	4317.85333	NaN	11.71814	0.00793	0.00793	816.56439	38.44567			815.55506		HMDB09309	815.54651
321	259.09259	259.09293	259.09259	7.28700	7.13000	7.28700	0.00000	8.21296	8.51770	4295.52400	NaN	9.36150	0.00921	0.00921	259.09270	7.23467		HMDB00884	258.08518		HMDB02331	258.08518
773	89.07127	89.07178	89.07127	2.97800	2.98600	2.97800	0.00000	8.27572	8.45354	4292.50886	NaN	10.57068	0.00968	0.00968	89.07144	2.98067	C16364		88.06366	C19299		88.06366
610	136.07192	136.07306	136.07192	1.12900	1.13800	1.12900	0.00000	8.61257	8.07889	4212.16333	NaN	8.55456	0.01015	0.01015	136.07230	1.13200	C02505	HMDB10715	135.06840	C07565		135.06840
751	98.51160	98.51312	98.51160	0.96500	0.97300	0.96500	0.00000	8.44274	8.21740	4146.69073	NaN	9.53711	0.01092	0.01092	98.51211	0.96767						
257	306.08594	306.08994	306.08594	3.82500	3.69200	3.82500	0.00000	8.29266	8.36740	4146.54038	NaN	10.74981	0.01176	0.01176	306.08727	3.78067	C13752		305.07920	C13752		305.07919
164	515.03888	515.04242	515.03888	4.42600	4.28100	4.42600	0.00000	8.36255	8.29448	4140.27791	NaN	9.07761	0.00947	0.00947	515.04006	4.37767			514.04166			514.04173
161	578.91553	578.91541	578.91553	2.84800	2.76200	2.84800	0.00000	8.43008	8.19740	4079.53851	NaN	9.96973	0.01057	0.01057	578.91549	2.81933	C03034		578.05500	C06017		578.05500
612	136.06163	136.06148	136.06163	2.57700	2.53900	2.57700	0.00000	8.15870	8.46630	4074.49356	NaN	8.91762	0.01073	0.01073	136.06158	2.56433	C03059		135.05320	C06056		135.05320
407	208.06386	208.06769	208.06386	3.24900	3.22200	3.24900	0.00000	8.35606	8.25481	4045.79930	NaN	8.88585	0.00908	0.00908	208.06514	3.24000			207.05653	C14876		207.05650
518	182.98526	182.98479	182.98436	10.67500	10.67400	10.71300	8.02752	8.44358	8.13944	3989.86717	3064.14341	9.98748	0.00884	0.00884	182.98480	10.68733	C07598		181.97080	C07719		181.97075
403	213.19533	213.19576	213.19533	0.85900	0.84300	0.85900	0.00000	8.81070	7.76371	3972.71008	NaN	11.62073	0.01086	0.01086	213.19547	0.85367			212.17763			212.17763
419	206.11559	206.11525	206.11449	1.17400	1.17300	1.15300	8.86219	8.43215	8.13063	3949.66393	7059.92686	11.65590	0.00992	0.00992	206.11511	1.16667			205.11028	C10869		205.11028
325	258.11005	258.10934	258.11005	2.93100	2.90400	2.93100	0.00000	8.35683	8.20001	3937.98439	NaN	10.56187	0.00980	0.00980	258.10981	2.92200			257.10117		HMDB00982	257.10117
369	231.09894	231.09735	231.09894	5.62700	5.51700	5.62700	0.00000	8.07521	8.47289	3920.78597	NaN	11.03299	0.01019	0.01019	231.09841	5.59033			230.09027			230.09027
472	190.91206	190.91272	190.91206	1.28200	1.29100	1.28200	0.00000	8.29361	8.24854	3909.13773	NaN	9.89933	0.01027	0.01027	190.91228	1.28500	C06670		189.95880	C06680		189.95884
344	243.13431	243.13516	243.13431	15.12800	15.12400	15.12800	0.00000	8.26614	8.27181	3900.94694	NaN	9.59536	0.00855	0.00855	243.13459	15.12667			242.12666			242.12666
495	185.13055	185.13237	185.13055	10.74800	10.36800	10.74800	0.00000	8.36138	8.13391	3818.62002	NaN	8.91623	0.00934	0.00934	185.13116	10.62133	C17235		184.12520	C09633		184.12520
379	227.17539	227.17360	227.17539	12.56100	12.51100	12.56100	0.00000	8.19707	8.29160	3806.01751	NaN	9.97198	0.00995	0.00995	227.17479	12.54433	C04277		226.16810			226.16813
395	215.08125	215.08141	215.08125	2.80100	2.75100	2.80100	0.00000	8.47329	7.99548	3768.32995	NaN	10.42333	0.01124	0.01124	215.08130	2.78433			214.07021			214.07760
438	199.98816	199.98749	199.98723	8.78000	8.14300	8.40500	8.32372	8.32218	8.13646	3749.28760	4120.44841	9.03582	0.00911	0.00911	199.98763	8.44267	C18905		198.97480	C19047		198.97477
311	267.20615	267.20691	267.20660	21.87200	21.87100	21.85000	9.16310	8.24483	8.18434	3694.43177	9538.53231	9.30553	0.01183	0.01183	267.20655	21.86433			266.19943	C04834		266.18820
134	888.32416	888.32349	888.32416	10.31300	10.28600	10.31300	0.00000	8.07437	8.34968	3685.00775	NaN	9.38657	0.01182	0.01182	888.32393	10.30400			887.26089			887.24562
426	204.08708	204.08723	204.08708	7.69900	7.75400	7.69900	0.00000	7.87598	8.53953	3669.28406	NaN	8.86895	0.00785	0.00785	204.08713	7.71733			203.07937	C12986		203.07940
496	185.13609	185.13428	185.13078	13.33600	12.95800	12.97300	6.77433	8.24566	8.16414	3658.82394	875.09032	8.83292	0.01035	0.01035	185.13372	13.08900	C17235		184.12520	C09633		184.12520
798	84.08028	84.08049	84.08028	15.30400	15.63100	15.30400	0.00000	9.50499	6.89511	3641.13039	NaN	10.07278	0.00988	0.00988	84.08035	15.41300			83.07350			83.07350
634	130.00824	130.00699	130.00813	0.55000	0.18400	0.17600	7.55507	8.15218	8.24256	3631.38818	1910.40522	9.87760	0.01047	0.01047	130.00779	0.30333	C06554		129.01740	C06560		129.01744
335	245.07898	245.07961	245.07898	3.40200	3.36300	3.40200	0.00000	8.15204	8.23691	3620.87618	NaN	8.85131	0.01078	0.01078	245.07919	3.38900			244.06954	C00299	HMDB00296	244.06954
440	199.98804	199.98782	199.98804	10.41800	10.67400	10.41800	0.00000	8.19743	8.18710	3612.89636	NaN	8.93226	0.00943	0.00943	199.98797	10.50333	C18905		198.97480	C19047		198.97477
711	112.07043	112.07140	112.07043	1.04700	1.03200	1.04700	0.00000	8.05814	8.31732	3596.54098	NaN	10.56045	0.01182	0.01182	112.07075	1.04200	C19548		111.06840			111.06841
312	263.12317	263.12378	263.12317	3.86100	3.76300	3.86100	0.00000	8.11079	8.25409	3577.57056	NaN	11.03478	0.00960	0.00960	263.12337	3.82833			262.11649	C01683		262.11650
796	84.96011	84.96195	84.96031	0.53800	0.46700	0.71700	7.81789	8.12118	8.22101	3537.20933	2484.66818	11.12337	0.00949	0.00949	84.96079	0.57400	C02390		83.95336	C02271		83.95340
681	118.01079	118.01433	118.01079	1.07000	1.05500	1.07000	0.00000	7.95192	8.37292	3506.65649	NaN	10.62029	0.00909	0.00909	118.01197	1.06500	C02231		117.00620	C02234		117.00621
434	201.10284	201.10333	201.10284	25.12300	25.04930	25.12300	0.00000	8.36433	7.94779	3484.43608	NaN	9.52023	0.01206	0.01206	201.10301	25.09843	C06537		200.09500	C14759		200.09500

218	374.15653	374.15756	374.15653	10.77200	10.73300	10.77200	0.00000	8.08422	8.22741	3483.58019	NaN	9.94579	0.01016	0.01016	374.15687	10.75900			373.14852			373.14852
437	199.98817	199.98735	199.98817	8.67600	8.72000	8.67600	0.00000	8.24057	8.02514	3404.50121	NaN	11.02461	0.01057	0.01057	199.98790	8.69067	C18905		198.97480	C19047		198.97477
757	93.03890	93.03867	93.03890	3.27200	3.25700	3.27200	0.00000	8.10269	8.11215	3319.00832	NaN	10.61175	0.01094	0.01094	93.03882	3.26700	C00116	HMDB00131	92.04730	C00116	HMDB00131	92.04734
420	206.12087	206.11806	206.11833	8.07300	7.95400	8.15800	7.95762	8.00553	8.20175	3306.47889	2857.25263	10.44151	0.00846	0.00846	206.11909	8.06167	C10846		205.11030			205.11028
481	186.95741	186.95740	186.95720	10.40400	10.70900	10.73600	7.69238	8.06146	8.14102	3298.55251	2191.57291	10.37144	0.01246	0.01246	186.95734	10.61633			185.93164	C14846		185.93160
310	267.20886	267.20804	267.20728	11.04000	10.39200	10.73600	7.77302	8.34752	7.81234	3229.00005	2375.62318	9.19829	0.00986	0.00986	267.20806	10.72267			266.19943	C04834		266.18820
448	199.14392	199.14349	199.14392	3.37800	3.24500	3.37800	0.00000	9.00995	7.14921	3227.86984	NaN	11.01858	0.00834	0.00834	199.14378	3.33367	C06185		198.13680	C10858	HMDB06548	198.13683
189	448.96100	448.96201	448.96100	4.40200	4.28100	4.40200	0.00000	8.30133	7.84841	3212.71720	NaN	10.20032	0.00907	0.00907	448.96134	4.36167	C05837		448.06100	C05837		448.06102
197	437.09811	437.09628	437.09811	12.97300	12.95800	12.97300	0.00000	8.19816	7.92488	3170.11281	NaN	10.58430	0.00859	0.00859	437.09750	12.96800	C10067		436.10056	C10093		436.10056
731	101.06470	101.06852	101.06470	8.14600	7.94250	8.14600	0.00000	8.07332	8.04095	3156.21961	NaN	10.57101	0.01209	0.01209	101.06597	8.07817	C08311		100.06366	C19296		100.06366
378	227.98348	227.98482	227.98348	0.95300	0.97300	0.95300	0.00000	8.11482	7.98946	3140.49575	NaN	10.54581	0.01069	0.01069	227.98392	0.95967	C01557		226.99047	C12469		226.99850
183	461.21805	461.21771	461.21774	8.89733	8.86100	8.75800	8.60710	8.09584	7.97133	3082.76948	5470.35392	9.88499	0.00925	0.00925	461.21783	8.83878	C10715		460.20972	C10831		460.20972
756	93.50569	93.50604	93.50569	1.05900	1.03200	1.05900	0.00000	8.20163	7.85305	3063.57293	NaN	11.77065	0.00977	0.00977	93.50581	1.05000						
314	263.08884	263.08936	263.08884	1.94200	1.93800	1.94200	0.00000	7.93800	8.09460	3029.94564	NaN	10.58257	0.00833	0.00833	263.08901	1.94067		HMDB11164	262.08011			262.08010
320	260.09473	260.09497	260.09473	4.44900	4.26900	4.44900	0.00000	7.85901	8.16836	3022.03170	NaN	9.86013	0.00908	0.00908	260.09481	4.38900			259.08579	C10701		259.08450
799	84.08019	84.08090	84.08019	14.45670	14.06500	14.45670	0.00000	8.56081	7.46621	3021.49557	NaN	8.78873	0.01125	0.01125	84.08043	14.32613			83.07350			83.07350
182	461.21777	461.21783	461.21777	10.40700	10.36800	10.40700	0.00000	8.11651	7.91034	3021.25606	NaN	12.66425	0.01039	0.01039	461.21779	10.39400	C10715		460.20972	C10831		460.20972
290	274.87360	274.87338	274.87360	1.29400	1.30300	1.29400	0.00000	7.98178	8.04192	3016.49322	NaN	9.48113	0.01182	0.01182	274.87353	1.29700	C15232		273.87050			273.87053
333	245.11356	245.11366	245.11356	2.87200	2.85700	2.87200	0.00000	8.02657	7.98518	2998.52986	NaN	10.17537	0.00895	0.00895	245.11359	2.86700			244.10592			244.10592
494	185.13838	185.13350	185.13059	10.07500	10.70900	10.34800	7.97284	7.91466	8.09625	2997.26281	2901.08114	10.34155	0.01072	0.01072	185.13416	10.37733	C17235		184.12520	C09633		184.12520
741	100.07884	100.07966	100.07884	39.91100	39.89600	39.91100	0.00000	7.95592	8.05006	2989.87624	NaN	9.38405	0.00887	0.00887	100.07911	39.90600		HMDB11749	99.06841	C11249		99.06841
387	223.08530	223.08463	223.08530	1.15300	1.16100	1.15300	0.00000	8.11283	7.88594	2979.12116	NaN	8.94799	0.01035	0.01035	223.08507	1.15567			222.07694		HMDB13068	222.07663
254	309.11237	309.11054	309.11237	7.76900	7.68400	7.76900	0.00000	7.59603	8.38858	2958.09892	NaN	8.72307	0.01123	0.01123	309.11176	7.74067			308.10484	C01541	HMDB01935	308.10486
309	267.20725	267.20746	267.20725	8.14600	8.08400	8.14600	0.00000	8.20819	7.77537	2956.54273	NaN	9.13252	0.01114	0.01114	267.20732	8.12533			266.19943	C04834		266.18820
732	101.06292	101.06480	101.06292	39.91100	39.90700	39.91100	0.00000	7.73769	8.23684	2943.23580	NaN	10.17572	0.01024	0.01024	101.06355	39.90967	C12518		100.05243		HMDB01862	100.05243
435	199.98839	199.98816	199.98839	10.04200	10.38000	10.04200	0.00000	8.65615	7.30474	2923.23309	NaN	10.47368	0.01059	0.01059	199.98831	10.15467	C18905		198.97480	C19047		198.97477
393	217.99721	217.99858	218.00157	1.23300	1.05500	1.05900	7.23404	8.20018	7.73686	2888.57406	1385.80405	8.93803	0.00928	0.00928	217.99912	1.11567	C18672		216.99410	C14229		217.00610
117	922.01025	922.00964	922.01025	8.94700	8.89600	8.94700	0.00000	6.84963	9.07079	2864.66997	NaN	9.29870	0.00819	0.00819	922.01005	8.93000			921.15707	C14120		921.15710
517	182.98392	182.98483	182.98392	8.32300	7.99000	8.32300	0.00000	7.87382	8.01432	2818.80410	NaN	8.94109	0.01032	0.01032	182.98422	8.21200	C07598		181.97080	C07719		181.97075
453	199.14320	199.14436	199.14320	9.31200	9.28500	9.31200	0.00000	7.62088	8.25099	2795.98001	NaN	9.88162	0.00959	0.00959	199.14359	9.30300	C06185		198.13680	C10858	HMDB06548	198.13683
316	261.48947	261.49191	261.48947	2.91900	2.75100	2.91900	0.00000	8.23972	7.62667	2788.33122	NaN	10.50645	0.01011	0.01011	261.49029	2.86300						
706	113.04663	113.04639	113.04663	0.91700	0.91400	0.91700	0.00000	7.93736	7.92417	2781.54239	NaN	9.36150	0.00823	0.00823	113.04655	0.91600			112.03851			112.03244
414	206.12834	206.13030	206.12834	19.51900	19.48100	19.51900	0.00000	8.24634	7.59701	2756.38477	NaN	12.01650	0.01004	0.01004	206.12899	19.50633	C17225		205.11370			205.11365
492	185.13133	185.13318	185.13133	8.99400	9.23800	8.99400	0.00000	8.13191	7.70478	2747.21793	NaN	10.43787	0.00929	0.00929	185.13195	9.07533	C17235		184.12520	C09633		184.12520
289	277.10678	277.10599	277.10678	4.32000	4.22200	4.32000	0.00000	7.85901	7.96029	2723.43641	NaN	11.69669	0.00952	0.00952	277.10652	4.28733			276.09977	C09492		276.09977
730	101.06302	101.06143	101.05879	21.38900	21.43500	21.35600	7.89751	7.96402	7.84329	2707.15960	2690.56956	9.54368	0.01088	0.01088	101.06108	21.39333	C12518		100.05243		HMDB01862	100.05243
181	461.21579	461.21686	461.21579	12.98500	12.95800	12.98500	0.00000	7.89554	7.90153	2693.33691	NaN	9.78343	0.01062	0.01062	461.21615	12.97600			460.20703			460.20703
776	88.50977	88.51007	88.50968	0.18500	0.17200	0.18700	8.01470	7.81647	7.97208	2681.87934	3025.11456	8.10691	0.00919	0.00919	88.50984	0.18133						
488	186.15886	186.15788	186.15624	14.60700	14.61800	14.62200	9.06786	7.83598	7.92833	2649.56299	8672.06665	8.35313	0.01161	0.01161	186.15766	14.61567			185.15281	C16649		185.14158
447	199.14407	199.14410	199.14407	5.42700	5.28200	5.42700	0.00000	8.67088	7.06688	2614.63763	NaN	10.67723	0.01090	0.01090	199.14408	5.37867	C06185		198.13680	C10858	HMDB06548	198.13683
740	100.07672	100.07654	100.07651	9.28600	9.26100	9.27600	8.05894	8.18642	7.55095	2614.12459	3161.92604	10.35126	0.00861	0.00861	100.07659	9.27433		HMDB11749	99.06841	C11249		99.06841
322	259.06534	259.06461	259.06534	1.27100	1.26700	1.27100	0.00000	7.83596	7.87524	2580.14800	NaN	8.02048	0.01017	0.01017	259.06509	1.26967			258.06169			258.06169
114	922.00842	922.00830	922.00842	36.93200	36.94000	36.93200	0.00000	8.23773	7.47174	2577.90674	NaN	11.58936	0.00955	0.00955	922.00838	36.93467			921.15707	C14120		921.15710
515	182.98560	182.98496	182.98369	9.06200	8.76700	8.72300	8.16132	8.19954	7.50517	2571.78523	3502.80744	9.06141	0.01069	0.01069	182.98475	8.85067	C07598		181.97080	C07719		181.97075
487	186.14998	186.15486	186.14998	10.41800	10.73300	10.41800	0.00000	8.31791	7.38290	2566.76550	NaN	10.68652	0.01101	0.01101	186.15161	10.52300	C16649		185.14158			185.15281
400	213.19487	213.19560	213.19487	0.18700	0.17200	0.18700	0.00000	8.32602	7.35601	2542.78247	NaN	10.95885	0.01142	0.01142	213.19511	0.18200			212.17763			212.17763
185	451.11487	451.11346	451.11487	16.63500	16.57300	16.63500	0.00000	8.09086	7.58988	2541.13725	NaN	10.41862	0.01076	0.01076	451.11440	16.61433			450.11616			450.11616
240	333.96661	333.96909	333.96661	4.42600	4.28100	4.42600	0.00000	7.89160	7.77871	2527.92742	NaN	9.10900	0.00900	0.00900	333.96744	4.37767	C08404		333.01880	C08404		333.01882
763	89.50728	89.50668	89.50728	36.79100	37.11700	36.79100	0.00000	8.26870	7.39075	2514.23770	NaN	10.94396	0.01064	0.01064	89.50708	36.89967						
418	206.11879	206.11859	206.11879	10.38300	10.36800	10.38300	0.00000	7.80355	7.81761	2466.55370	NaN	11.28164	0.00966	0.00966	206.11872	10.37800	C10846		205.11030			205.11028
308	267.20670	267.20682	267.20670	2.40100	2.31500	2.40100	0.00000	7.96797	7.64592	2457.61248	NaN	9.63192	0.00931	0.00931	267.20674	2.37233			266.19943	C04834		266.18820
729	101.05846	101.06216	101.05846	19.99000	19.70400	19.99000	0.00000	7.81240	7.80059	2456.50444	NaN	10.50794	0.01267	0.01267	101.05970	19.89467	C02240		100.05240	C08279	HMDB01470	100.05240
401	213.19373	213.19591	213.19373	12.96200	12.94600	12.96200	0.00000	8.23408	7.36759	2442.64145	NaN	9.10974	0.01007	0.01007	213.19445	12.95667			212.17763			212.17763
704	113.06989	113.06987	113.06989	12.98500	12.94600	12.98500	0.00000	7.96364	7.62098	2421.90719	NaN	7.09083	0.00690	0.00690	113.06989	12.97200			112.05243			112.05243
604	138.09433	138.09915	138.09433	9.15900	9.09600	9.15900	0.00000	7.75800	7.80636	2397.49902	NaN	11.73556	0.01051	0.01051	138.09594	9.13800	C00483	HMDB00306	137.08410	C01183		137.08410
212	391.28330	391.28662	391.28330	3.55500	3.55100	3.55500	0.00000	6.78256	8.77722	2392.01780	NaN	9.90926	0.01001	0.01001	391.28440	3.55367			390.27699			390.27699
548	167.01239	167.01173	167.01306	0.17300	0.71400	0.48200	7.57646	7.92151	7.62468	2375.81746	1951.70549	9.35649	0.00895	0.00895	167.01240	0.45633			166.00311	C17948		166.00310
402	213.19621	213.19640	213.19591	17.13900	16.71400	17.00000	7.85903	8.10124	7.43827	2367.88099	2588.99772	9.66513	0.01040	0.01040	213.19617	16.95100			212.17763			212.17763
762	89.50742	89.50737	89.50742	19.29600	19.25700	19.29600	0.00000	8.42740	7.10654	2361.30738	NaN	10.09590	0.01067	0.01067	89.50741	19.28300						
417	206.11940	206.11870	206.11600	9.13300	9.01400	8.99400	8.07360	7.75277	7.76987	2347.99608	3208.63856	10.91240	0.00836	0.00836	206.11803	9.04700			205.11028	C10869		205.11028
724	102.09780	102.09269	102.09780	39.34600	39.24800	39.34600	0.00000	8.38458	7.12400	2331.54741	NaN	9.93901	0.00948	0.00948	102.09610	39.31333	C00576	HMDB01252	101.08410	C01842		101.08410
433	201.10303	201.10249	201.10303	10.43000	10.36800	10.43000	0.00000	7.75595	7.73926	2316.01745	NaN	9.91836	0.01049	0.01049	201.10285	10.40933	C06537		200.09500	C14759		200.09500
705	113.07042	113.07068	113.07042	10.76000	10.38000	10.76000	0.00000	7.84047	7.64377	2303.34662	NaN	10.49017	0.01015	0.01015	113.07051	10.63333			112.05243			112.05243
719	107.99998	108.00150	107.99998	2.43600	2.27975	2.43600	0.00000	7.94977	7.48030	2241.80786	NaN	9.45536	0.00975	0.00975	108.00049	2.38392			107.01379	C19178		107.01379
282	280.19537	280.19928	280.19537	17.97700	17.92600	17.97700	0.00000	7.65671	7.75277	2218.83159	NaN	9.20585	0.01099	0.01099	280.19668	17.96000	C09923		279.18344	C09901		279.18340
480	186.95725	186.95654	186.95665	8.14400	8.14300	8.24000	9.00640	7.62939	7.77581	2214.09856	8155.13441	8.93285	0.01087	0.01087	186.95681	8.17567			185.93164	C14846		185.93160
180	461.21845	461.22040	461.21845	9.93600	9.87400	9.93600	0.00000	7.71074	7.69242	2211.83985	NaN	10.69702	0.00917	0.00917	461.21910	9.91533	C10715		460.20972	C10831		460.20972
178	461.21887	461.21628	461.21887	38.55700	38.35300	38.55700	0.00000	8.32568	7.07549	2209.64656	NaN	9.54339	0.01207	0.01207	461.21801	38.48900	C10715		460.20972	C10831		460.20972
271	291.08350	291.08179	291.08350	3.70800	3.65700	3.70800	0.00000	7.56089	7.81798	2185.14194	NaN	8.51546	0.01143	0.01143	291.08293	3.69100			290.07252	C03648		290.07900
599	141.95882	141.95804	141.95850	8.85000	8.95533	8.94700	8.54112	7.74686	7.60985	2161.05892	5121.05206	10.78183	0.00930	0.00930	141.95845	8.91744	C00169	HMDB01096	140.98270	C00169	HMDB01096	140.98271
343	243.17172	243.16408	243.16174	13.08900	13.33500	12.96200	6.47807	7.81650	7.49693	2114.79867	650.71235	9.48146	0.01100	0.01100	243.16585	13.12867			242.15315			242.15314
113	922.00830	922.00989	922.00830	34.16500	33.83200	34.16500	0.00000	8.28447	7.02782	2113.59180	NaN	9.72281	0.00960	0.00960	922.00883	34.05400			921.15707	C14120		921.15710
653	122.96444	122.96479	122.96444	12.29000	12.59300	12.29000	0.00000	8.10306	7.17499	2077.71448	NaN	8.77556	0.00937	0.00937	122.96456	12.39100		HMDB12216	121.97128	C08270	HMDB12251	121.97129

586	146.04140	146.03526	146.04140	10.76000	11.02700	10.76000	0.00000	7.37971	7.89137	2070.49190	NaN	9.62986	0.01183	0.01183	146.03935	10.84900	C05746		145.03232	C00940	HMDB01552	145.03750
468	191.93796	191.93604	191.94032	0.92700	0.74900	0.76400	7.61643	7.71785	7.55256	2069.80001	2031.30623	7.43943	0.01041	0.01041	191.93811	0.81333			190.95408	C18779		190.95410
815	81.52158	81.52107	81.52125	39.90800	39.53100	39.89900	8.40732	7.14960	8.10138	2049.78431	4479.72853	9.25841	0.00966	0.00966	81.52130	39.77933						
577	148.11099	148.11134	148.11099	9.85300	9.77900	9.85300	0.00000	7.55173	7.63231	1982.30775	NaN	10.08026	0.01020	0.01020	148.11111	9.82833	C09960		147.10480	C09910		147.10480
415	206.11992	206.11881	206.11539	11.68800	11.73400	11.78400	7.32454	7.57987	7.59087	1969.16823	1517.07486	8.25213	0.00995	0.00995	206.11804	11.73533			205.11028	C10869		205.11028
195	437.09592	437.09677	437.09592	34.82500	34.67950	34.82500	0.00000	8.56718	6.59303	1958.83352	NaN	10.95936	0.00974	0.00974	437.09620	34.77650	C10067		436.10056	C10093		436.10056
619	132.10033	132.09424	132.10033	11.65500	11.68700	11.65500	0.00000	7.68054	7.47816	1957.35762	NaN	9.63014	0.01010	0.01010	132.09830	11.66567	C00123	HMDB00687	131.09460	C00407	HMDB00172	131.09460
145	791.22510	791.22681	791.22510	3.83700	3.65700	3.83700	0.00000	7.53987	7.61050	1949.22068	NaN	10.75146	0.01050	0.01050	791.22567	3.77700	C04488		790.27860	C04488		790.27862
761	89.50733	89.50745	89.50733	37.35600	37.47000	37.35600	0.00000	8.09325	7.04753	1939.90520	NaN	10.58329	0.00845	0.00845	89.50737	37.39400						
451	199.14053	199.14389	199.14053	8.06400	8.01300	8.06400	0.00000	7.31647	7.81469	1930.58325	NaN	8.17756	0.01018	0.01018	199.14165	8.04700	C06185		198.13680	C10858	HMDB06548	198.13683
814	81.52113	81.52107	81.52113	18.63600	18.98600	18.63600	0.00000	7.70118	7.42698	1927.69821	NaN	10.18006	0.00940	0.00940	81.52111	18.75267						
231	351.18137	351.19098	351.18137	9.39400	9.35500	9.39400	0.00000	7.25027	7.81905	1871.81251	NaN	10.93990	0.01111	0.01111	351.18457	9.38100			350.17294			350.17294
412	206.12015	206.12007	206.12015	0.64700	0.82000	0.64700	0.00000	7.64706	7.41135	1861.62899	NaN	8.16819	0.01041	0.01041	206.12012	0.70467			205.11365	C17225		205.11370
281	280.20169	280.20166	280.19803	11.71100	11.80400	11.93700	6.82534	7.52536	7.52277	1852.07851	920.89343	10.65995	0.01185	0.01185	280.20046	11.81733		HMDB12535	279.19601	C09923		279.18344
598	141.95857	141.95940	141.95857	12.98500	13.32300	12.98500	0.00000	7.55981	7.48673	1850.61052	NaN	9.64754	0.00999	0.00999	141.95885	13.09767	C00169	HMDB01096	140.98270	C00169	HMDB01096	140.98271
177	461.21732	461.21832	461.21732	38.18000	37.98800	38.18000	0.00000	8.17647	6.86829	1848.96924	NaN	9.43533	0.00822	0.00822	461.21765	38.11600	C10715		460.20972	C10831		460.20972
411	207.05096	207.04935	207.05096	7.46300	7.30700	7.46300	0.00000	7.32618	7.68366	1816.95336	NaN	10.14269	0.00945	0.00945	207.05043	7.41100		HMDB00379	206.04265		HMDB03518	206.04265
812	81.52161	81.52129	81.52161	21.99200	21.80000	21.99200	0.00000	7.89662	7.10909	1813.21331	NaN	9.60656	0.00860	0.00860	81.52150	21.92800						
485	186.15544	186.15747	186.15544	33.38800	33.03200	33.38800	0.00000	8.06656	6.93179	1806.55171	NaN	9.30297	0.01232	0.01232	186.15612	33.26933			185.15281	C16649		185.14158
465	192.95195	192.94745	192.95195	0.17600	0.17200	0.17600	0.00000	7.07133	7.89550	1778.30128	NaN	9.28850	0.00856	0.00856	192.95045	0.17467	C18315		191.97449	C18302		191.97450
416	206.12012	206.11949	206.12012	5.08500	4.90500	5.08500	0.00000	7.27340	7.69159	1776.66553	NaN	8.84353	0.01057	0.01057	206.11991	5.02500			205.11365	C17225		205.11370
587	146.01154	146.01152	146.01154	0.17600	0.18400	0.17600	0.00000	7.55878	7.39787	1769.27106	NaN	10.33813	0.01018	0.01018	146.01153	0.17867	C19324		144.99460	C19345		144.99460
584	146.07632	146.07712	146.07632	8.18200	8.11900	8.18200	0.00000	7.69442	7.25288	1761.02118	NaN	9.28790	0.01010	0.01010	146.07659	8.16100			145.07388	C03656	HMDB12131	145.07388
725	102.07809	102.07589	102.07809	8.15800	8.08400	8.15800	0.00000	7.52765	7.41891	1760.36727	NaN	8.40355	0.01028	0.01028	102.07736	8.13333	C07672		101.07010	C08063		101.07015
342	243.17931	243.17889	243.17792	12.33500	12.32200	12.33800	7.72028	7.40454	7.53326	1752.67772	2253.58962	9.51649	0.00903	0.00903	243.17871	12.33167	C08451		242.16710	C17716		242.16710
739	100.07709	100.07731	100.07709	18.31800	17.93800	18.31800	0.00000	7.72138	7.21396	1750.52073	NaN	10.30920	0.01105	0.01105	100.07716	18.19133		HMDB11749	99.06841	C11249		99.06841
646	126.03894	126.03947	126.03472	0.16100	0.17200	0.16400	7.88380	7.94595	6.98467	1746.39889	2653.94054	11.76852	0.01150	0.01150	126.03771	0.16567	C03557	HMDB11747	125.02420	C03782		125.02420
179	461.21857	461.21646	461.21857	7.92300	8.16600	7.92300	0.00000	7.64467	7.28445	1745.08534	NaN	9.87752	0.00912	0.00912	461.21787	8.00400	C10715		460.20972	C10831		460.20972
276	286.06845	286.06903	286.06845	7.88700	7.68400	7.88700	0.00000	6.93520	7.96359	1718.82105	NaN	8.69428	0.00876	0.00876	286.06864	7.81933	C19014		285.06220	C19017		285.06222
700	113.06940	113.07135	113.06940	8.15800	8.11900	8.15800	0.00000	7.78053	7.05832	1668.07630	NaN	10.77566	0.00974	0.00974	113.07005	8.14500			112.05243			112.05243
645	126.09059	126.09067	126.08695	9.10900	9.10800	9.25300	8.36132	7.48926	7.32172	1644.98878	4278.33210	10.03674	0.01098	0.01098	126.08940	9.15667			125.09530			125.09530
677	118.08732	118.08682	118.08732	12.96200	13.32300	12.96200	0.00000	7.44516	7.36254	1642.29640	NaN	8.55155	0.00962	0.00962	118.08715	13.08233	C00183	HMDB00883	117.07900	C00431	HMDB03355	117.07900
703	113.07034	113.07088	113.07046	9.01500	9.37900	9.01700	7.95652	7.22446	7.56973	1631.24321	2854.11600	10.98293	0.01166	0.01166	113.07056	9.13700			112.05243			112.05243
288	277.12231	277.11798	277.12231	11.37200	11.68700	11.37200	0.00000	7.24836	7.54442	1630.08910	NaN	10.06481	0.00938	0.00938	277.12087	11.47700	C04732		276.10700		HMDB11106	276.10700
486	186.15733	186.15675	186.15408	0.17300	0.18400	0.18700	8.84327	7.64120	7.14838	1627.48977	6927.57823	8.78450	0.01115	0.01115	186.15606	0.18133			185.15281	C16649		185.14158
328	249.12477	249.13216	249.12477	3.53100	3.49200	3.53100	0.00000	7.30856	7.46538	1614.81095	NaN	11.41870	0.01102	0.01102	249.12723	3.51800			248.11947			248.11947
597	141.95834	141.95841	141.95834	8.18200	8.09600	8.18200	0.00000	7.46139	7.29578	1601.32211	NaN	10.53492	0.00932	0.00932	141.95836	8.15333	C00169	HMDB01096	140.98270	C00169	HMDB01096	140.98271
425	204.09212	204.08797	204.09212	10.05400	9.69700	10.05400	0.00000	6.96306	7.79390	1601.15444	NaN	9.06095	0.01106	0.01106	204.09073	9.93500	C01365		203.08210			203.08071
560	158.96080	158.96054	158.96080	31.54000	31.56000	31.54000	0.00000	7.67367	7.08223	1600.30364	NaN	9.71024	0.01099	0.01099	158.96071	31.54667	C19212		157.97238	C19164		157.97240
526	181.13449	181.13376	181.13449	10.92500	11.31000	10.92500	0.00000	7.52444	7.21434	1586.66329	NaN	8.86769	0.00953	0.00953	181.13425	11.05333	C11120		180.12630	C11283		180.12626
582	147.04306	147.04572	147.04306	4.46100	4.30500	4.46100	0.00000	7.29193	7.42362	1568.34098	NaN	11.50095	0.01083	0.01083	147.04395	4.40900	C05851	HMDB01218	146.03677		HMDB02359	146.03677
299	270.22012	270.21832	270.21652	14.19530	14.17100	14.46850	8.30816	7.59451	7.11830	1566.18981	4056.85287	9.82651	0.01003	0.01003	270.21832	14.27827			269.19909	C05763		269.19391
563	158.96129	158.96089	158.96129	8.17000	8.02500	8.17000	0.00000	7.42726	7.27709	1559.58429	NaN	8.93990	0.01039	0.01039	158.96116	8.12167	C19212		157.97238	C19164		157.97240
603	138.09447	138.10153	138.09447	10.77200	10.75700	10.77200	0.00000	8.00739	6.66980	1538.55122	NaN	10.41424	0.01117	0.01117	138.09682	10.76700	C00483	HMDB00306	137.08410	C01183		137.08410
296	270.21594	270.21994	270.21594	0.19900	0.18400	0.19900	0.00000	7.85314	6.82169	1536.73363	NaN	9.72979	0.00992	0.00992	270.21728	0.19400			269.19909	C05763		269.19391
585	146.07680	146.07622	146.07680	9.26500	9.63800	9.26500	0.00000	7.38442	7.25649	1510.89049	NaN	11.54548	0.01086	0.01086	146.07660	9.38933			145.07388	C03656	HMDB12131	145.07388
351	242.13843	242.14095	242.13208	18.65700	18.98600	18.86000	7.34206	7.09886	7.54106	1510.14557	1543.88140	10.37181	0.00984	0.00984	242.13715	18.83433	C11841		241.13139	C11841		241.13139
675	119.08156	119.08095	119.08156	10.40700	10.72100	10.40700	0.00000	7.44213	7.18701	1502.02387	NaN	8.67167	0.01013	0.01013	119.08136	10.51167	C03283	HMDB06284	118.07420	C08291		118.07420
562	158.96142	158.96146	158.96132	31.83400	32.19600	31.83400	0.00000	7.46939	7.15891	1501.39923	NaN	8.99604	0.01084	0.01084	158.96137	31.95467	C19212		157.97238	C19164		157.97240
466	192.13178	192.13512	192.13178	10.10100	9.97900	10.10100	0.00000	7.41026	7.19924	1487.34403	NaN	8.27372	0.01011	0.01011	192.13289	10.06033	C07904		191.13100	C10935		191.13100
685	116.06127	116.05821	116.06127	9.26500	9.04900	9.26500	0.00000	7.44705	7.14699	1475.89262	NaN	9.51084	0.00947	0.00947	116.06025	9.19300	C00148	HMDB00162	115.06330	C00763	HMDB03411	115.06330
399	213.19550	213.19482	213.19550	12.19600	12.24000	12.19600	0.00000	7.41547	7.17761	1475.18472	NaN	10.37272	0.01024	0.01024	213.19527	12.21067			212.17763			212.17763
158	608.08911	608.08771	608.08911	10.78300	10.75700	10.78300	0.00000	7.59649	6.99367	1473.03338	NaN	8.24849	0.00961	0.00961	608.08864	10.77433	C00203	HMDB00304	607.08148	C00043	HMDB00290	607.08154
484	186.15120	186.15453	186.15120	12.38500	12.25200	12.38500	0.00000	7.95868	6.60438	1453.21316	NaN	10.63078	0.00827	0.00827	186.15231	12.34067	C16649		185.14158			185.15281
811	81.52184	81.52132	81.52127	34.59900	34.78600	34.71900	8.33771	7.51190	7.03839	1443.96069	4178.50751	10.89720	0.00993	0.00993	81.52148	34.70133						
736	100.07835	100.07756	100.07652	16.90300	16.78400	16.50500	7.67263	7.54407	7.00484	1442.95999	2148.73380	9.70544	0.00904	0.00904	100.07747	16.73067		HMDB11749	99.06841	C11249		99.06841
536	174.03999	174.04047	174.03999	3.08400	3.06900	3.08400	0.00000	7.27384	7.27483	1442.79507	NaN	8.19891	0.00976	0.00976	174.04015	3.07900			173.04366	C19253		173.04366
300	270.20398	270.21350	270.20398	13.60900	13.61700	13.60900	0.00000	7.40170	7.14475	1441.18470	NaN	10.73898	0.00939	0.00939	270.20715	13.61167			269.19909	C05763		269.19391
204	419.08704	419.08804	419.08704	20.24900	20.44600	20.24900	0.00000	6.97910	7.55495	1432.27850	NaN	8.40270	0.01162	0.01162	419.08737	20.31467			418.08897	C06435		418.08900
297	270.21951	270.21881	270.21707	12.33500	12.32200	12.29000	8.25666	7.47301	7.03627	1414.64993	3853.20396	10.11716	0.01061	0.01061	270.21847	12.31567			269.19909	C05763		269.19391
692	114.09174	114.09143	114.09070	18.29200	18.22100	18.23600	7.41279	7.19593	7.30457	1408.45412	1657.04190	9.70361	0.00991	0.00991	114.09129	18.24967			113.08406	C05853		113.08406
150	712.48804	712.48755	712.48804	36.55500	36.26900	36.55500	0.00000	7.31097	7.17650	1399.30637	NaN	10.64529	0.01117	0.01117	712.48787	36.45967			711.48386			711.48386
226	358.19821	358.20337	358.19821	10.38300	10.36800	10.38300	0.00000	7.43990	7.03106	1387.80373	NaN	8.16581	0.01015	0.01015	358.19993	10.37800	C07251		357.19400	C09558		357.19400
196	437.10315	437.10205	437.10315	10.40700	10.36800	10.40700	0.00000	7.41537	7.05482	1387.27719	NaN	10.74883	0.01205	0.01205	437.10278	10.39400	C10067		436.10056	C10093		436.10056
684	116.06678	116.06670	116.06678	10.90100	10.82700	10.90100	0.00000	7.42969	7.02723	1378.09921	NaN	12.06091	0.01065	0.01065	116.06676	10.87633	C00148	HMDB00162	115.06330	C00763	HMDB03411	115.06330
350	242.13161	242.13374	242.13161	21.03800	20.89300	21.03800	0.00000	7.08142	7.36320	1369.65257	NaN	10.29108	0.00931	0.00931	242.13232	20.98967			241.12334			241.12334
686	116.06504	116.06580	116.06504	11.11300	11.11000	11.11300	0.00000	7.26463	7.17608	1366.96728	NaN	9.07201	0.00943	0.00943	116.06530	11.11200	C00148	HMDB00162	115.06330	C00763	HMDB03411	115.06330
279	280.20041	280.20017	280.20041	12.22000	12.47500	12.22000	0.00000	7.68065	6.75984	1366.82169	NaN	9.12146	0.00905	0.00905	280.20033	12.30500		HMDB12535	279.19601	C09923		279.18344
710	112.07062	112.07352	112.07062	12.97300	13.32300	12.97300	0.00000	7.44421	6.99442	1365.55712	NaN	11.53322	0.00902	0.00902	112.07159	13.08967	C19548		111.06840			111.06841
176	461.21716	461.21558	461.21716	29.83300	29.91200	29.83300	0.00000	8.06351	6.37137	1362.99412	NaN	10.04718	0.01030	0.01030	461.21663	29.85933	C10672		460.20970	C10704		460.20970
693	114.09116	114.09124	114.09116	17.09400	17.11400	17.09400	0.00000	7.06946	7.34143	1346.74507	NaN	9.77170	0.01240	0.01240	114.09119	17.10067			113.08406	C05853		113.08406
701	113.06906	113.07086	113.06906	10.40700	10.09700	10.40700	0.00000	7.08974	7.29049	1326.24948	NaN	11.58533	0.00937	0.00937	113.06966	10.30367			112.05243			112.05243
291	274.09042	274.09030	274.09042	3.09500	3.10400	3.09500	0.00000	7.24281	7.13190	1322.59925	NaN	10.98324	0.00982	0.00982	274.09038	3.09800			273.08235	C10849		273.08570

676	118.08671	118.08582	118.08671	10.76000	10.73300	10.76000	0.00000	7.39467	6.97438	1318.86079	NaN	10.03426	0.01164	0.01164	118.08641	10.75100			117.07897			117.07897
500	184.13452	184.13327	184.13336	19.49300	18.96300	19.22500	6.76363	7.15802	7.20592	1315.50150	865.78150	9.64552	0.01053	0.01053	184.13372	19.22700	C12452		183.12590	C12453		183.12590
460	194.12016	194.12126	194.12016	8.12300	8.09600	8.12300	0.00000	7.27060	7.08776	1311.83013	NaN	9.11672	0.01047	0.01047	194.12053	8.11400	C07577		193.11030	C07875		193.11030
361	238.15469	238.15540	238.15469	10.36000	10.75700	10.36000	0.00000	7.25934	7.08379	1301.88237	NaN	8.94862	0.01081	0.01081	238.15493	10.49233			237.15175	C05314		237.15180
298	270.21707	270.22119	270.21707	7.15700	7.31900	7.15700	0.00000	7.23864	7.08491	1289.19427	NaN	8.33574	0.00955	0.00955	270.21845	7.21100			269.19909	C05763		269.19391
630	130.00678	130.00728	130.00678	10.41800	10.38000	10.41800	0.00000	7.33706	6.98315	1287.04629	NaN	10.67498	0.00835	0.00835	130.00694	10.40533	C06554		129.01740	C06560		129.01744
283	279.98288	279.98062	279.98288	2.67200	2.71500	2.67200	0.00000	7.29306	6.99851	1268.74311	NaN	9.00927	0.01032	0.01032	279.98213	2.68633	C01783		279.00980	C06909		279.06200
341	243.18131	243.17993	243.17151	9.18000	9.85000	9.53500	8.12660	7.36833	6.90942	1260.01344	3383.27896	10.04325	0.00815	0.00815	243.17758	9.52167	C08451		242.16710	C17716		242.16710
269	291.12125	291.12012	291.12125	7.35700	7.28300	7.35700	0.00000	6.92364	7.32080	1239.19616	NaN	8.23905	0.00889	0.00889	291.12087	7.33233		HMDB12267	290.11140	C04421		290.11140
810	81.52129	81.52157	81.52119	31.40800	31.26600	31.45700	7.92273	7.55789	6.66964	1228.76202	2759.28054	8.98559	0.01000	0.01000	81.52135	31.37700						
388	222.09082	222.09528	222.09082	1.16450	1.17300	1.16450	0.00000	7.10926	7.10014	1217.67565	NaN	10.62391	0.00802	0.00802	222.09231	1.16733	C00140	HMDB00215	221.08990	C00645	HMDB01129	221.08990
397	213.19214	213.19565	213.19214	28.92600	28.73400	28.92600	0.00000	7.51687	6.66493	1200.98944	NaN	9.13245	0.00893	0.00893	213.19331	28.86200			212.17763			212.17763
148	739.54736	739.55121	739.54736	6.69800	6.70633	6.69800	0.00000	6.73248	7.44346	1197.47729	NaN	10.38825	0.00996	0.00996	739.54865	6.70078			738.55631			738.55631
138	850.04486	850.04846	850.04486	8.13400	8.04900	8.13400	0.00000	6.91292	7.24119	1184.47579	NaN	9.14704	0.00963	0.00963	850.04606	8.10567	C04739		849.10070			849.10072
262	301.99240	301.99750	301.99240	7.47500	7.29500	7.47500	0.00000	7.02629	7.12444	1182.47976	NaN	9.54945	0.01145	0.01145	301.99410	7.41500	C15249		301.02720	C15249		301.02725
702	113.06884	113.07049	113.06884	11.87800	11.81600	11.87800	0.00000	6.73963	7.40511	1178.93845	NaN	12.00097	0.00985	0.00985	113.06939	11.85733			112.05243			112.05243
575	154.98006	154.97942	154.98006	1.12900	1.14900	1.12900	0.00000	6.98958	7.14020	1170.15250	NaN	9.71972	0.01075	0.01075	154.97984	1.13567	C02876		154.00310	C03505		154.00310
764	89.50755	89.50724	89.50755	28.89100	29.22900	28.89100	0.00000	6.51563	7.60860	1166.91225	NaN	9.34712	0.01124	0.01124	89.50744	29.00367						
188	450.01932	450.01975	450.01932	2.77800	2.75100	2.77800	0.00000	7.33814	6.76183	1152.84130	NaN	8.38909	0.01082	0.01082	450.01946	2.76900			449.01630	C08106		449.03270
224	358.19955	358.20358	358.19955	12.86700	12.84000	12.86700	0.00000	7.26695	6.83256	1152.57772	NaN	9.21249	0.00925	0.00925	358.20090	12.85800	C07251		357.19400	C09558		357.19400
359	238.15674	238.15706	238.15674	12.95000	12.93500	12.95000	0.00000	7.27047	6.81123	1142.35449	NaN	10.10377	0.00830	0.00830	238.15685	12.94500			237.15175	C05314		237.15180
594	141.95883	141.95857	141.95883	26.81900	27.03900	26.81900	0.00000	7.69669	6.36077	1128.59787	NaN	10.29952	0.01016	0.01016	141.95875	26.89233	C00169	HMDB01096	140.98270	C00169	HMDB01096	140.98271
214	382.88171	382.88104	382.88171	4.66100	4.62300	4.66100	0.00000	7.53187	6.52509	1128.31345	NaN	9.89742	0.01007	0.01007	382.88149	4.64833	C18464		381.96540	C18486		381.96543
247	318.16315	318.16827	318.16315	3.20100	3.08000	3.20100	0.00000	7.07063	6.96994	1119.10561	NaN	10.58421	0.01059	0.01059	318.16486	3.16067			317.15869			317.15869
513	182.98554	182.98459	182.98554	13.60900	13.84100	13.60900	0.00000	6.99445	7.03630	1113.62157	NaN	10.96971	0.01000	0.01000	182.98522	13.68633	C07598		181.97080	C07719		181.97075
478	186.95912	186.96074	186.95912	29.85600	29.88800	29.85600	0.00000	7.03886	6.94233	1086.36889	NaN	11.08452	0.01142	0.01142	186.95966	29.86667			185.93164	C14846		185.93160
615	134.07304	134.07205	134.07253	9.27425	9.57900	9.54700	8.10383	6.86807	7.08220	1069.70175	3307.09482	9.90286	0.01071	0.01071	134.07254	9.46675	C10901		133.06400			133.06400
157	608.08746	608.09119	608.08746	10.40700	10.36800	10.40700	0.00000	7.32315	6.62658	1069.41424	NaN	11.94619	0.00943	0.00943	608.08870	10.39400	C00203	HMDB00304	607.08148	C00043	HMDB00290	607.08154
377	227.98438	227.98373	227.98317	10.52200	10.75700	10.41800	8.04714	7.04879	6.89873	1068.22983	3124.83390	10.37257	0.01041	0.01041	227.98376	10.56567	C01557		226.99047	C12469		226.99850
295	270.21436	270.22070	270.21436	10.41800	10.73300	10.41800	0.00000	7.44250	6.48750	1058.91666	NaN	11.07242	0.00920	0.00920	270.21647	10.52300			269.19909	C05763		269.19391
347	242.18588	242.18544	242.18588	0.17600	0.17200	0.17600	0.00000	7.03959	6.86985	1048.08315	NaN	9.36793	0.01062	0.01062	242.18574	0.17467			241.18305	C11788		241.18310
111	922.00964	922.01007	922.00964	21.27400	21.65900	21.27400	0.00000	8.39230	5.48459	1031.16089	NaN	9.62764	0.00931	0.00931	922.00979	21.40233			921.15707	C14120		921.15710
709	112.07622	112.07474	112.07207	8.06100	8.08400	7.87500	7.79274	7.33475	6.54103	1030.59375	2422.94619	10.26362	0.01016	0.01016	112.07434	8.00667	C19548		111.06840			111.06841
683	116.97812	116.97786	116.97613	0.97400	0.87833	0.88200	9.57818	6.98334	6.89225	1030.49487	14446.06247	10.02941	0.00901	0.00901	116.97737	0.91144	C00122	HMDB00134	116.01096	C01384	HMDB00176	116.01096
392	218.11572	218.11343	218.11572	4.08400	3.94000	4.08400	0.00000	6.86888	6.99231	1023.10225	NaN	10.15415	0.01065	0.01065	218.11496	4.03600	C15532		217.10630		HMDB00856	217.10626
820	81.03349	81.04295	81.03349	9.64100	9.54400	9.64100	0.00000	6.94186	6.90491	1015.74844	NaN	11.04167	0.01040	0.01040	81.03664	9.60867	C00396		80.03740		HMDB03361	80.03745
137	850.04572	850.04810	850.04572	10.40700	10.33300	10.40700	0.00000	6.98082	6.84938	1007.37007	NaN	11.35200	0.00992	0.00992	850.04651	10.38233	C04739		849.10070			849.10072
745	98.98645	98.98608	98.98645	10.40700	10.23800	10.40700	0.00000	6.78722	7.03800	1004.86480	NaN	10.69379	0.00944	0.00944	98.98633	10.35067	C12893		97.97701	C12554		97.97700
707	112.07377	112.07515	112.07377	10.40700	10.73300	10.40700	0.00000	7.32419	6.48229	995.49322	NaN	8.29620	0.00960	0.00960	112.07423	10.51567	C19548		111.06840			111.06841
581	147.05792	147.05176	147.05792	3.39000	3.32800	3.39000	0.00000	6.89624	6.89196	986.43918	NaN	8.20670	0.00932	0.00932	147.05587	3.36933	C06577	HMDB02214	146.04801	C14508		146.04801
477	186.96053	186.95879	186.96053	30.92800	30.75900	30.92800	0.00000	7.27286	6.51377	985.65930	NaN	8.90638	0.01034	0.01034	186.95995	30.87167			185.93164	C14846		185.93160
376	227.98305	227.98218	227.98048	8.05000	7.54200	7.85200	7.80727	6.90958	6.85622	975.45242	2458.41739	7.82590	0.01004	0.01004	227.98190	7.81467	C01557		226.99047	C12469		226.99850
524	181.13419	181.13219	181.13333	10.05100	9.90900	10.00600	7.74035	7.82137	5.93602	971.36117	2299.27063	10.39554	0.01062	0.01062	181.13324	9.98867	C11283		180.12626	C11120		180.12630
445	199.14533	199.14374	199.14533	36.65000	36.96400	36.65000	0.00000	7.13609	6.59102	956.75772	NaN	9.55950	0.00852	0.00852	199.14480	36.75467	C10858	HMDB06548	198.13683	C06185		198.13680
792	84.95963	84.96051	84.96029	8.07300	7.74250	7.84000	7.45331	6.98093	6.74393	955.68545	1725.56553	11.01346	0.00914	0.00914	84.96014	7.88517	C02390		83.95336	C02271		83.95340
273	289.96228	289.96417	289.96228	2.82500	2.76200	2.82500	0.00000	7.00019	6.71703	952.04344	NaN	9.80792	0.01093	0.01093	289.96291	2.80400	C03822		288.96730	C03822		288.96733
753	97.02834	97.02947	97.02834	2.73100	2.72700	2.73100	0.00000	6.78387	6.93202	951.41089	NaN	11.62627	0.01135	0.01135	97.02872	2.72967	C07090		96.02110	C14279		96.02110
356	238.15610	238.15794	238.15318	0.17300	0.17200	0.19900	7.62093	7.27467	6.43871	950.21248	2040.46559	9.34053	0.01016	0.01016	238.15574	0.18133			237.15175	C05314		237.15180
294	270.21948	270.21857	270.21948	9.99500	10.35600	9.99500	0.00000	7.29087	6.42147	949.72305	NaN	9.89265	0.01190	0.01190	270.21918	10.11533			269.19909	C05763		269.19391
141	822.01282	822.01068	822.01282	8.12300	8.06000	8.12300	0.00000	6.83805	6.86768	946.58905	NaN	9.44309	0.00929	0.00929	822.01211	8.10200	C00894	HMDB02307	821.12578	C00894	HMDB02307	821.12579
595	141.96185	141.96118	141.96185	3.01300	2.68000	3.01300	0.00000	7.03380	6.67096	946.12700	NaN	9.76442	0.00987	0.00987	141.96163	2.90200	C00169	HMDB01096	140.98270	C00169	HMDB01096	140.98271
614	134.06966	134.06993	134.06966	11.96100	12.21670	11.96100	0.00000	6.74341	6.94694	939.33549	NaN	8.51113	0.01053	0.01053	134.06975	12.04623			133.06400	C10901		133.06400
559	158.96150	158.96172	158.96153	17.83300	17.63200	17.58800	6.41136	6.78317	6.86995	922.01670	608.72371	9.32219	0.00948	0.00948	158.96158	17.68433	C19212		157.97238	C19164		157.97240
229	352.31586	352.30612	352.31586	0.48200	0.17200	0.48200	0.00000	7.20256	6.42669	911.07270	NaN	10.01184	0.00977	0.00977	352.31261	0.37867			351.30712			351.31372
512	182.98442	182.98708	182.98442	2.76600	2.49200	2.76600	0.00000	6.92319	6.66799	893.89219	NaN	9.55950	0.00944	0.00944	182.98531	2.67467	C07598		181.97080	C07719		181.97075
357	238.15509	238.15500	238.15509	9.37100	9.23800	9.37100	0.00000	6.91554	6.67551	893.83574	NaN	10.68217	0.00943	0.00943	238.15506	9.32667			237.15175	C05314		237.15180
136	850.04321	850.04608	850.04321	0.18700	0.19600	0.18700	0.00000	6.99600	6.55020	874.01525	NaN	10.33825	0.00836	0.00836	850.04417	0.19000	C04739		849.10070			849.10072
543	170.11766	170.12314	170.11766	0.90600	0.90200	0.90600	0.00000	7.09064	6.45549	873.98342	NaN	9.34590	0.00817	0.00817	170.11949	0.90467	C17730		169.11030			169.11028
760	89.50707	89.50677	89.50677	6.33300	6.01200	6.33300	0.00000	7.37899	6.16356	872.42405	NaN	9.67258	0.01165	0.01165	89.50687	6.22600						
242	330.60745	330.60907	330.60745	28.64400	28.55800	28.64400	0.00000	7.34809	6.14214	849.89318	NaN	10.72203	0.01046	0.01046	330.60799	28.61533						
609	136.06120	136.06299	136.06120	3.70800	3.77500	3.70800	0.00000	7.18291	6.30164	847.48354	NaN	9.11450	0.01016	0.01016	136.06180	3.73033	C00147	HMDB00034	135.05449	C00147	HMDB00034	135.05450
682	116.97671	116.97643	116.97671	0.18700	0.17200	0.18700	0.00000	6.76685	6.71640	846.93600	NaN	11.81046	0.00794	0.00794	116.97661	0.18200	C00122	HMDB00134	116.01096	C01384	HMDB00176	116.01096
691	114.09322	114.09209	114.09254	38.77800	38.68300	38.39200	7.94315	6.51517	6.94813	838.52893	2816.22392	11.20592	0.01091	0.01091	114.09262	38.61767	C06593		113.08410			113.08406
793	84.96372	84.96153	84.96372	10.40700	10.36800	10.40700	0.00000	6.65622	6.77225	824.05519	NaN	9.29400	0.00953	0.00953	84.96299	10.39400	C02271		83.95340	C02390		83.95336
542	170.11977	170.11968	170.12042	9.30900	9.33200	9.57100	8.41015	7.24183	6.15953	812.95778	4492.44343	9.61336	0.00972	0.00972	170.11995	9.40400	C17730		169.11030			169.11028
635	128.94371	128.94090	128.94371	0.17600	0.18400	0.17600	0.00000	6.68283	6.70685	808.22112	NaN	7.85346	0.01082	0.01082	128.94277	0.17867	C19034		127.93765	C18902		127.93770
608	136.06360	136.06949	136.06360	5.28500	4.89333	5.28500	0.00000	7.29641	6.07656	801.50042	NaN	10.05415	0.00916	0.00916	136.06556	5.15444	C00147	HMDB00034	135.05450	C00147	HMDB00034	135.05450
750	98.51403	98.51265	98.51403	12.25500	12.46400	12.25500	0.00000	6.48007	6.87355	793.78009	NaN	9.82014	0.00931	0.00931	98.51357	12.32467						
625	130.96520	130.96579	130.96520	7.72250	8.04900	7.72250	0.00000	6.85677	6.48077	787.42546	NaN	11.66746	0.01076	0.01076	130.96539	7.83133	C18627	HMDB13592	129.95790	C18586		129.95790
429	201.10243	201.10382	201.10243	16.07000	16.34900	16.07000	0.00000	6.38786	6.92794	778.91073	NaN	9.18481	0.01075	0.01075	201.10290	16.16300	C06537		200.09500	C14759		200.09500
578	148.05902	148.06085	148.05902	4.17900	4.10500	4.17900	0.00000	6.68138	6.60848	768.87800	NaN	10.81906	0.01062	0.01062	148.05963	4.15433			147.05316			147.05316
216	381.87317	381.87598	381.87317	4.21400	3.95200	4.21400	0.00000	6.73673	6.54370	765.25606	NaN	10.26833	0.00955	0.00955	381.87411	4.12667		HMDB00843	381.00357			381.00357
794	84.96101	84.95934	84.96101	7.64000	7.33050	7.64000	0.00000	6.38702	6.87415	757.92395	NaN	10.58055	0.00850	0.00850	84.96045	7.53683	C02390		83.95336	C02271		83.95340

602	140.03435	140.04102	140.03435	8.09900	7.94300	8.09900	0.00000	6.68383	6.55436	749.26780	NaN	9.87585	0.01024	0.01024	140.03657	8.04700	C03349		139.03030	C03349		139.03031
514	182.98441	182.98387	182.98441	35.73100	35.55100	35.73100	0.00000	5.80739	7.40665	740.27087	NaN	10.77761	0.01039	0.01039	182.98423	35.67100	C07598		181.97080	C07719		181.97075
360	238.15707	238.15532	238.15707	2.62450	2.76200	2.62450	0.00000	6.26846	6.94382	739.62370	NaN	9.70910	0.01023	0.01023	238.15649	2.67033			237.15175	C05314		237.15180
143	815.99738	816.00562	815.99738	6.56900	6.63600	6.56900	0.00000	6.71024	6.50077	739.15123	NaN	8.97853	0.00927	0.00927	816.00012	6.59133						
302	267.20691	267.21530	267.20691	30.90400	30.77100	30.90400	0.00000	8.05407	5.13737	731.95633	NaN	10.03840	0.00926	0.00926	267.20971	30.85967			266.19943	C04834		266.18820
718	108.00217	107.99979	108.00217	4.12000	4.09300	4.12000	0.00000	6.93046	6.22607	719.29024	NaN	9.83752	0.01227	0.01227	108.00138	4.11100			107.01379	C19178		107.01379
348	242.14679	242.14957	242.14679	7.58100	7.33000	7.58100	0.00000	6.47990	6.65773	712.52619	NaN	9.93738	0.00762	0.00762	242.14772	7.49733			241.13612	C18819		241.13612
629	130.00882	130.00827	130.00882	9.79500	10.10900	9.79500	0.00000	6.38074	6.72678	701.87769	NaN	10.85348	0.01149	0.01149	130.00864	9.89967	C06554		129.01740	C06560		129.01744
156	608.08783	608.09735	608.08783	11.52500	11.47470	11.52500	0.00000	6.93340	6.17055	700.62917	NaN	11.39500	0.00980	0.00980	608.09100	11.50823	C00043	HMDB00290	607.08160	C00203	HMDB00304	607.08160
511	182.98462	182.98483	182.98462	15.39900	15.19500	15.39900	0.00000	6.60538	6.48205	694.86503	NaN	9.69403	0.01019	0.01019	182.98469	15.33100	C07598		181.97080	C07719		181.97075
241	331.90469	331.90723	331.90469	4.92000	4.78700	4.92000	0.00000	6.50056	6.55683	684.50376	NaN	10.64372	0.01068	0.01068	331.90554	4.87567	C07763		330.99080	C07763		330.99084
698	113.07051	113.07150	113.07051	13.60900	13.77000	13.60900	0.00000	7.01956	6.03650	684.04825	NaN	11.50603	0.01060	0.01060	113.07084	13.66267			112.05243			112.05243
650	122.96500	122.96414	122.96500	20.97900	20.92900	20.97900	0.00000	7.01688	6.00654	672.97724	NaN	10.71549	0.00946	0.00946	122.96472	20.96233		HMDB12216	121.97128	C08270	HMDB12251	121.97129
749	98.51370	98.51172	98.51370	11.93700	12.16900	11.93700	0.00000	6.15413	6.81196	653.96162	NaN	10.04648	0.00873	0.00873	98.51304	12.01433						
554	164.09500	164.09963	164.09500	7.35700	7.43600	7.35700	0.00000	6.54699	6.41630	653.04320	NaN	10.09408	0.00967	0.00967	164.09654	7.38333		HMDB00473	163.08580			163.08580
651	122.96442	122.96463	122.96344	19.92900	19.95100	19.76700	7.54178	6.79601	6.15799	650.01638	1885.17541	9.27139	0.01050	0.01050	122.96416	19.88233		HMDB12216	121.97128	C08270	HMDB12251	121.97129
734	100.08041	100.07839	100.07773	35.84600	35.62200	35.62500	8.15467	6.66487	6.19918	621.42993	3479.58801	12.84670	0.00990	0.00990	100.07884	35.69767		HMDB11749	99.06841	C11249		99.06841
428	201.10275	201.10252	201.10275	24.27600	24.47250	24.27600	0.00000	7.52451	5.29973	609.18376	NaN	9.12378	0.01044	0.01044	201.10268	24.34150	C06537		200.09496			200.09496
476	186.95900	186.95956	186.95900	28.50200	28.55800	28.50200	0.00000	6.31695	6.49135	604.34873	NaN	10.60245	0.01090	0.01090	186.95919	28.52067			185.93164	C14846		185.93160
442	199.14418	199.14490	199.14397	18.54000	18.48000	18.61300	8.00412	7.87388	4.89624	592.92144	2993.26416	10.91974	0.00919	0.00919	199.14435	18.54433	C06185		198.13680	C10858	HMDB06548	198.13683
305	267.20773	267.20615	267.20743	21.43600	20.83400	21.22600	8.88882	6.25817	6.44663	573.86812	7250.48194	10.64595	0.00879	0.00879	267.20710	21.16533			266.19943	C04834		266.18820
499	184.13347	184.13472	184.13347	23.34600	23.11900	23.34600	0.00000	6.06643	6.62689	570.58489	NaN	9.26177	0.01039	0.01039	184.13389	23.27033			183.12593	C10865		183.12593
613	134.06085	134.06311	134.06085	2.94250	2.69200	2.94250	0.00000	6.53415	6.14204	565.71633	NaN	9.22613	0.00915	0.00915	134.06161	2.85900	C03766		133.05280	C02040		133.05280
462	193.92210	193.92281	193.92210	4.24900	4.45800	4.24900	0.00000	6.11997	6.48436	545.75140	NaN	8.90009	0.00958	0.00958	193.92234	4.31867			193.02312	C01693		193.03750
490	185.13051	185.13275	185.13051	20.20200	20.22200	20.20200	0.00000	6.32204	6.21491	527.66986	NaN	9.07646	0.00952	0.00952	185.13126	20.20867	C17235		184.12520	C09633		184.12520
461	193.92064	193.92134	193.92064	2.97800	3.04500	2.97800	0.00000	6.19989	6.29932	517.80837	NaN	9.81888	0.01186	0.01186	193.92087	3.00033			193.02312	C01693		193.03750
215	381.87647	381.87439	381.87647	3.66100	3.58700	3.66100	0.00000	6.33065	6.10481	501.56352	NaN	8.51116	0.01032	0.01032	381.87577	3.63633		HMDB00843	381.00357			381.00357
168	497.87274	497.87460	497.87274	4.09600	4.08100	4.09600	0.00000	6.74764	5.63494	488.47612	NaN	9.75868	0.00997	0.00997	497.87336	4.09100	C18861		496.93487	C18740		496.93490
572	156.09236	156.09993	156.09236	3.06000	3.26900	3.06000	0.00000	6.43358	5.93300	484.58512	NaN	9.84438	0.01078	0.01078	156.09488	3.12967			155.08071	C06557		155.08070
648	124.96911	124.96780	124.96911	5.88567	5.97700	5.88567	0.00000	5.57857	6.75812	477.39587	NaN	9.46372	0.00726	0.00726	124.96867	5.91611			123.95240	C07295	HMDB12259	123.95060
186	450.88617	450.88632	450.88617	4.16700	4.08100	4.16700	0.00000	6.54519	5.67869	451.21290	NaN	9.72661	0.00849	0.00849	450.88622	4.13833			450.01856			
712	111.04429	111.03588	111.04429	4.24900	4.58700	4.24900	0.00000	6.25296	5.95992	448.73714	NaN	9.33358	0.01018	0.01018	111.04149	4.36167			110.03677			110.03677
349	242.13438	242.13971	242.13438	17.71800	17.42000	17.71800	0.00000	5.62671	6.57952	447.24996	NaN	9.65199	0.01148	0.01148	242.13616	17.61867	C11841		241.13139	C11841		241.13139
717	108.00065	107.99869	108.00065	4.60200	4.89367	4.60200	0.00000	5.94417	6.19447	432.38750	NaN	10.63057	0.00944	0.00944	108.00000	4.69922			107.01379	C19178		107.01379
475	186.95865	186.95935	186.95865	18.93100	18.82100	18.93100	0.00000	6.54208	5.52991	418.21370	NaN	9.32163	0.00921	0.00921	186.95888	18.89433			185.93164	C14846		185.93160
775	88.51019	88.50868	88.51019	4.63800	4.48100	4.63800	0.00000	6.10708	5.95370	415.87590	NaN	9.71530	0.00986	0.00986	88.50968	4.58567						
457	197.12659	197.13086	197.12659	3.73100	4.12800	3.73100	0.00000	6.26186	5.73629	403.05690	NaN	10.83778	0.01021	0.01021	197.12801	3.86333	C13688		196.12118	C13311		196.12120
690	114.09181	114.09151	114.09164	30.65400	31.08900	30.84500	6.99252	6.98015	5.01448	402.34786	1088.46065	9.99352	0.01016	0.01016	114.09165	30.86267			113.08406	C05853		113.08406
353	239.18893	239.17950	239.18893	5.43800	5.64667	5.43800	0.00000	6.39235	5.57387	396.67222	NaN	11.45830	0.01070	0.01070	239.18579	5.50756			238.19327			238.19327
354	239.16419	239.16988	239.16419	3.14300	3.51600	3.14300	0.00000	6.00918	5.95691	396.64732	NaN	8.27650	0.01052	0.01052	239.16608	3.26733			238.15690			238.15690
553	164.11055	164.10945	164.11055	5.87400	5.61200	5.87400	0.00000	6.19498	5.77063	396.55070	NaN	7.88945	0.01159	0.01159	164.11018	5.78667			163.09971			163.09971
272	290.88239	290.88812	290.88239	3.16625	3.05700	3.16625	0.00000	5.87189	6.08810	395.43890	NaN	11.71923	0.00974	0.00974	290.88430	3.12983	C17258		289.83920	C11065		289.92236
589	144.09911	144.09410	144.09911	4.66100	4.99900	4.66100	0.00000	6.39950	5.55978	395.29709	NaN	10.00698	0.00994	0.00994	144.09744	4.77367	C04114		143.09460	C10172	HMDB04827	143.09460
624	130.96562	130.96483	130.96562	4.81400	4.50500	4.81400	0.00000	6.51272	5.41547	389.20142	NaN	11.35559	0.01032	0.01032	130.96536	4.71100	C18627	HMDB13592	129.95790	C18586		129.95790
373	228.00728	228.00557	228.00728	3.20100	3.15100	3.20100	0.00000	5.91752	5.98539	384.31149	NaN	11.41340	0.01153	0.01153	228.00671	3.18433			226.99854	C12469		226.99850
337	243.18338	243.18196	243.18323	6.31900	6.29400	6.00300	7.00455	5.85498	6.03082	381.03848	1101.62815	10.05248	0.00921	0.00921	243.18286	6.20533	C09917		242.17830	C09876		242.17830
187	450.88498	450.89093	450.88498	3.38967	3.68100	3.38967	0.00000	5.88798	5.90583	363.90933	NaN	9.88857	0.00913	0.00913	450.88696	3.48678			450.01856			
557	158.96120	158.96179	158.96120	28.18400	27.95700	28.18400	0.00000	5.35828	6.41164	359.58972	NaN	10.21501	0.00782	0.00782	158.96140	28.10833	C19212		157.97238	C19164		157.97240
175	461.21851	461.21475	461.21851	28.12600	28.40500	28.12600	0.00000	6.36070	5.18039	320.71266	NaN	9.49671	0.01131	0.01131	461.21726	28.21900	C10672		460.20970	C10704		460.20970
153	693.90857	693.90631	693.90857	3.79000	3.64500	3.79000	0.00000	6.29931	5.13520	304.06839	NaN	10.10121	0.00947	0.00947	693.90782	3.74167			692.70463			
301	267.20676	267.20734	267.20676	28.53800	28.14600	28.53800	0.00000	7.45010	3.15547	200.89587	NaN	9.54100	0.01075	0.01075	267.20695	28.40733			266.19943	C04834		266.18820
209	399.22800	399.23120	399.22800	5.17900	5.21100	5.17900	0.00000	5.55389	4.71908	170.11627	NaN	11.25703	0.01239	0.01239	399.22907	5.18967	C02673		398.22060	C09226		398.22060

Appendix - D - Wild Type Avicel Non Polar Metabolites

ID	MZ_blank	MZ_WTAv_NonPolar_Rep1	MZ_WTAv_NonPolar_Rep2	RT_blank	RT_WTAv_NonPolar_Rep1	RT_WTAv_NonPolar_Rep2	Int_blank	Int_WTAv_NonPolar_Rep2	Int_WTAv_NonPolar_Rep1	exp(mean.grp1)	exp(mean.grp2)	fold.mean	p.ttest	p.wilcox	mean_m/z	mean_rt	KEGG_ID_1	HMDB_ID_1	Match_mass_1	KEGG_ID_2	HMDB_ID_2	Match_mass_2
85	721.50549	721.50482	721.50806	29.65100	29.65600	29.89600	11.04093	5.29892	9.66077	1771.96988	62375.31333	11.44966	0.00983	0.00983	721.50612	29.73433		HMDB10571	720.49414		HMDB10585	720.49414
339	69.07013	69.06999	69.07045	2.42000	3.00200	3.91400	9.31685	5.93957	7.93852	1031.78546	11123.85427	8.27537	0.01061	0.01061	69.07019	3.11200	C17530		68.06260	C16521		68.06260
87	721.50586	721.50537	721.50531	28.78000	29.33800	29.07200	11.44459	6.38037	9.81874	3292.98700	93394.73409	9.37388	0.00959	0.00959	721.50551	29.06333		HMDB10571	720.49414		HMDB10585	720.49414
79	721.50641	721.50653	721.50732	31.53600	30.93970	31.92250	11.32931	6.86149	8.96487	2733.07405	83225.76363	9.58575	0.01041	0.01041	721.50676	31.46607		HMDB10571	720.49414		HMDB10585	720.49414
314	100.11092	100.11092	100.11130	7.08900	7.08900	7.49400	0.00000	7.10641	6.67055	980.91096	NaN	9.78242	0.00939	0.00939	100.11105	7.22400			99.10480	C00571		99.10480
303	102.12772	102.12820	102.12802	25.93000	26.27600	26.72800	9.10602	7.11817	7.89812	1822.82587	9009.32294	9.16524	0.01096	0.01096	102.12798	26.31133	C08306		101.12040	C14691		101.12040
88	721.50659	721.50452	721.50678	28.14400	28.53700	28.28270	11.26369	7.24280	9.89124	5255.45505	77939.83541	9.85840	0.01051	0.01051	721.50596	28.32123		HMDB10571	720.49414		HMDB10585	720.49414
84	721.50665	721.50531	721.50629	27.29600	27.67700	27.52900	10.57187	7.56303	9.48520	5034.72391	39021.64875	9.38757	0.00910	0.00910	721.50608	27.50067		HMDB10571	720.49414		HMDB10585	720.49414
307	102.12803	102.12785	102.12792	32.10100	31.92900	31.13300	9.14826	7.59938	8.36957	2935.03575	9398.04591	10.61676	0.01017	0.01017	102.12794	31.72100	C08306		101.12040	C14691		101.12040
304	102.12809	102.12800	102.12796	29.32200	30.08000	29.96700	7.92942	7.74987	8.15574	2843.54159	2777.81289	10.11675	0.00769	0.00769	102.12802	29.78967	C08306		101.12040	C14691		101.12040
74	721.50549	721.50617	721.50659	32.67800	33.23600	34.06600	10.03089	7.75485	6.77685	1430.59964	22717.36878	9.47006	0.00998	0.00998	721.50608	33.32667		HMDB10571	720.49414		HMDB10585	720.49414
257	270.21936	270.21936	270.21777	3.47300	3.47300	4.07900	0.00000	7.81444	5.81341	910.43868	NaN	8.19378	0.00880	0.00880	270.21883	3.67500			269.19909	C05763		269.19391
316	100.11127	100.11127	100.11161	7.46600	7.46600	8.20100	0.00000	7.88385	6.97673	1686.29303	NaN	11.34585	0.01014	0.01014	100.11138	7.71100			99.10480	C00571		99.10480
319	100.10960	100.10960	100.11182	8.29000	8.29000	8.47200	0.00000	7.92126	8.58829	3845.93237	NaN	8.33167	0.00856	0.00856	100.11034	8.35067			99.10480	C00571		99.10480
306	102.12800	102.12800	102.12767	32.28200	32.28200	31.73400	0.00000	7.92962	8.34533	3420.25893	NaN	10.80151	0.00851	0.00851	102.12789	32.09933	C08306		101.12040	C14691		101.12040
308	102.12790	102.12804	102.12785	33.68000	33.76700	32.90000	9.92590	8.01900	8.61862	4100.27266	20453.20551	10.71755	0.00920	0.00920	102.12793	33.44900	C08306		101.12040	C14691		101.12040
75	721.50623	721.50623	721.50806	34.54400	34.54400	34.46630	0.00000	8.09240	6.94060	1838.11847	NaN	8.43574	0.00947	0.00947	721.50684	34.51810		HMDB10571	720.49414		HMDB10585	720.49414
80	721.50592	721.50592	721.50812	26.98200	26.98200	26.81100	0.00000	8.11261	9.21672	5794.51340	NaN	9.62232	0.00828	0.00828	721.50665	26.92500		HMDB10571	720.49414		HMDB10585	720.49414
76	721.50494	721.50592	721.50708	34.94000	34.95600	35.32600	8.30145	8.29311	7.22084	2337.82412	4029.70010	9.74115	0.00958	0.00958	721.50598	35.07400		HMDB10571	720.49414		HMDB10585	720.49414
341	69.07015	69.07089	69.07075	2.05475	2.48400	2.66500	9.74178	8.33744	8.70976	5032.12012	17013.79141	11.22452	0.00946	0.00946	69.07059	2.40125	C17530		68.06260	C16521		68.06260
340	69.07035	69.07038	69.07011	6.11900	6.51150	6.75275	8.90250	8.38250	8.65834	5016.15442	7350.28884	6.66384	0.01103	0.01103	69.07028	6.46108	C17530		68.06260	C16521		68.06260
78	721.50427	721.50427	721.50665	26.32300	26.32300	26.17500	0.00000	8.42806	8.82954	5590.37905	NaN	10.25254	0.00996	0.00996	721.50507	26.27367		HMDB10571	720.49414		HMDB10585	720.49414
296	118.12193	118.12186	118.12160	3.13900	3.24900	2.66500	10.00192	8.44986	8.66715	5210.89227	22068.79034	11.19100	0.01350	0.01350	118.12179	3.01767	C00183	HMDB00883	117.07900	C00431	HMDB03355	117.07900
309	102.12824	102.12824	102.12811	36.08700	36.08700	35.26700	0.00000	8.46201	9.10761	6534.24932	NaN	9.18617	0.01068	0.01068	102.12819	35.81367	C08306		101.12040	C14691		101.12040
17	922.01093	922.00958	922.01038	6.31900	7.00600	6.06900	7.63387	8.46297	6.48111	1758.18745	2067.04119	10.64251	0.01042	0.01042	922.01030	6.46467			921.15707	C14120		921.15710
298	118.12236	118.12228	118.12182	10.28800	9.72700	9.75567	8.97093	8.47799	8.88358	5888.67272	7870.87995	9.75065	0.00998	0.00998	118.12215	9.92356	C00183	HMDB00883	117.07900	C00431	HMDB03355	117.07900
297	118.12292	118.12194	118.12071	2.38500	2.41300	2.33500	9.76066	8.53929	8.67259	5464.00024	17337.98060	9.29211	0.00768	0.00768	118.12185	2.37767	C00183	HMDB00883	117.07900	C00431	HMDB03355	117.07900
269	202.21677	202.21677	202.21585	16.08720	16.08720	16.54020	0.00000	8.57627	9.38101	7931.82899	NaN	9.33884	0.00911	0.00911	202.21646	16.23820	C19325		201.17290			201.17287
299	118.12227	118.12227	118.12212	39.91500	39.91500	39.90800	0.00000	8.63124	8.91393	6454.84584	NaN	11.68006	0.00897	0.00897	118.12222	39.91267	C00183	HMDB00883	117.07900	C00431	HMDB03355	117.07900
19	922.01093	922.00781	922.00879	1.08900	1.08200	1.08700	9.85422	8.65064	8.89720	6463.43395	19038.50356	9.75746	0.00990	0.00990	922.00918	1.08600			921.15707	C14120		921.15710
273	179.03537	179.03537	179.03471	3.43800	3.43800	2.94800	0.00000	8.69876	9.05744	7173.14296	NaN	9.54584	0.00956	0.00956	179.03515	3.27467	C19495		178.02661			178.02661
266	202.21680	202.21680	202.21631	18.91400	18.91400	19.62600	0.00000	8.70660	7.78226	3806.35762	NaN	11.82991	0.01079	0.01079	202.21663	19.15133	C19325		201.17290			201.17287
322	100.10996	100.11140	100.11198	39.89800	39.17300	38.96600	10.32805	8.71979	9.08231	7339.67377	30578.36662	10.54838	0.00850	0.00850	100.11111	39.34567			99.10480	C00571		99.10480
272	179.03542	179.03542	179.03522	3.16700	3.16700	2.19400	0.00000	8.92675	8.47349	6003.63037	NaN	10.70803	0.00963	0.00963	179.03535	2.84267	C19495		178.02661			178.02661
259	270.21851	270.21393	270.21146	1.63100	1.58800	1.59300	10.46175	8.93451	9.01910	7917.31434	34952.82030	10.80567	0.01028	0.01028	270.21463	1.60400			269.19909	C05763		269.19391
150	551.50220	551.50220	551.50348	33.75500	33.75500	33.97200	0.00000	8.93665	9.87262	12144.53219	NaN	10.64417	0.01040	0.01040	551.50262	33.82733			550.49609	C13864		550.49610
326	100.10974	100.10929	100.11166	1.07800	1.14100	1.08700	10.20722	9.02673	9.47509	10414.01163	27098.10380	10.78393	0.00986	0.00986	100.11023	1.10200			99.10480	C00571		99.10480
291	121.05088	121.05087	121.05076	37.51920	37.96000	38.41200	10.80717	9.03625	8.97568	8151.55295	49373.73829	9.87108	0.01095	0.01095	121.05083	37.96373		HMDB01366	120.04359		HMDB01366	120.04360
342	59.06152	59.06152	59.06102	27.70100	27.70100	28.28300	0.00000	9.06739	8.63408	6979.51060	NaN	10.60991	0.00975	0.00975	59.06135	27.89500	C00207	HMDB01659	58.04190	C00479	HMDB03366	58.04190
230	393.33054	393.33054	393.33017	10.65800	10.65800	10.68600	0.00000	9.07547	9.35906	10069.50315	NaN	11.31812	0.00831	0.00831	393.33041	10.66733			392.30389			392.30389
343	59.06150	59.06150	59.06110	28.39600	28.39600	28.86000	0.00000	9.12355	8.69234	7390.46171	NaN	12.82041	0.01092	0.01092	59.06137	28.55067	C00207	HMDB01659	58.04190	C00479	HMDB03366	58.04190
345	59.06149	59.06149	59.06120	13.39000	13.39000	13.43100	0.00000	9.16195	9.06940	9096.80775	NaN	11.30596	0.00981	0.00981	59.06139	13.40367	C00207	HMDB01659	58.04190	C00479	HMDB03366	58.04190
346	59.06148	59.06148	59.06126	12.64800	12.64800	12.64100	0.00000	9.16954	9.30680	10282.16201	NaN	9.48420	0.00939	0.00939	59.06141	12.64567	C00207	HMDB01659	58.04190	C00479	HMDB03366	58.04190
11	983.66168	983.66168	983.66303	11.57600	11.57600	11.62800	0.00000	9.20309	9.49055	11462.28255	NaN	10.72441	0.00991	0.00991	983.66213	11.59333			982.72613			982.72614
289	121.05077	121.05091	121.05096	22.86700	22.08300	22.64100	9.69102	9.25946	8.13407	5983.53403	16171.69167	12.02087	0.00970	0.00970	121.05088	22.53033		HMDB01366	120.04359		HMDB01366	120.04360
109	660.48969	660.48969	660.49152	10.30400	10.30400	10.34500	0.00000	9.33497	9.47163	12128.34729	NaN	9.03867	0.01094	0.01094	660.49030	10.31767			659.48895			659.46755
252	301.28497	301.28497	301.28433	9.35000	9.35000	9.41400	0.00000	9.34166	9.57783	12832.65435	NaN	10.52166	0.01018	0.01018	301.28476	9.37133		HMDB10737	300.26645			300.26645
255	285.17947	285.17947	285.17798	1.53000	1.53000	1.52300	0.00000	9.38222	9.74513	14238.02557	NaN	9.91438	0.00903	0.00903	285.17898	1.52767	C14257		284.17760	C15194		284.17760
156	550.62817	550.62817	550.62817	25.74600	25.74600	25.43300	0.00000	9.39013	9.12246	10470.25848	NaN	10.23182	0.00849	0.00849	550.62817	25.64167			549.51207			
197	473.26898	473.26898	473.26547	8.91500	8.91500	9.19000	0.00000	9.39672	9.39299	12026.33049	NaN	8.49813	0.00963	0.00963	473.26781	9.00667			472.25896		HMDB02522	472.24948
256	279.09409	279.09409	279.09345	6.37000	6.37000	6.36400	0.00000	9.40702	9.51765	12865.86616	NaN	11.22400	0.00871	0.00871	279.09387	6.36800			278.08605			278.08623
34	851.58423	851.58423	851.58301	11.77700	11.77700	11.75800	0.00000	9.42765	9.75434	14632.45701	NaN	10.66041	0.01094	0.01094	851.58382	11.77067			850.57234			850.57234
292	121.05079	121.05125	121.05077	24.74000	24.46200	25.40900	10.47203	9.43188	9.23368	11302.49043	35313.93738	8.28440	0.00940	0.00940	121.05094	24.87033		HMDB01366	120.04359		HMDB01366	120.04360
318	100.11234	100.11234	100.11198	32.64800	32.64800	32.48800	0.00000	9.45286	8.27408	7068.97021	NaN	9.89253	0.01132	0.01132	100.11222	32.59467			99.10480	C00571		99.10480
313	100.11218	100.11255	100.11220	29.74600	30.10300	30.33200	9.65066	9.46217	6.22113	2544.40045	15531.95513	10.53388	0.01136	0.01136	100.11231	30.06033			99.10480	C00571		99.10480
317	100.11224	100.11226	100.11220	29.18000	29.52600	29.86150	9.95377	9.48118	7.83395	5753.50026	21031.24889	10.18197	0.00839	0.00839	100.11223	29.52250			99.10480	C00571		99.10480
225	411.32129	411.32129	411.32138	12.40100	12.40100	12.44100	0.00000	9.49122	9.57096	13781.62352	NaN	9.53304	0.00921	0.00921	411.32132	12.41433			410.31443			410.31847
133	579.53528	579.53528	579.53772	25.46300	25.46300	25.36200	0.00000	9.51113	9.82019	15766.75628	NaN	8.96036	0.00904	0.00904	579.53609	25.42933		HMDB07074	578.49103		HMDB07242	578.49103
26	895.61078	895.61078	895.60944	11.70600	11.70600	11.78200	0.00000	9.51903	9.68607	14802.51286	NaN	10.19427	0.01035	0.01035	895.61033	11.73133			894.60980			894.61967
32	855.58014	855.58014	855.58209	12.88400	12.88400	12.88900	0.00000	9.56139	9.79994	16005.13710	NaN	9.44338	0.01068	0.01068	855.58079	12.88567			854.60364			854.60364
132	587.42712	587.42712	587.42590	12.04800	12.04800	12.11100	0.00000	9.56601	10.07547	18411.64769	NaN	8.69543	0.01038	0.01038	587.42672	12.06900			586.43858			586.43858
45	807.55890	807.55890	807.55859	11.82400	11.82400	11.87600	0.00000	9.57701	9.81211	16229.01523	NaN	10.17568	0.01062	0.01062	807.55880	11.84133			806.54613			806.53086
113	650.47534	650.47534	650.47583	19.11400	19.11400	19.10800	0.00000	9.59456	10.01576	18127.06699	NaN	10.59686	0.01105	0.01105	650.47551	19.11200			649.46821			649.46821
218	428.38431	428.38431	428.38339	12.02400	12.02400	12.01700	0.00000	9.60589	9.85901	16855.75079	NaN	11.26493	0.00997	0.00997	428.38400	12.02167			427.36616			427.36616
81	721.50659	721.50964	721.51032	23.49100	23.20100	23.17100	11.81282	9.61047	9.34954	13095.25814	134972.00830	10.67051	0.01003	0.01003	721.50885	23.28767		HMDB10571	720.49414		HMDB10585	720.49414
348	59.06132	59.06127	59.06112	31.37100	32.05900	32.93500	11.73840	9.61275	9.74485	15975.32468	125291.54211	9.69038	0.00853	0.00853	59.06124	32.12167	C00207	HMDB01659	58.04190	C00479	HMDB03366	58.04190
251	302.24405	302.24405	302.24347	5.73400	5.73400	5.71600	0.00000	9.61760	9.70586	15704.92451	NaN	10.02015	0.01087	0.01087	302.24386	5.72800	C07171		301.24056	C08454		301.24057
253	300.20239	300.20239	300.20142	1.48200	1.48200	1.48700	0.00000	9.63798	9.76850	16370.60331	NaN	11.09094	0.01040	0.01040	300.20207	1.48367			299.18853	C11819		299.18853
271	184.14476	184.14533	184.14464	36.69500	36.86400	36.76300	11.05802	9.63812	9.85828	17123.35682	63450.74287	10.33823	0.01073	0.01073	184.14491	36.77400			183.12593	C10865		183.12593
82	721.50531	721.50507	721.50574	36.54150	36.36900	36.52800	11.01005	9.66565	9.38634	13711.56109	60478.90856	11.48020	0.00964	0.00964	721.50537	36.47950		HMDB10571	720.49414		HMDB10585	720.49414
38	834.59589	834.59589	834.59656	20.71600	20.71600	20.66200	0.00000	9.68497	9.96084	18451.52111	NaN	9.12819	0.01062	0.01062	834.59611	20.69800			833.58638		HMDB08057	833.59341
52	790.61047	790.61047	790.61176	21.74100	21.74100	21.72200	0.00000	9.70463	10.05803	19561.71347	NaN	10.26570	0.01024	0.01024	790.61090	21.73467			789.58832			789.58832
93	718.53803	718.53803	718.53980	21.30500	21.30500	21.28700	0.00000	9.70559	10.00212	19031.65965	NaN	9.30127	0.00900	0.00900	718.53862	21.29900			717.53081			717.53081
254	286.24826	286.24826	286.24780	6.46500	6.46500	6.45800	0.00000	9.71776	9.66333	16164.02910	NaN	10.31122	0.01016	0.01016	286.24811	6.46267			285.24564			285.24565

121	616.46198	616.46198	616.46338	10.32800	10.32800	10.34500	0.00000	9.71904	9.86196	17863.23316	NaN	9.09033	0.01090	0.01090	616.46244	10.33367			615.49885	C08712		615.30435
163	543.40076	543.40076	543.40064	12.09500	12.09500	12.22900	0.00000	9.73677	10.01722	19477.08342	NaN	9.90381	0.01160	0.01160	543.40072	12.13967			542.43349			542.43351
65	747.53491	747.53491	747.53729	15.89900	15.89900	15.93900	0.00000	9.73844	9.86947	18105.20603	NaN	10.59370	0.01015	0.01015	747.53571	15.91233			746.53462			746.50979
353	59.06143	59.06152	59.06125	10.02900	9.42100	9.45000	10.63076	9.75038	10.27601	22319.02731	41388.43391	10.10511	0.00953	0.00953	59.06140	9.63333	C00207	HMDB01659	58.04190	C00479	HMDB03366	58.04190
349	59.06125	59.06141	59.06117	32.64300	33.13000	33.32400	11.95225	9.76078	9.85755	18199.74423	155165.11830	10.77289	0.01101	0.01101	59.06128	33.03233	C00207	HMDB01659	58.04190	C00479	HMDB03366	58.04190
194	482.38425	482.38425	482.38532	12.27100	12.27100	12.34700	0.00000	9.76618	9.80588	17783.57313	NaN	9.80724	0.01070	0.01070	482.38460	12.29633			481.35323			481.35323
40	827.54816	827.54816	827.55011	12.15330	12.15330	12.17000	0.00000	9.77545	9.96657	19360.82173	NaN	10.87365	0.01116	0.01116	827.54881	12.15887			826.57234			826.57234
149	552.41986	552.41986	552.41846	12.87200	12.87200	12.90100	0.00000	9.78109	10.01555	19896.91735	NaN	8.75336	0.01083	0.01083	552.41939	12.88167			551.39509			551.39509
209	445.23447	445.23447	445.23526	6.99500	6.99500	7.01100	0.00000	9.78306	9.86817	18501.63711	NaN	9.77117	0.01072	0.01072	445.23473	7.00033	C12959		444.22604	C12959		444.22600
119	631.45343	631.45343	631.45209	12.00000	12.00000	12.02900	0.00000	9.78934	10.20498	21964.00302	NaN	8.82672	0.01000	0.01000	631.45298	12.00967			630.46241			630.46241
216	429.28995	429.28995	429.29022	11.01100	11.01100	11.02800	0.00000	9.79277	9.97974	19658.27986	NaN	9.45028	0.01065	0.01065	429.29004	11.01667			428.27737			428.27737
270	202.21664	202.21664	202.21587	37.49600	37.51200	37.51700	10.54475	9.79457	9.40550	14765.32045	37977.38586	9.26282	0.00909	0.00909	202.21633	37.50833	C19325		201.17290			201.17287
53	783.66296	783.66296	783.66425	16.21700	16.21700	16.25700	0.00000	9.81179	10.13411	21438.60833	NaN	9.81023	0.01042	0.01042	783.66339	16.23033			782.63014			782.59080
69	732.55298	732.55298	732.55304	21.69400	21.69400	21.68700	0.00000	9.82166	10.09400	21116.91641	NaN	10.61259	0.01010	0.01010	732.55300	21.69167			731.54646			731.54646
300	118.12255	118.12265	118.12274	37.44900	37.46500	37.45800	11.39045	9.83310	10.08477	21140.31918	88472.48349	8.08176	0.00929	0.00929	118.12265	37.45733	C00183	HMDB00883	117.07900	C00431	HMDB03355	117.07900
157	550.62750	550.62750	550.62836	24.94500	24.94500	24.89100	0.00000	9.83406	9.96757	19946.53547	NaN	9.33569	0.01026	0.01026	550.62779	24.92700			549.51207			
48	799.51843	799.51843	799.51941	11.38800	11.38800	11.39300	0.00000	9.86961	10.01508	20792.43966	NaN	11.62555	0.01099	0.01099	799.51876	11.38967			798.52815			798.52820
77	721.50629	721.50494	721.50745	35.22250	35.59200	35.82100	9.42137	9.87767	7.91993	7323.16543	12349.43585	11.10292	0.01003	0.01003	721.50623	35.54517		HMDB10571	720.49414		HMDB10585	720.49414
123	612.50397	612.50397	612.50537	15.69900	15.69900	15.77400	0.00000	9.88393	10.04269	21232.93861	NaN	8.93393	0.00978	0.00978	612.50444	15.72400			611.46755	C10015		611.36830
13	964.71478	964.71478	964.71655	15.13300	15.13300	15.19700	0.00000	9.89516	10.10980	22081.19328	NaN	9.44048	0.00932	0.00932	964.71537	15.15433			963.76556			963.76556
189	491.37573	491.37653	491.37653	15.13300	15.13300	15.19700	0.00000	9.90831	10.03620	21423.70297	NaN	9.54683	0.00938	0.00938	491.37600	15.15433	C08972		490.36583	C16859		490.36583
57	776.58923	776.58923	776.59412	21.41100	21.41100	21.39300	0.00000	9.91219	10.09408	22095.57017	NaN	9.76586	0.01071	0.01071	776.59086	21.40500			775.57267			775.57267
129	591.08637	591.08637	591.08618	7.37200	7.37200	7.37700	0.00000	9.92694	9.63239	17670.70335	NaN	10.01595	0.01116	0.01116	591.08630	7.37367			590.06432	C04630		590.10260
86	721.50690	721.52240	721.52374	23.29100	22.93100	22.90000	11.81345	9.93184	9.79209	19186.56580	135056.82641	10.07415	0.01201	0.01201	721.51768	23.04067		HMDB10571	720.49414		HMDB10585	720.49414
31	860.68243	860.68243	860.68506	22.88300	22.88300	22.86500	0.00000	9.93406	10.26747	24361.73218	NaN	11.90197	0.01017	0.01017	860.68331	22.87700			859.66657			859.66657
215	436.30948	436.30948	436.30966	11.70600	11.70600	11.74600	0.00000	9.94954	9.90304	20461.34428	NaN	10.86802	0.01082	0.01082	436.30954	11.71933	C16889		435.31150	C16889		435.31154
243	344.22830	344.22830	344.22781	1.48200	1.48200	1.48700	0.00000	9.95011	10.12955	22921.44961	NaN	10.13684	0.00893	0.00893	344.22814	1.48367	C07879		343.22598	C07879		343.22600
198	473.25339	473.25339	473.25299	9.66800	9.66800	9.69700	0.00000	9.95046	9.89655	20404.41499	NaN	11.57794	0.01130	0.01130	473.25326	9.67767			472.24610			472.24610
232	388.25461	388.25461	388.25281	1.49400	1.49400	1.48700	0.00000	9.95912	10.15954	23372.78846	NaN	9.10743	0.01172	0.01172	388.25401	1.49167			387.24431			387.24817
234	383.19321	383.19321	383.18185	10.54000	10.54000	10.58000	0.00000	9.97216	10.16177	23552.02912	NaN	10.90250	0.01036	0.01036	383.18942	10.55333	C19435		382.18660			382.17400
214	437.26141	437.26141	437.26187	8.54900	8.54900	8.56600	0.00000	9.97384	10.09081	22750.09240	NaN	10.74170	0.00965	0.00965	437.26157	8.55467		HMDB07855	436.25896			436.25896
89	721.52832	721.52832	721.53259	22.08300	22.08300	22.08800	0.00000	9.97461	10.01442	21905.93241	NaN	9.92584	0.00974	0.00974	721.52974	22.08467			720.53048			720.53048
99	689.49249	689.49249	689.49139	14.68600	14.68600	14.75000	0.00000	9.98094	10.10764	23023.91638	NaN	10.26794	0.01105	0.01105	689.49213	14.70733			688.50427			688.50427
302	116.05328	116.05328	116.05296	7.40700	7.40700	7.41200	0.00000	10.02684	9.97571	22054.48755	NaN	9.11742	0.00953	0.00953	116.05317	7.40867	C00148	HMDB00162	115.06330	C00763	HMDB03411	115.06330
30	860.66742	860.66742	860.66742	16.75900	16.75900	16.82300	0.00000	10.03726	10.25027	25432.04695	NaN	8.72534	0.01014	0.01014	860.66742	16.78033			859.66657			859.66657
174	523.47296	523.47296	523.47278	23.73100	23.73100	23.72500	0.00000	10.04109	10.46699	28397.07590	NaN	8.57755	0.01058	0.01058	523.47290	23.72900			522.53757			522.53757
236	366.17099	366.17099	366.17014	7.69000	7.69000	7.69500	0.00000	10.05235	9.99666	22572.90599	NaN	9.27108	0.01060	0.01060	366.17071	7.69167			365.15869			365.15869
140	572.43683	572.43683	572.43732	10.35100	10.35100	10.39200	0.00000	10.05576	10.25416	25718.22676	NaN	12.34198	0.00968	0.00968	572.43699	10.36467			571.47532			571.36379
192	483.36148	483.36148	483.36218	11.40000	11.40000	11.41600	0.00000	10.08301	10.16760	24966.85734	NaN	10.61982	0.01031	0.01031	483.36172	11.40533	C19992		482.35487	C19892		482.35490
245	337.14703	337.14703	337.14621	6.38200	6.38200	6.38700	0.00000	10.08630	10.26293	26228.75091	NaN	8.46674	0.00985	0.00985	337.14676	6.38367	C02590		336.13950			336.13953
55	780.54932	780.54932	780.55188	19.24400	19.24400	19.19000	0.00000	10.09681	10.28859	26707.51973	NaN	10.76364	0.01080	0.01080	780.55017	19.22600		HMDB07984	779.54646		HMDB08015	779.54646
49	795.58557	795.58557	795.58630	21.14000	21.14000	21.11000	0.00000	10.10707	10.32495	27337.28519	NaN	10.20651	0.00906	0.00906	795.58582	21.13000			794.58252			794.58252
67	734.57739	734.57739	734.57935	21.08100	21.08100	21.06300	0.00000	10.11762	10.17975	25557.47041	NaN	8.38382	0.00971	0.00971	734.57804	21.07500			733.56216			733.56216
101	678.45343	678.45343	678.45422	11.27000	11.27000	11.31000	0.00000	10.12407	10.29790	27200.23302	NaN	9.80649	0.01242	0.01242	678.45370	11.28333			677.46312		HMDB12331	677.42676
106	664.49133	664.49133	664.49146	19.79800	19.79800	19.77900	0.00000	10.13923	10.40192	28870.56870	NaN	9.46512	0.01096	0.01096	664.49137	19.79167			663.48386			663.48386
164	538.40472	538.40472	538.40320	12.16500	12.16500	12.18200	0.00000	10.14019	10.38721	28672.60238	NaN	9.60630	0.01055	0.01055	538.40422	12.17067		HMDB11490	537.37946		HMDB11520	537.37946
158	550.62756	550.62756	550.62903	23.75500	23.75500	23.70100	0.00000	10.14236	10.39717	28847.15442	NaN	7.52905	0.00918	0.00918	550.62805	23.73700			549.51207			
70	732.61548	732.61548	732.61786	24.16700	24.16700	24.14900	0.00000	10.14472	10.50107	30421.05959	NaN	11.23301	0.01023	0.01023	732.61627	24.16100		HMDB01348	731.60669			731.61924
96	699.59259	699.59259	699.59705	24.60300	24.60300	24.57300	0.00000	10.15394	10.46066	29950.44689	NaN	10.79213	0.00840	0.00840	699.59408	24.59300			698.58493			698.58493
203	457.30533	457.30533	457.30484	10.95200	10.95200	10.99200	0.00000	10.15939	10.06754	24673.01514	NaN	10.78561	0.00999	0.00999	457.30517	10.96533			456.29878			456.30509
185	500.30124	500.30124	500.30051	8.54900	8.54900	8.56600	0.00000	10.16104	10.16092	25873.60586	NaN	9.68417	0.00897	0.00897	500.30100	8.55467	C05465	HMDB00951	499.29673		HMDB00896	499.29673
250	308.18527	308.18527	308.18533	5.71100	5.71100	5.71600	0.00000	10.16490	10.04132	24418.83020	NaN	11.55176	0.01127	0.01127	308.18529	5.71267	C07219	HMDB05023	307.16850	C07219	HMDB05023	307.16846
145	565.41394	565.41394	565.41480	11.40000	11.40000	11.40500	0.00000	10.20146	10.34875	29001.66225	NaN	11.11110	0.01027	0.01027	565.41423	11.40167		HMDB02198	564.39673	C08583	HMDB03154	564.39673
211	443.30490	443.30490	443.30554	11.74100	11.74100	11.77000	0.00000	10.21950	10.38060	29734.20971	NaN	9.38512	0.00963	0.00963	443.30512	11.75067			442.30829			442.30829
115	644.49469	644.49469	644.49609	12.69500	12.69500	12.72400	0.00000	10.25249	10.42896	30968.55937	NaN	11.28532	0.00977	0.00977	644.49516	12.70467			643.50228			643.50228
14	963.73828	963.73828	963.73737	23.39000	23.39000	23.36000	0.00000	10.25347	10.47776	31748.94969	NaN	7.93227	0.01071	0.01071	963.73798	23.38000			962.73631			962.73631
219	428.38477	428.38477	428.38525	12.48300	12.48300	12.51200	0.00000	10.25961	10.04713	25677.51074	NaN	11.11759	0.00958	0.00958	428.38493	12.49267			427.36616			427.36616
337	74.09747	74.09747	74.09742	1.40000	1.40000	1.39300	0.00000	10.26731	10.07527	26141.74628	NaN	9.36903	0.00915	0.00915	74.09746	1.39767			73.08915	C05985		73.08915
151	551.50250	551.50250	551.50354	21.58800	21.58800	21.58100	0.00000	10.27344	10.55750	33371.78230	NaN	9.07901	0.00987	0.00987	551.50285	21.58567			550.49609	C13864		550.49610
23	904.69251	904.69251	904.69318	16.68800	16.68800	16.71700	0.00000	10.30406	10.54250	33633.56413	NaN	11.73116	0.01236	0.01236	904.69273	16.69767			903.69279			
107	664.48895	664.48895	664.48920	20.44500	20.44500	20.43900	0.00000	10.31569	10.69367	36485.69418	NaN	9.49260	0.00918	0.00918	664.48903	20.44300			663.48386			663.48386
242	348.31122	348.31122	348.31055	14.78000	14.78000	14.82000	0.00000	10.31624	10.76203	37764.89212	NaN	12.43703	0.00921	0.00921	348.31099	14.79333	C11695	HMDB04080	347.28244		HMDB13655	347.28244
170	528.41010	528.41010	528.41058	10.39900	10.39900	10.42700	0.00000	10.32843	10.51171	33525.72624	NaN	10.30240	0.01001	0.01001	528.41026	10.40833	C15755		527.34582	C15755		527.34580
105	667.48102	667.48102	667.48187	14.74500	14.74500	14.79700	0.00000	10.33249	10.51902	33716.97337	NaN	10.20340	0.01090	0.01090	667.48130	14.76233			666.48353			666.44714
176	523.47174	523.47174	523.47327	23.39000	23.39000	23.36000	0.00000	10.36824	10.92261	42000.03487	NaN	9.87725	0.00950	0.00950	523.47225	23.38000			522.53757			522.53757
71	725.52033	725.52033	725.52295	15.97000	15.97000	16.01000	0.00000	10.36932	10.45729	33299.73055	NaN	9.98641	0.01074	0.01074	725.52120	15.98333			724.51286			724.50427
265	203.17606	203.17606	203.17552	1.43500	1.43500	1.41700	0.00000	10.37023	10.49225	33902.41858	NaN	8.72156	0.01072	0.01072	203.17588	1.42900		HMDB13076	202.16812			202.17215
355	59.06137	59.06142	59.06120	36.50600	36.49900	37.05800	12.82407	10.38229	11.01070	44200.63775	371040.79461	8.24277	0.00946	0.00946	59.06133	36.68767	C00207	HMDB01659	58.04190	C00479	HMDB03366	58.04190
165	537.48810	537.48810	537.48792	20.01000	20.01000	19.95600	0.00000	10.38488	10.64570	36875.03328	NaN	10.82683	0.00891	0.00891	537.48804	19.99200		HMDB07041	536.44409		HMDB07125	536.44409
193	483.33649	483.33649	483.33765	10.64600	10.64600	10.67400	0.00000	10.38502	10.73078	38480.19320	NaN	9.04562	0.01065	0.01065	483.33687	10.65533			482.30660			482.30657
15	948.71857	948.71857	948.71979	16.61700	16.61700	16.65800	0.00000	10.39687	10.58345	35959.87856	NaN	10.95340	0.01013	0.01013	948.71897	16.63067			947.72723			947.77889
223	412.38968	412.38968	412.38934	14.58000	14.58000	14.64400	0.00000	10.40424	10.59470	36296.18486	NaN	10.77697	0.00917	0.00917	412.38957	14.60133		HMDB13314	411.37125			411.37124
191	484.35696	484.35696	484.35617	12.88400	12.88400	12.90100	0.00000	10.45558	10.69438	39142.95021	NaN	9.40540	0.01073	0.01073	484.35670	12.88967			483.31960	C09959		483.38248
182	505.38998	505.38998	505.39017	16.55900	16.55900	16.58700	0.00000	10.47732	10.67314	39152.93787	NaN	9.27931	0.01041	0.01041	505.39005	16.56833			504.38145			504.38145
148	556.44177	556.44177	556.44226	12.80100	12.80100	12.85300	0.00000	10.49174	10.66923	39359.18448	NaN	8.94355	0.00700	0.00700	556.44194	12.81833		HMDB10697	555.52264		HMDB10697	555.52264
126	600.46814	600.46814	600.46881	12.74200	12.74200	12.78300	0.00000	10.50449	10.64722	39177.31922	NaN	8.93804	0.00980	0.00980	600.46836	12.75567			599.45835			599.45832
179	513.38886	513.38886	513.38825	15.09800	15.09800	15.15000	0.00000	10.50971	10.58358	38049.57260	NaN	11.44015	0.00934	0.00934	513.38865	15.11533	C17734		512.35020			512.35018
180	512.41425	512.41425	512.41431	12.88400	12.88400	12.93600	0.00000	10.51414	10.59231	38300.63685	NaN	10.32228	0.01093	0.01093	512.41427	12.90133			511.32977			511.32975
28	876.64404	876.64404	876.64349	20.45700	20.45700	20.41500	0.00000	10.52388	10.76865	42035.45632	NaN	10.48185	0.01011	0.01011	876.64386	20.44300			875.64036			875.64036

72	722.54224	722.54224	722.54321	19.80900	19.80900	19.79100	0.00000	10.52631	10.74048	41497.82188	NaN	9.48809	0.01066	0.01066	722.54256	19.80300			721.52572			721.52572
8	992.74426	992.74426	992.74567	16.54700	16.54700	16.58700	0.00000	10.53350	10.73128	41456.25286	NaN	11.36454	0.01031	0.01031	992.74473	16.56033						
47	804.62152	804.62152	804.62268	20.46900	20.46900	20.45000	0.00000	10.53621	10.64553	39770.12820	NaN	8.91396	0.00895	0.00895	804.62191	20.46267			803.60397			803.60397
177	522.59735	522.59735	522.59784	21.28900	21.10500	21.14500	12.32058	10.53698	10.68622	40603.06361	224264.66685	9.62596	0.01230	0.01230	522.59751	21.17967			521.48078			
134	579.53375	579.53375	579.53552	22.03500	22.03500	22.00500	0.00000	10.53889	10.88560	44902.28205	NaN	10.77317	0.00992	0.00992	579.53434	22.02500		HMDB07074	578.49103		HMDB07242	578.49103
102	678.50671	678.50671	678.50678	21.01100	21.01100	20.99200	0.00000	10.55834	10.83841	44283.96998	NaN	9.60604	0.00877	0.00877	678.50673	21.00467			677.49951			677.49951
190	484.38495	484.38495	484.38345	10.45700	10.45700	10.49800	0.00000	10.56589	10.65962	40650.13959	NaN	10.07701	0.01129	0.01129	484.38445	10.47067	C09959		483.38248	C09968		483.38248
175	523.47095	523.47095	523.47186	19.89200	19.89200	19.83800	0.00000	10.57228	10.80922	43947.44341	NaN	11.32123	0.00870	0.00870	523.47125	19.87400			522.53757			522.53757
29	864.64179	864.64179	864.64557	22.44800	22.44800	22.41700	0.00000	10.57404	10.80448	43881.99182	NaN	9.35052	0.00989	0.00989	864.64305	22.43767			863.63333		HMDB08287	863.64036
220	426.36896	426.36896	426.36853	12.74200	12.74200	12.75900	0.00000	10.58842	10.79013	43882.66768	NaN	9.06355	0.00886	0.00886	426.36882	12.74767			425.35051		HMDB05065	425.35049
354	59.06147	59.06147	59.06109	35.93400	35.93400	36.53900	0.00000	10.60928	10.41133	36691.64600	NaN	10.77945	0.01206	0.01206	59.06134	36.13567	C00207	HMDB01659	58.04190	C00479	HMDB03366	58.04190
166	537.48792	537.48792	537.48737	20.48100	20.48100	20.42700	0.00000	10.61166	10.92801	47564.12884	NaN	11.05441	0.01023	0.01023	537.48773	20.46300		HMDB07041	536.44409		HMDB07125	536.44409
206	455.34885	455.34885	455.34940	12.33000	12.33000	12.37000	0.00000	10.64414	10.76113	44472.89378	NaN	11.53348	0.01137	0.01137	455.34903	12.34333			454.34468			454.34468
186	497.37753	497.37753	497.37720	12.16500	12.16500	12.20600	0.00000	10.64931	10.88533	47444.68954	NaN	10.00426	0.01152	0.01152	497.37742	12.17867	C04102		496.34030	C11175		496.34000
42	818.63702	818.63702	818.63953	21.12900	21.12900	21.11000	0.00000	10.65788	10.91982	48477.22150	NaN	9.39542	0.01089	0.01089	818.63786	21.12267			817.61962			817.61962
228	405.27182	405.27182	405.27216	11.57600	11.57600	11.61700	0.00000	10.69003	10.83805	47289.43255	NaN	10.51592	0.00968	0.00968	405.27193	11.58967	C07074		404.25630	C15568		404.25630
114	645.46454	645.46454	645.46722	14.80400	14.80400	14.85600	0.00000	10.69163	10.81455	46774.32777	NaN	9.97802	0.01057	0.01057	645.46543	14.82133			644.44167			644.44167
90	721.50610	721.50855	721.51025	21.96000	21.34100	21.31000	12.30310	10.69409	10.90825	49078.15541	220377.03708	8.66028	0.00838	0.00838	721.50830	21.53700		HMDB10571	720.49414		HMDB10585	720.49414
135	579.53565	579.53565	579.53522	25.00400	25.00400	24.92600	0.00000	10.70221	10.91598	49468.53485	NaN	10.40718	0.01122	0.01122	579.53550	24.97800		HMDB07074	578.49103		HMDB07242	578.49103
95	703.50861	703.50861	703.50873	16.02900	16.02900	16.05700	0.00000	10.70270	10.90105	49112.85034	NaN	10.09954	0.00918	0.00918	703.50865	16.03833			702.51992			702.51992
224	412.38886	412.38886	412.38907	14.26200	14.26200	14.31400	0.00000	10.72055	10.82052	47597.48596	NaN	8.20871	0.00985	0.00985	412.38893	14.27933		HMDB13314	411.37125			411.37124
112	654.33270	654.33270	654.33228	13.60200	13.60200	13.65400	0.00000	10.74114	11.03527	53541.02819	NaN	9.84659	0.01157	0.01157	654.33256	13.61933	C15681		653.32133	C15661		653.32130
213	440.35855	440.35855	440.35931	10.46900	10.46900	10.49800	0.00000	10.75253	10.97435	52231.48302	NaN	9.31611	0.00909	0.00909	440.35881	10.47867			439.30864			439.30863
111	656.44135	656.44135	656.44110	11.31700	11.31700	11.34600	0.00000	10.75590	10.93452	51287.96188	NaN	8.70848	0.01054	0.01054	656.44126	11.32667			655.43625			655.42986
137	579.43103	579.43103	579.42981	12.16500	12.16500	12.17000	0.00000	10.75659	10.97344	52313.72789	NaN	9.41722	0.00853	0.00853	579.43062	12.16667			578.43111	C16280		578.41240
240	352.30609	352.30609	352.30548	10.59900	10.59900	10.62700	0.00000	10.78018	10.93409	51903.08669	NaN	10.43089	0.00918	0.00918	352.30589	10.60833			351.30712			351.31372
222	414.32251	414.32251	414.32181	12.28300	12.28300	12.32300	0.00000	10.78160	10.91868	51541.42633	NaN	8.90793	0.00909	0.00909	414.32228	12.29633		HMDB13333	413.31412			413.31410
249	316.19446	316.19446	316.19479	10.59900	10.59900	10.60400	0.00000	10.79079	10.98105	53418.82116	NaN	9.25114	0.01029	0.01029	316.19457	10.60067			315.18344			315.18344
139	577.51148	577.51148	577.51105	24.74400	24.74400	24.67900	0.00000	10.79097	11.09067	56433.41976	NaN	9.66151	0.00967	0.00967	577.51133	24.72233		HMDB07075	576.47540		HMDB07076	576.47540
237	364.18277	364.18277	364.18243	6.38200	6.38200	6.38700	0.00000	10.79418	10.94538	52563.60908	NaN	9.48341	0.01059	0.01059	364.18266	6.38367			363.17942			363.17942
246	331.28458	331.28458	331.28391	14.78000	14.78000	14.83200	0.00000	10.80116	11.08171	56468.11142	NaN	9.96372	0.00997	0.00997	331.28435	14.79733			330.27699		HMDB11564	330.27699
227	410.17893	410.17893	410.17889	10.54000	10.54000	10.58000	0.00000	10.81618	11.02700	55358.79282	NaN	10.99867	0.00890	0.00890	410.17892	10.55333			409.16714			409.16714
167	537.48810	537.48810	537.48877	24.04900	24.04900	24.01900	0.00000	10.84050	11.24852	62599.23606	NaN	10.21728	0.00758	0.00758	537.48832	24.03900		HMDB07041	536.44409		HMDB07125	536.44409
127	593.44690	593.44690	593.44580	12.89600	12.89600	12.91200	0.00000	10.85053	11.08795	58060.33485	NaN	9.55248	0.01062	0.01062	593.44653	12.90133			592.44676		HMDB12299	592.44916
169	535.40222	535.40222	535.40155	15.03900	15.03900	15.10300	0.00000	10.85507	11.01593	56133.90867	NaN	11.34206	0.00997	0.00997	535.40200	15.06033			534.42255			534.42255
264	244.20253	244.20253	244.20235	1.43500	1.43500	1.42900	0.00000	10.85720	11.16497	60541.46527	NaN	11.66932	0.00985	0.00985	244.20247	1.43300	C07673		243.19870	C07575		243.19870
46	806.63831	806.63831	806.63977	23.43700	23.43700	23.43000	0.00000	10.86266	11.07144	57933.48670	NaN	8.89770	0.01050	0.01050	806.63879	23.43467			805.63489			805.63493
22	910.64575	910.64575	910.64746	21.14000	21.14000	21.13300	0.00000	10.88206	11.14254	60615.22915	NaN	10.82939	0.01154	0.01154	910.64632	21.13767						
168	537.48853	537.48853	537.48865	23.74300	23.74300	23.70100	0.00000	10.89499	11.43562	70636.41761	NaN	10.63042	0.00970	0.00970	537.48857	23.72900		HMDB07041	536.44409		HMDB07125	536.44409
229	396.33328	396.33328	396.33182	10.54000	10.54000	10.58000	0.00000	10.90151	11.01961	57558.69506	NaN	9.29992	0.01079	0.01079	396.33279	10.55333			395.33993			395.33993
120	623.45374	623.45374	623.45380	14.85100	14.85100	14.91500	0.00000	10.92371	11.08851	60241.13143	NaN	8.57284	0.01018	0.01018	623.45376	14.87233			622.48082			622.48082
356	59.06144	59.06149	59.06115	1.08900	1.11700	1.12200	12.67991	10.95852	11.55133	77259.30863	321228.56274	9.00421	0.00947	0.00947	59.06136	1.10933	C00207	HMDB01659	58.04190	C00479	HMDB03366	58.04190
12	977.75299	977.75299	977.75385	23.74300	23.74300	23.71300	0.00000	10.98548	11.20663	65910.44919	NaN	8.80791	0.01004	0.01004	977.75328	23.73300			976.75196			976.75196
171	527.40460	527.40460	527.40393	16.48800	16.48800	16.52800	0.00000	10.98962	11.16728	64760.36112	NaN	8.73443	0.00942	0.00942	527.40438	16.50133			526.36342			526.43858
147	557.41394	557.41394	557.41486	15.00400	15.00400	15.05600	0.00000	11.02959	11.17659	66375.91860	NaN	10.33789	0.01015	0.01015	557.41425	15.02133			556.42401	C15892		556.46440
100	681.49530	681.49530	681.49536	16.07600	16.07600	16.11600	0.00000	11.03883	11.26022	69530.73974	NaN	8.50512	0.00932	0.00932	681.49532	16.08933			680.47806			680.47806
331	90.97769	90.97769	90.97713	1.34100	1.34100	1.34600	0.00000	11.04650	11.32196	71986.26418	NaN	11.08417	0.01012	0.01012	90.97750	1.34267	C06613		89.98720	C16348		89.98720
248	323.14011	323.14011	323.13959	7.40700	7.40700	7.41200	0.00000	11.05260	11.12990	65594.78331	NaN	9.95081	0.00959	0.00959	323.13993	7.40867	C09559		322.14160	C09568		322.14160
125	601.44061	601.44061	601.44080	14.89800	14.89800	14.96200	0.00000	11.09862	11.24254	71010.13280	NaN	8.51954	0.00933	0.00933	601.44067	14.91933	C08585		600.41790	C08606	HMDB03020	600.41790
233	385.17297	385.17297	385.17249	2.03600	2.03600	2.00600	0.00000	11.10183	11.10936	66542.57846	NaN	9.23026	0.00956	0.00956	385.17281	2.02600			384.16634			384.16639
138	579.42645	579.42645	579.42773	14.94500	14.94500	14.99700	0.00000	11.10597	11.28036	72632.21917	NaN	10.47719	0.00849	0.00849	579.42688	14.96233	C16280		578.41240			578.43111
36	846.66895	846.66895	846.67120	22.34200	22.34200	22.33500	0.00000	11.11476	11.41971	78216.05080	NaN	10.75414	0.01179	0.01179	846.66970	22.33967			845.65092			845.68731
63	748.58466	748.58466	748.58777	23.46100	23.46100	23.44200	0.00000	11.12154	11.60374	86046.12064	NaN	8.72613	0.00958	0.00958	748.58569	23.45467		HMDB07937	747.57782		HMDB08033	747.57782
205	456.32645	456.32645	456.32596	11.42300	11.42300	11.44000	0.00000	11.15042	11.37046	77686.79919	NaN	9.45928	0.01063	0.01063	456.32628	11.42867			455.30354			455.30354
332	86.09749	86.09746	86.09737	3.52700	3.20200	3.27800	12.30898	11.15393	11.75149	94155.72705	221677.31461	10.72491	0.01086	0.01086	86.09744	3.33567	C03219		85.08915	C01746		85.08910
200	470.34161	470.34161	470.34241	12.16500	12.16500	12.18200	0.00000	11.21825	11.39891	81517.90894	NaN	9.12377	0.00908	0.00908	470.34188	12.17067			469.31921	C11995		469.30400
160	549.41510	549.41510	549.41724	16.42900	16.42900	16.46970	0.00000	11.26257	11.43755	84970.60022	NaN	9.10882	0.00978	0.00978	549.41581	16.44257	C03855		548.40770			548.40769
24	904.67365	904.67365	904.67658	21.57600	21.57600	21.53400	0.00000	11.26675	11.63268	93874.42973	NaN	10.66192	0.00937	0.00937	904.67462	21.56200			903.69279			
142	565.51862	565.51862	565.52002	21.54100	21.54100	21.51000	0.00000	11.28327	11.60132	93180.86502	NaN	8.21505	0.00743	0.00743	565.51908	21.53067		HMDB07016	564.47540		HMDB07043	564.47540
136	579.53424	579.53424	579.53650	21.61100	21.61100	21.56900	0.00000	11.28672	11.56251	91547.57488	NaN	9.82771	0.00905	0.00905	579.53499	21.59700		HMDB07074	578.49103		HMDB07242	578.49103
110	659.48169	659.48169	659.48346	16.12300	16.12300	16.17500	0.00000	11.30410	11.46118	87784.27991	NaN	10.11065	0.00939	0.00939	659.48228	16.14033			658.45732			658.45732
117	634.42731	634.42731	634.42957	11.34100	11.34100	11.39300	0.00000	11.33356	11.42984	87701.64436	NaN	10.36222	0.01208	0.01208	634.42806	11.35833			633.43691			633.43691
146	563.50018	563.50018	563.50098	24.41500	24.41500	24.39600	0.00000	11.35387	11.73612	103259.00737	NaN	9.09851	0.01015	0.01015	563.50045	24.40867			562.45973			562.45973
201	458.32321	458.32321	458.32306	11.64700	11.64700	11.68700	0.00000	11.44289	11.51518	96667.77066	NaN	9.42145	0.00957	0.00957	458.32316	11.66033			457.28280			457.24375
196	476.37415	476.37415	476.37332	15.93400	15.93400	15.97500	0.00000	11.44496	11.54214	98080.96143	NaN	8.05911	0.00792	0.00792	476.37387	15.94767			475.36953	C13142		475.31452
108	663.45331	663.45410	663.45435	20.71200	20.61000	20.59200	12.78442	11.44735	11.65410	103851.92654	356616.91599	10.91481	0.01042	0.01042	663.45392	20.63800			662.44072			662.41584
116	637.46960	637.46960	637.47131	16.17000	16.17000	16.22200	0.00000	11.46012	11.58876	101158.02460	NaN	9.02070	0.01002	0.01002	637.47017	16.18733		HMDB07317	636.47535			636.47538
62	757.64825	757.64911	757.65094	24.76350	24.61500	24.58400	13.03613	11.46395	11.60140	101994.94528	458689.90236	9.31650	0.01105	0.01105	757.64943	24.65417		HMDB07702	756.66315		HMDB07814	756.66315
141	571.42993	571.42993	571.43018	16.37000	16.37000	16.41000	0.00000	11.48490	11.61467	103754.52602	NaN	11.07881	0.00971	0.00971	571.43001	16.38333			570.43966		HMDB02746	570.44367
210	444.38007	444.38007	444.38049	15.35700	15.35700	15.40900	0.00000	11.49018	11.67634	107286.30959	NaN	9.49508	0.00847	0.00847	444.38021	15.37433		HMDB13154	443.36108			443.30356
122	615.45459	615.45459	615.45636	16.24100	16.24100	16.28100	0.00000	11.52850	11.69470	110370.33696	NaN	9.97512	0.00952	0.00952	615.45518	16.25433			614.42296		HMDB07250	614.49100
311	102.12768	102.12855	102.12824	1.07800	1.44700	1.44000	10.66862	11.55099	11.67719	110645.79966	42985.57480	10.40422	0.00919	0.00919	102.12815	1.32167	C08306		101.12040	C14691		101.12040
128	593.44257	593.44257	593.44305	16.31100	16.31100	16.35200	0.00000	11.55344	11.71015	112622.24890	NaN	11.57806	0.01019	0.01019	593.44273	16.32467			592.44676		HMDB12299	592.44916
235	376.34232	376.34232	376.34232	16.26400	16.26400	16.30400	0.00000	11.58842	11.96093	129919.59146	NaN	9.08334	0.00996	0.00996	376.34232	16.27733		HMDB13626	375.31373		HMDB13626	375.31372
172	525.38495	525.38495	525.38422	12.89600	12.89600	12.91200	0.00000	11.64557	11.89811	129552.37342	NaN	10.26351	0.00829	0.00829	525.38471	12.90133			524.34777			524.31138
187	497.35324	497.35324	497.35373	11.43500	11.43500	11.42800	0.00000	11.65570	11.86570	128116.98224	NaN	9.91168	0.00860	0.00860	497.35340	11.43267	C04102		496.34030	C11175		496.34000
143	565.51971	565.51971	565.52020	24.68600	24.68600	24.64300	0.00000	11.66795	11.96729	135620.79427	NaN	10.47616	0.01156	0.01156	565.51988	24.67167		HMDB07016	564.47540		HMDB07043	564.47540
336	79.02229	79.02229	79.02188	1.47100	1.47100	1.46400	0.00000	11.68199	11.65966	117104.91151	NaN	10.85689	0.00912	0.00912	79.02215	1.46867	C11143	HMDB02151	78.01394	C11143	HMDB02151	78.01394
54	781.57172	781.57172	781.57227	20.62200	20.62200	20.56800	0.00000	11.70129	11.94880	136632.32974	NaN	9.45704	0.01108	0.01108	781.57190	20.60400			780.56687			780.56687

199	473.26572	473.26572	473.26538	8.53800	8.53800	8.55400	0.00000	11.70521	11.84578	130026.73695	NaN	9.86899	0.00988	0.00988	473.26561	8.54333			472.25896		HMDB02522	472.24948
181	511.36859	511.36859	511.36923	12.20100	12.20100	12.20600	0.00000	11.73973	11.98489	141819.13792	NaN	10.00360	0.00827	0.00827	511.36881	12.20267			510.37089			510.37089
238	359.31574	359.31574	359.31543	16.26400	16.26400	16.30400	0.00000	11.79137	12.13834	157134.28663	NaN	9.30768	0.00856	0.00856	359.31563	16.27733			358.30829			358.30829
144	565.51898	565.51898	565.52057	21.12900	21.12900	21.09800	0.00000	11.79670	12.09951	154523.44272	NaN	9.47662	0.00848	0.00848	565.51951	21.11867		HMDB07016	564.47540		HMDB07043	564.47540
124	612.41461	612.41461	612.41583	11.38800	11.38800	11.42800	0.00000	11.79749	11.96435	144482.90996	NaN	10.58299	0.00823	0.00823	612.41502	11.40133	C10015		611.36830	C10242		611.36828
56	779.61066	779.61066	779.61322	22.34200	22.34200	22.33500	0.00000	11.85703	12.09281	158724.21385	NaN	11.00473	0.01193	0.01193	779.61151	22.33967	C02970		778.60290			778.60290
221	415.27487	415.27487	415.27521	10.63400	10.63400	10.63900	0.00000	11.88827	12.08706	160760.06239	NaN	10.35667	0.01041	0.01041	415.27498	10.63567			414.26175	C11171		414.27460
239	358.24170	358.24170	358.24161	12.91900	12.91900	12.93600	0.00000	11.96832	12.16004	173542.65948	NaN	8.61998	0.01035	0.01035	358.24167	12.92467	C07360		357.23040	C08707		357.23040
333	86.09744	86.09744	86.09728	4.63900	4.63900	3.92600	0.00000	12.00868	12.75295	238187.86492	NaN	8.75036	0.01142	0.01142	86.09738	4.40133	C03219		85.08915	C01746		85.08910
202	458.34845	458.34845	458.34854	12.22400	12.22400	12.26400	0.00000	12.03881	12.14404	178335.74934	NaN	10.47616	0.00914	0.00914	458.34848	12.23733			457.39197			457.39197
231	391.28479	391.28519	391.28494	16.02400	15.93400	15.97500	12.31793	12.05085	12.21700	186078.45613	223669.73987	9.92132	0.00923	0.00923	391.28497	15.97767			390.27701			390.27701
183	502.37512	502.37512	502.37555	12.14200	12.14200	12.18200	0.00000	12.06663	12.32936	198391.38254	NaN	9.44923	0.01032	0.01032	502.37526	12.15533			501.38518	C06999	HMDB05030	501.28791
66	736.56097	736.56097	736.56207	20.46900	20.46900	20.46200	0.00000	12.09923	12.27016	195770.35577	NaN	12.41621	0.01083	0.01083	736.56134	20.46667			735.54137			735.54137
130	590.40216	590.40216	590.40234	11.42300	11.42300	11.46400	0.00000	12.13347	12.28582	200715.62826	NaN	10.44159	0.01028	0.01028	590.40222	11.43667			589.37435			589.47060
64	748.59070	748.59070	748.59381	21.57600	21.57600	21.56900	0.00000	12.13875	12.38761	211752.96044	NaN	11.28735	0.01005	0.01005	748.59174	21.57367		HMDB07937	747.57782		HMDB08033	747.57782
247	330.21072	330.21072	330.21069	11.43500	11.43500	11.45200	0.00000	12.15877	12.36335	211304.88867	NaN	9.25217	0.00923	0.00923	330.21071	11.44067	C08687		329.19910	C12580		329.19910
195	480.33643	480.33643	480.33627	11.61150	11.61150	11.65200	0.00000	12.17569	12.31981	208511.68588	NaN	10.52067	0.01059	0.01059	480.33638	11.62500			479.33754			479.33754
10	986.66327	986.66327	986.66486	11.57600	11.57600	11.61700	0.00000	12.19424	12.34145	212744.62663	NaN	9.14422	0.01119	0.01119	986.66380	11.58967			985.84381			985.84386
35	850.62909	850.62909	850.63190	22.04700	22.04700	22.01700	0.00000	12.19634	12.40799	220172.73355	NaN	7.79288	0.00957	0.00957	850.63003	22.03700			849.62471			849.62471
60	765.59552	765.59552	765.59699	21.78800	21.78800	21.76900	0.00000	12.25483	12.38155	223728.84318	NaN	10.71841	0.01024	0.01024	765.59601	21.78167			764.59308			764.59308
39	832.65466	832.65466	832.65595	21.80000	21.80000	21.74600	0.00000	12.26157	12.43911	231039.03074	NaN	10.35110	0.00905	0.00905	832.65509	21.78200			831.63527			831.63527
97	695.35944	695.35944	695.35992	13.60200	13.60200	13.65400	0.00000	12.26187	12.38758	225195.84904	NaN	9.28338	0.01074	0.01074	695.35960	13.61933	C08692		694.34655	C08681		694.34650
184	502.34967	502.34967	502.34961	11.58800	11.58800	11.61700	0.00000	12.31529	12.46407	240308.95807	NaN	10.35562	0.00919	0.00919	502.34965	11.59767			501.38518	C06999	HMDB05030	501.28791
27	890.65912	890.65912	890.66034	21.04600	21.04600	21.01600	0.00000	12.33144	12.64769	265551.85789	NaN	10.54862	0.00874	0.00874	890.65953	21.03600		HMDB04834	889.64905		HMDB11591	889.64905
16	942.63751	942.63751	942.63837	11.62300	11.62300	11.65200	0.00000	12.34205	12.49741	247639.89665	NaN	10.14218	0.00913	0.00913	942.63780	11.63267			941.49975			
103	678.50769	678.50769	678.50879	20.50400	20.50400	20.48600	0.00000	12.40351	12.65194	275880.91873	NaN	10.92705	0.01184	0.01184	678.50806	20.49800		HMDB07866	677.49957		HMDB08890	677.49957
217	429.29080	429.29080	429.29050	11.42300	11.42300	11.44000	0.00000	12.41630	12.56198	265439.63216	NaN	11.67088	0.00783	0.00783	429.29070	11.42867			428.27737			428.27737
244	344.22641	344.22641	344.22635	12.20100	12.20100	12.21700	0.00000	12.43100	12.61877	275098.52265	NaN	11.48124	0.00918	0.00918	344.22639	12.20633	C07879		343.22598	C07879		343.22600
51	792.62335	792.62335	792.62512	22.94200	22.94200	22.91200	0.00000	12.43705	12.58848	271785.56244	NaN	9.56488	0.01015	0.01015	792.62394	22.93200			791.60397			791.60397
204	457.32138	457.32138	457.32187	12.93100	12.93100	12.94800	0.00000	12.44347	12.61654	276510.30536	NaN	9.99407	0.00898	0.00898	457.32154	12.93667			456.30509			456.30509
152	551.50403	551.50403	551.50513	21.02200	21.02200	20.98000	0.00000	12.45972	12.73551	295852.34489	NaN	10.43296	0.01112	0.01112	551.50439	21.00800			550.49611	C13864		550.49610
98	692.52301	692.52301	692.52551	21.61100	21.61100	21.59300	0.00000	12.47132	12.75529	300531.31677	NaN	9.49009	0.01023	0.01023	692.52384	21.60500			691.51521			691.51521
58	776.62225	776.62225	776.62549	22.35300	22.35300	22.33500	0.00000	12.47292	12.70026	292607.72287	NaN	10.30980	0.01231	0.01231	776.62333	22.34700		HMDB07944	775.60913		HMDB08264	775.60913
50	794.56574	794.56574	794.56726	19.89200	19.89200	19.85000	0.00000	12.47844	12.71592	295723.59587	NaN	9.83832	0.00962	0.00962	794.56624	19.87800			793.56211			793.56211
25	898.61023	898.61023	898.61139	11.65900	11.65900	11.69900	0.00000	12.49372	12.65878	289598.47557	NaN	9.85470	0.00918	0.00918	898.61062	11.67233			897.64583			897.64583
68	734.57044	734.57044	734.57178	22.93100	22.93100	22.91200	0.00000	12.50170	12.82356	315725.80828	NaN	10.77780	0.00791	0.00791	734.57088	22.92467			733.56216			733.56216
9	991.76892	991.76892	991.77124	24.07300	24.07300	24.04300	0.00000	12.50924	12.74738	305073.12540	NaN	9.84544	0.01115	0.01115	991.76969	24.06300			990.86151			990.86151
212	443.30634	443.30634	443.30627	12.20100	12.20100	12.21700	0.00000	12.51060	12.67253	294067.37966	NaN	10.49682	0.01071	0.01071	443.30632	12.20633			442.30829			442.30829
161	546.37573	546.37573	546.37628	11.49400	11.49400	11.53400	0.00000	12.51243	12.63864	289392.34503	NaN	11.00583	0.00937	0.00937	546.37592	11.50733		HMDB10393	545.34815		HMDB10394	545.34815
226	410.37488	410.37488	410.37479	13.64900	13.64900	13.70100	0.00000	12.54517	12.70696	304390.19827	NaN	10.07078	0.01077	0.01077	410.37485	13.66633			409.39197			409.39198
173	524.36469	524.36469	524.36554	11.54100	11.54100	11.59300	0.00000	12.57032	12.73720	312939.11087	NaN	8.62199	0.01013	0.01013	524.36497	11.55833			523.36375		HMDB10384	523.36375
241	350.17661	350.17661	350.17575	7.40700	7.40700	7.41200	0.00000	12.57662	12.69898	307981.93020	NaN	11.75636	0.00972	0.00972	350.17632	7.40867	C18411		349.16780	C18411		349.16779
159	550.62927	550.62885	550.62994	22.38400	22.18900	22.22900	14.21600	12.60355	12.86497	339169.93469	1492558.57036	10.05927	0.01001	0.01001	550.62935	22.26733			549.51207			
33	854.58600	854.58600	854.58508	11.70600	11.70600	11.74600	0.00000	12.61349	12.75685	322922.03798	NaN	9.78199	0.01036	0.01036	854.58569	11.71933			853.58323			853.58323
178	520.38556	520.38556	520.38538	9.65700	9.65700	9.68500	0.00000	12.62485	12.77924	328418.61260	NaN	8.25008	0.01187	0.01187	520.38550	9.66633			519.36888			519.36884
153	551.50494	551.50494	551.50513	24.37900	24.37900	24.33700	0.00000	12.65270	13.00656	373110.39096	NaN	10.25842	0.00867	0.00867	551.50501	24.36500			550.49611	C13864		550.49610
44	808.58203	808.58203	808.58423	20.44500	20.44500	20.40300	0.00000	12.71143	12.84974	355252.86113	NaN	10.35892	0.01157	0.01157	808.58276	20.43100		HMDB07989	807.57776		HMDB07990	807.57776
43	810.55920	810.55920	810.56030	11.75300	11.75300	11.79300	0.00000	12.71617	12.86590	358984.85431	NaN	11.30306	0.00892	0.00892	810.55957	11.76633		HMDB12394	809.52069		HMDB12404	809.52069
162	546.40149	546.40149	546.40192	12.07100	12.07100	12.12300	0.00000	12.76761	12.95017	384188.99019	NaN	11.01254	0.01081	0.01081	546.40163	12.08833		HMDB10393	545.34815		HMDB10394	545.34815
274	176.13445	176.13445	176.13611	1.40000	1.40000	1.38100	0.00000	12.78397	12.88673	375249.04436	NaN	10.65202	0.01117	0.01117	176.13500	1.39367	C05575		175.13208	C18174		175.13210
61	762.59320	762.59320	762.60169	21.77650	21.77650	21.76900	0.00000	12.81164	12.93731	390222.97011	NaN	9.40485	0.00867	0.00867	762.59603	21.77400			761.59341			761.59341
59	766.53284	766.53284	766.53363	11.80000	11.80000	11.84000	0.00000	12.81902	12.96298	396727.01872	NaN	8.82089	0.01154	0.01154	766.53310	11.81333			765.53081			765.53081
73	722.50690	722.50690	722.50726	11.85900	11.85900	11.89900	0.00000	12.88976	13.03702	426508.27477	NaN	10.18217	0.01057	0.01057	722.50702	11.87233			721.50460		HMDB09215	721.50464
154	551.50476	551.50476	551.50549	20.61000	20.61000	20.56800	0.00000	12.90323	13.18243	461773.10517	NaN	9.22598	0.00815	0.00815	551.50501	20.59600			550.49611	C13864		550.49610
37	836.61316	836.61316	836.61517	21.51700	21.51700	21.48700	0.00000	12.92815	13.09475	447508.97071	NaN	9.72625	0.01021	0.01021	836.61383	21.50700		HMDB08055	835.60906		HMDB08056	835.60906
131	590.42731	590.42731	590.42822	12.01200	12.01200	12.05200	0.00000	12.93852	13.11711	454891.75865	NaN	10.79438	0.01007	0.01007	590.42761	12.02533			589.37435			589.47060
104	678.47980	678.47980	678.48151	11.90600	11.90600	11.94600	0.00000	12.97483	13.12398	464818.88450	NaN	10.15990	0.00978	0.00978	678.48037	11.91933			677.46312			677.49951
118	634.45361	634.45361	634.45422	11.95300	11.95300	11.99400	0.00000	12.99277	13.16005	477542.73106	NaN	8.45815	0.00943	0.00943	634.45382	11.96667			633.43696			633.43696
208	449.33807	449.33920	449.33875	16.02400	15.92300	15.97500	13.51573	13.11713	13.25156	531970.11524	740978.15371	11.45001	0.01088	0.01088	449.33867	15.97400			448.33526			448.33526
155	551.50501	551.50501	551.50543	24.08500	24.08500	24.05400	0.00000	13.12854	13.49376	603891.65487	NaN	10.52534	0.01076	0.01076	551.50515	24.07467			550.49611	C13864		550.49610
92	720.55487	720.55487	720.55731	22.35300	22.35300	22.33500	0.00000	13.19402	13.44997	610475.89049	NaN	8.84810	0.00988	0.00988	720.55569	22.34700		HMDB07935	719.54651		HMDB07967	719.54651
275	127.13206	127.13206	127.12402	27.44200	27.44200	27.42300	0.00000	13.28416	13.50859	657612.49848	NaN	9.89603	0.00904	0.00904	127.12938	27.43567	C07287		126.10450		HMDB06024	126.10447
276	127.12364	127.12364	127.12347	3.26100	3.26100	3.57200	0.00000	13.28487	13.81040	765001.46393	NaN	10.39392	0.00977	0.00977	127.12359	3.36467	C07287		126.10450		HMDB06024	126.10447
91	721.50855	721.50946	721.51001	20.72400	20.63400	20.62700	15.43091	13.37844	13.50305	687447.46646	5029873.57168	9.05687	0.00836	0.00836	721.50934	20.66167		HMDB10571	720.49414		HMDB10585	720.49414
207	452.32361	452.32361	452.32312	9.65700	9.65700	9.68500	0.00000	13.63908	13.73740	880495.44468	NaN	9.57550	0.01095	0.01095	452.32345	9.66633			451.31988	C05150		451.31990
301	118.10165	118.08730	118.08736	1.37200	1.40000	1.39300	10.47911	13.67830	13.83214	941493.62745	35564.87093	8.71363	0.00967	0.00967	118.09210	1.38833	C00183	HMDB00883	117.07900	C00431	HMDB03355	117.07900
41	822.59863	822.59863	822.60004	21.02200	21.02200	20.98000	0.00000	13.70996	13.89367	986396.80672	NaN	9.95942	0.00952	0.00952	822.59910	21.00800			821.59341			821.59341
277	127.13234	127.13234	127.12420	31.78800	31.78800	31.68700	0.00000	13.94918	14.04055	1196442.77517	NaN	10.81934	0.01161	0.01161	127.12963	31.75433	C07287		126.10450		HMDB06024	126.10447
94	706.53992	706.53992	706.54205	21.75300	21.75300	21.74600	0.00000	14.02049	14.26290	1385666.59886	NaN	9.16291	0.01008	0.01008	706.54063	21.75067		HMDB07869	705.53088		HMDB07934	705.53088
188	493.34992	493.34992	493.34946	9.65700	9.65700	9.68500	0.00000	14.14634	14.30342	1505865.11900	NaN	10.16140	0.01096	0.01096	493.34976	9.66633			492.32530			492.32528
335	86.09738	86.09746	86.09742	39.91000	39.91500	39.90800	15.74165	14.15281	14.38869	1576552.26292	6862984.82929	9.72575	0.01060	0.01060	86.09742	39.91100	C03219		85.08915	C01746		85.08910
279	127.13213	127.13210	127.12415	33.70300	33.95500	33.63000	14.93621	14.18754	14.11798	1401085.22970	3066982.61400	9.99699	0.01057	0.01057	127.12946	33.76267	C07287		126.10450		HMDB06024	126.10447
280	127.13213	127.13229	127.12411	34.91600	35.40400	35.05500	15.25636	14.31576	14.32616	1657732.76024	4224261.62259	8.89067	0.01119	0.01119	127.12951	35.12500	C07287		126.10450		HMDB06024	126.10447
282	127.12366	127.12387	127.12370	2.11400	2.13000	2.11200	16.07704	14.48887	14.70599	2185662.13517	9597728.53052	8.22170	0.01074	0.01074	127.12374	2.11867	C07287		126.10450		HMDB06024	126.10447
281	127.12375	127.12367	127.12348	1.54900	1.51800	1.51100	16.12812	14.50368	14.66293	2155000.46861	10100715.88769	10.94923	0.01037	0.01037	127.12363	1.52600	C07287		126.10450		HMDB06024	126.10447
283	127.12364	127.12364	127.12353	1.07800	1.09400	1.09900	16.09121	14.55314	14.73275	2287433.01642	9734677.76084	8.03362	0.00881	0.00881	127.12360	1.09033	C07287		126.10450		HMDB06024	126.10447
284	127.13277	127.13277	127.12434	36.68700	36.68700	36.75100	0.00000	14.90226	14.95510	3043997.07448	NaN	10.66212	0.00963	0.00963	127.12996	36.70833	C07287		126.10450		HMDB06024	126.10447

Appendix - E - Proteomics Data HOV: COGs

CLASS	HOV	HOV-description	locus	locus-description	AV	AVR	CB	CBR	CB2D	iTRAQ
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0126	Tfu_0126 putative integral membrane protein						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0127	Tfu_0127 putative integral membrane protein						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0128	Tfu_0128 pilus assembly protein CpaF						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0185	Tfu_0185 hypothetical protein						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0381	Tfu_0381 sec-independent translocase						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0387	Tfu_0387 SecD/SecF/SecDF export membrane protein	19.33	19.06	19.71	19.81	23.88	1.494
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0477	Tfu_0477 ATPase	16.09	16.9	16.47	16.17	22	1.209
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0579	Tfu_0579 peptidase S49, protease IV:Peptidase S49, SppA	21.99	21.86	21.35	20.93	25.08	1.204
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0658	Tfu_0658 cell division transporter substrate-binding protein FtsY	17.49	17.82	18.43	17.13	21.68	1.002
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0661	Tfu_0661 Signal recognition particle protein	17.98	18.05	17.79	18.57	22.6	0.989
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0667	Tfu_0667 peptidase S26A, signal peptidase I						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0671	Tfu_0671 SMF protein						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0715	Tfu_0715 similar to Rossmann fold nucleotide-binding protein involved in DNA uptake						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_0761	Tfu_0761 translocase	17.24	16.09	18.23	18.27	23.03	
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_1089	Tfu_1089 hypothetical protein						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_1122	Tfu_1122 signal peptidase II					18.28	
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_1768	Tfu_1768 sec-independent periplasmic protein translocase						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_1769	Tfu_1769 Twin-arginine translocation protein TatA/E		16.06		13.71	20.32	
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2092	Tfu_2092 YajC	18.01	17.71	17.08		19.96	
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2133	Tfu_2133 hypothetical protein						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2193	Tfu_2193 ATP-dependent Clp protease proteolytic subunit	20.29	20.62	21.31	20.84	24.1	0.798
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2194	Tfu_2194 endopeptidase Clp	21.36	21.68	21.56	21.35	24.71	1.134
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2226	Tfu_2226 putative integral membrane protein		16.29			21.74	
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2271	Tfu_2271 hypothetical protein					15.94	
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2272	Tfu_2272 putative septum site-determining protein	16.98	17.27	14.31	15.22	20.58	0.787
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2273	Tfu_2273 hypothetical protein						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2274	Tfu_2274 putative secretory protein					18.11	
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2275	Tfu_2275 hypothetical protein						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2276	Tfu_2276 putative integral membrane protein						
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2490	Tfu_2490 translocase	20.43	20.09	21.04	20.76	24.79	
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2626	Tfu_2626 preprotein translocase SecY	15.35	15.15	18.03	17.57	21.22	0.946
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_2660	Tfu_2660 SecE subunit of protein translocation complex	16.2	15.85			16.67	
COG	U	Intracellular trafficking, secretion, and vesicular transport	Tfu_3114	Tfu_3114 hypothetical protein		14.35	14.79		19.03	
COG	R	General function prediction only	Tfu_0005	Tfu_0005 hypothetical protein						
COG	R	General function prediction only	Tfu_0009	Tfu_0009 putative transferase						
COG	R	General function prediction only	Tfu_0050	Tfu_0050 conserved hypothetical protein with similarity to AbiLI: abortive pha	15.72	15.02	15.33		21.18	
COG	R	General function prediction only	Tfu_0056	Tfu_0056 Tyrosine protein kinase:WD-40 repeat:Serine/threonine protein kinase						
COG	R	General function prediction only	Tfu_0061	Tfu_0061 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal					17.56	
COG	R	General function prediction only	Tfu_0072	Tfu_0072 putative quinone oxidoreductase	17.09	17.49	17.07	16.8	21.43	0.775
COG	R	General function prediction only	Tfu_0079	Tfu_0079 similar to hydrolase or acyltransferase (alpha/beta hydrolase superf	20.25	20.39	18.27	17.83	22.46	
COG	R	General function prediction only	Tfu_0081	Tfu_0081 3-hydroxybutyrate dehydrogenase	21.11	21.46	19.94	20.31	23.95	1.187
COG	R	General function prediction only	Tfu_0096	Tfu_0096 Phenazine biosynthesis PhzC/PhzF protein	16.45		13.57		20.67	
COG	R	General function prediction only	Tfu_0107	Tfu_0107 hypothetical protein	17.17	16.4	17.6	16.97	21.52	
COG	R	General function prediction only	Tfu_0116	Tfu_0116 putative hydrolase					18.08	
COG	R	General function prediction only	Tfu_0123	Tfu_0123 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal						
COG	R	General function prediction only	Tfu_0132	Tfu_0132 putative hydrolase					11.79	
COG	R	General function prediction only	Tfu_0140	Tfu_0140 putative integral membrane protein						
COG	R	General function prediction only	Tfu_0141	Tfu_0141 metal-dependent phosphohydrolase, HD region					18.39	
COG	R	General function prediction only	Tfu_0147	Tfu_0147 similar to Metal-dependent hydrolase	17.84	17.87	14.57	15	19.62	
COG	R	General function prediction only	Tfu_0162	Tfu_0162 b-ketoadipate enol-lactone hydrolase				14.37	20.07	
COG	R	General function prediction only	Tfu_0163	Tfu_0163 Tyrosine protein kinase:Serine/threonine protein kinase	15.1	14.83	14.91	14.78	20.69	
COG	R	General function prediction only	Tfu_0176	Tfu_0176 putative short chain dehydrogenase					17.3	
COG	R	General function prediction only	Tfu_0193	Tfu_0193 similar to Carbonic anhydrase/acetyltransferase isoleucine patch sup	17.63	16.71	16.02	14.98	20.92	

COG	R	General function prediction only	Tfu_0240	Tfu_0240 putative xanthine/uracil permease	17.93	17.55	18.36	18.34	21.43	
COG	R	General function prediction only	Tfu_0275	Tfu_0275 putative short chain dehydrogenase	19.38	19.27	18.64	18.26	23.3	
COG	R	General function prediction only	Tfu_0298	Tfu_0298 hypothetical protein						
COG	R	General function prediction only	Tfu_0321	Tfu_0321 hypothetical protein					15.44	
COG	R	General function prediction only	Tfu_0360	Tfu_0360 putative oxidoreductase					16.95	
COG	R	General function prediction only	Tfu_0361	Tfu_0361 oxidoreductase, short chain dehydrogenase/reductase family					14.74	
COG	R	General function prediction only	Tfu_0386	Tfu_0386 hypothetical protein					18.93	
COG	R	General function prediction only	Tfu_0397	Tfu_0397 ATPase						
COG	R	General function prediction only	Tfu_0402	Tfu_0402 ATPase	19.44	18.53	17.68	16.7	20.92	0.582
COG	R	General function prediction only	Tfu_0406	Tfu_0406 Tyrosine protein kinase:Serine/threonine protein kinase	15.36	16.04			20.09	0.675
COG	R	General function prediction only	Tfu_0409	Tfu_0409 ABC transporter, ATP-binding subunit				14.91	20	
COG	R	General function prediction only	Tfu_0426	Tfu_0426 MazG, bacterial			13.43		19.98	
COG	R	General function prediction only	Tfu_0439	Tfu_0439 putative sugar acetyltransferase						
COG	R	General function prediction only	Tfu_0442	Tfu_0442 von Willebrand factor, type A						
COG	R	General function prediction only	Tfu_0454	Tfu_0454 Tyrosine protein kinase:Serine/threonine protein kinase					16.34	
COG	R	General function prediction only	Tfu_0469	Tfu_0469 hypothetical protein	15.96	16.6			19.23	
COG	R	General function prediction only	Tfu_0496	Tfu_0496 Conserved hypothetical protein 730	18.3	17.9	19.29	19.3	23.28	1.271
COG	R	General function prediction only	Tfu_0500	Tfu_0500 Tyrosine protein kinase:Serine/threonine protein kinase	16.56	16			20.28	
COG	R	General function prediction only	Tfu_0508	Tfu_0508 ATP-binding protein involved in chromosome partitioning					18.22	1.361
COG	R	General function prediction only	Tfu_0509	Tfu_0509 hypothetical protein		14.46	14.87		20.16	1.408
COG	R	General function prediction only	Tfu_0511	Tfu_0511 phosphoesterase PHP, N-terminal						
COG	R	General function prediction only	Tfu_0512	Tfu_0512 similar to Zn-dependent hydrolase including glyoxylases	17.87	17.61	18.82	18.28	22.55	
COG	R	General function prediction only	Tfu_0513	Tfu_0513 putative hydrolase					17.33	
COG	R	General function prediction only	Tfu_0533	Tfu_0533 similar to metal-dependent hydrolase						
COG	R	General function prediction only	Tfu_0535	Tfu_0535 hypothetical protein						
COG	R	General function prediction only	Tfu_0543	Tfu_0543 hypothetical protein			13.59	14.81	19.36	
COG	R	General function prediction only	Tfu_0552	Tfu_0552 hypothetical protein	16.41	15.3	15.91	15.63	20.32	
COG	R	General function prediction only	Tfu_0557	Tfu_0557 diacylglycerol kinase, catalytic region	17.83	17.28	18.34	17.87	22.19	1.054
COG	R	General function prediction only	Tfu_0569	Tfu_0569 hypothetical protein					16.63	1.359
COG	R	General function prediction only	Tfu_0577	Tfu_0577 HAD-superfamily hydrolase, subfamily IA, variant 1	15.04	16.24	17.06	16.18	21.77	1.066
COG	R	General function prediction only	Tfu_0578	Tfu_0578 putative reductase	14.53	14.06	14.22	14.23	18.82	1.061
COG	R	General function prediction only	Tfu_0588	Tfu_0588 ATPase						2.621
COG	R	General function prediction only	Tfu_0592	Tfu_0592 Tyrosine protein kinase:Serine/threonine protein kinase	18.18	17.59	17.18	17.09	21.25	
COG	R	General function prediction only	Tfu_0601	Tfu_0601 serine/threonine protein kinase	14.82	14.92	15.29		19.56	
COG	R	General function prediction only	Tfu_0619	Tfu_0619 hypothetical protein	18	17.8	17.81	17.81	22.14	
COG	R	General function prediction only	Tfu_0649	Tfu_0649 hypothetical protein					17.33	
COG	R	General function prediction only	Tfu_0663	Tfu_0663 hypothetical protein					19.3	
COG	R	General function prediction only	Tfu_0683	Tfu_0683 Conserved hypothetical protein 48						
COG	R	General function prediction only	Tfu_0689	Tfu_0689 putative hydrolase	14.4					
COG	R	General function prediction only	Tfu_0701	Tfu_0701 Tyrosine protein kinase:Serine/threonine protein kinase	18.86	18.29	16.43	15.99	22.51	0.6
COG	R	General function prediction only	Tfu_0712	Tfu_0712 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal					12.98	
COG	R	General function prediction only	Tfu_0746	Tfu_0746 hypothetical protein						
COG	R	General function prediction only	Tfu_0751	Tfu_0751 hypothetical protein						
COG	R	General function prediction only	Tfu_0757	Tfu_0757 regulatory protein, LuxR:TPR repeat						
COG	R	General function prediction only	Tfu_0758	Tfu_0758 regulatory protein, LuxR						
COG	R	General function prediction only	Tfu_0760	Tfu_0760 putative ATP/GTP-binding protein					15.52	
COG	R	General function prediction only	Tfu_0769	Tfu_0769 hypothetical protein					15.06	
COG	R	General function prediction only	Tfu_0785	Tfu_0785 mitochondrial processing peptidase					18.09	0.986
COG	R	General function prediction only	Tfu_0792	Tfu_0792 putative hydrolase of the metallo-beta-lactamase superfamily	19.38	19.05	18.75	18.41	22.78	1.171
COG	R	General function prediction only	Tfu_0797	Tfu_0797 CinA, C-terminal					17.18	
COG	R	General function prediction only	Tfu_0801	Tfu_0801 probable acetyltransferase						
COG	R	General function prediction only	Tfu_0804	Tfu_0804 RecA regulator RecX					15.98	
COG	R	General function prediction only	Tfu_0805	Tfu_0805 metal-dependent phosphohydrolase, HD region					17.98	
COG	R	General function prediction only	Tfu_0820	Tfu_0820 Small GTP-binding protein domain			12.64	12.78	19.31	
COG	R	General function prediction only	Tfu_0822	Tfu_0822 hypothetical protein						
COG	R	General function prediction only	Tfu_0825	Tfu_0825 ComEC/Rec2-related protein						
COG	R	General function prediction only	Tfu_0843	Tfu_0843 putative protein kinase C inhibitor (HIT family	16.7	16.41		15.7	19.5	0.726
COG	R	General function prediction only	Tfu_0845	Tfu_0845 hypothetical protein			15.25	14.89	19.08	
COG	R	General function prediction only	Tfu_0846	Tfu_0846 hypothetical protein			15.34		20.56	

COG	R	General function prediction only	Tfu_0848	Tfu_0848 GTP-binding protein Era		13.43	14.99		20.75	
COG	R	General function prediction only	Tfu_0862	Tfu_0862 HylII					15.53	
COG	R	General function prediction only	Tfu_0874	Tfu_0874 Alpha/beta hydrolase	16.84	15.52	17.31	18.48	22.22	0.937
COG	R	General function prediction only	Tfu_0882	Tfu_0882 hypothetical protein						
COG	R	General function prediction only	Tfu_0885	Tfu_0885 putative glutathione-dependent aldehyde dehydrogenase						
COG	R	General function prediction only	Tfu_0888	Tfu_0888 ketoacyl reductase					17	
COG	R	General function prediction only	Tfu_0890	Tfu_0890 hypothetical protein						
COG	R	General function prediction only	Tfu_0895	Tfu_0895 hypothetical protein					15.66	
COG	R	General function prediction only	Tfu_0925	Tfu_0925 hypothetical protein	14.35	12.95		15.05	20.91	0.717
COG	R	General function prediction only	Tfu_0926	Tfu_0926 hypothetical protein					16.47	
COG	R	General function prediction only	Tfu_0941	Tfu_0941 hypothetical protein					18.87	
COG	R	General function prediction only	Tfu_0943	Tfu_0943 putative ATP/GTP-binding protein					16.53	
COG	R	General function prediction only	Tfu_0956	Tfu_0956 putative phosphatase						
COG	R	General function prediction only	Tfu_0960	Tfu_0960 n-acylamino acid racemase : O-succinylbenzoate-CoA synthase					19.49	
COG	R	General function prediction only	Tfu_0966	Tfu_0966 caffeoyl-CoA O-methyltransferase		13.62			16.15	
COG	R	General function prediction only	Tfu_0970	Tfu_0970 NADPH-dependent F420 reductase	18.24	17.08	19.7	19.23	23.5	0.891
COG	R	General function prediction only	Tfu_0983	Tfu_0983 NAD+ synthase	16.91	16.85	17.72	17.22	22.21	0.82
COG	R	General function prediction only	Tfu_1026	Tfu_1026 hypothetical protein						
COG	R	General function prediction only	Tfu_1028	Tfu_1028 hypothetical protein	18.33	17.53	16.66	15.99	21.87	
COG	R	General function prediction only	Tfu_1034	Tfu_1034 hypothetical protein						
COG	R	General function prediction only	Tfu_1040	Tfu_1040 hypothetical protein						
COG	R	General function prediction only	Tfu_1041	Tfu_1041 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA		13.51			20.01	
COG	R	General function prediction only	Tfu_1084	Tfu_1084 serine/threonine protein kinase	14.81				19.13	
COG	R	General function prediction only	Tfu_1099	Tfu_1099 hypothetical protein						
COG	R	General function prediction only	Tfu_1100	Tfu_1100 putative regulatory protein						
COG	R	General function prediction only	Tfu_1115	Tfu_1115 hypothetical protein	15.62	16.69	16.19	13.82	20.84	
COG	R	General function prediction only	Tfu_1119	Tfu_1119 hypothetical protein	14.84	16.22	15.38		20.86	
COG	R	General function prediction only	Tfu_1124	Tfu_1124 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal						
COG	R	General function prediction only	Tfu_1141	Tfu_1141 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	R	General function prediction only	Tfu_1149	Tfu_1149 peptidase S16, lon N-terminal					15.29	
COG	R	General function prediction only	Tfu_1172	Tfu_1172 similar to methyltransferase		14.12			17.4	
COG	R	General function prediction only	Tfu_1174	Tfu_1174 glutamate synthase, NADH/NADPH, small subunit 1						
COG	R	General function prediction only	Tfu_1178	Tfu_1178 peptidase C56, PfpI					15.89	
COG	R	General function prediction only	Tfu_1187	Tfu_1187 hypothetical protein					18.5	
COG	R	General function prediction only	Tfu_1193	Tfu_1193 similar to GTPase	16.85	16.47	15.45		20.59	
COG	R	General function prediction only	Tfu_1195	Tfu_1195 putative regulator					17.25	
COG	R	General function prediction only	Tfu_1200	Tfu_1200 hypothetical protein			14.4	14.71	20.54	
COG	R	General function prediction only	Tfu_1210	Tfu_1210 GTP-binding protein EngA	16.26	15.44	17.76	17.39	22.44	1.024
COG	R	General function prediction only	Tfu_1221	Tfu_1221 hypothetical protein						
COG	R	General function prediction only	Tfu_1224	Tfu_1224 putative 3-oxoacyl-(acyl-carrier protein) reductase						
COG	R	General function prediction only	Tfu_1230	Tfu_1230 hypothetical protein						
COG	R	General function prediction only	Tfu_1236	Tfu_1236 putative reductase						
COG	R	General function prediction only	Tfu_1239	Tfu_1239 putative hydrolase						
COG	R	General function prediction only	Tfu_1242	Tfu_1242 short chain dehydrogenase					18.48	
COG	R	General function prediction only	Tfu_1250	Tfu_1250 hypothetical protein	16.02	15.73	17.23	17.11	22.06	0.98
COG	R	General function prediction only	Tfu_1260	Tfu_1260 maltose O-acetyltransferase	17.34	17.54		16.06	20.06	
COG	R	General function prediction only	Tfu_1263	Tfu_1263 hypothetical protein						
COG	R	General function prediction only	Tfu_1273	Tfu_1273 putative oxidoreductase						
COG	R	General function prediction only	Tfu_1276	Tfu_1276 alcohol dehydrogenase	18.91	18.85	17.84	17.04	22.33	1.13
COG	R	General function prediction only	Tfu_1279	Tfu_1279 short chain dehydrogenase					16.87	
COG	R	General function prediction only	Tfu_1283	Tfu_1283 probable short-chain type dehydrogenase/reductase						
COG	R	General function prediction only	Tfu_1297	Tfu_1297 amidohydrolase family protein						
COG	R	General function prediction only	Tfu_1298	Tfu_1298 2-deoxy-D-gluconate 3-dehydrogenase	15.48	14.84		13.51	17.6	
COG	R	General function prediction only	Tfu_1328	Tfu_1328 hypothetical protein						
COG	R	General function prediction only	Tfu_1333	Tfu_1333 hypothetical protein						
COG	R	General function prediction only	Tfu_1342	Tfu_1342 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	R	General function prediction only	Tfu_1350	Tfu_1350 hypothetical protein						
COG	R	General function prediction only	Tfu_1354	Tfu_1354 transmembrane transport protein						
COG	R	General function prediction only	Tfu_1367	Tfu_1367 hypothetical protein	19.6	19.51	20.09	19.92	24.2	0.919

COG	R	General function prediction only	Tfu_1368	Tfu_1368 hypothetical protein	19.62	19.42	20.1	20.36	23.98	1.045
COG	R	General function prediction only	Tfu_1376	Tfu_1376 hypothetical protein						
COG	R	General function prediction only	Tfu_1378	Tfu_1378 helix-turn-helix motif					14.23	
COG	R	General function prediction only	Tfu_1392	Tfu_1392 hypothetical protein					17.09	
COG	R	General function prediction only	Tfu_1410	Tfu_1410 O-succinylbenzoate synthase					15.48	
COG	R	General function prediction only	Tfu_1418	Tfu_1418 hypothetical protein	18.89	18.42	20.57	20.44	23.75	0.572
COG	R	General function prediction only	Tfu_1420	Tfu_1420 hypothetical protein	16.65	17.03			16.02	
COG	R	General function prediction only	Tfu_1425	Tfu_1425 hypothetical protein						
COG	R	General function prediction only	Tfu_1430	Tfu_1430 putative ATP/GTP-binding protein					15.81	
COG	R	General function prediction only	Tfu_1432	Tfu_1432 hypothetical protein	16.74	17.98	17.57	18.36	21.6	1.179
COG	R	General function prediction only	Tfu_1444	Tfu_1444 hypothetical protein						
COG	R	General function prediction only	Tfu_1459	Tfu_1459 hypothetical protein	16.4	16.48	16.64	15.83	21.56	1.633
COG	R	General function prediction only	Tfu_1461	Tfu_1461 von Willebrand factor, type A					17.39	
COG	R	General function prediction only	Tfu_1466	Tfu_1466 short-chain alcohol dehydrogenase						
COG	R	General function prediction only	Tfu_1469	Tfu_1469 hypothetical protein						
COG	R	General function prediction only	Tfu_1472	Tfu_1472 short-chain dehydrogenase/reductase (SDR) family protein						
COG	R	General function prediction only	Tfu_1474	Tfu_1474 short chain dehydrogenase						
COG	R	General function prediction only	Tfu_1485	Tfu_1485 hypothetical protein						
COG	R	General function prediction only	Tfu_1489	Tfu_1489 oxidoreductase						
COG	R	General function prediction only	Tfu_1498	Tfu_1498 putative flavin-dependent reductase						
COG	R	General function prediction only	Tfu_1499	Tfu_1499 hypothetical protein						
COG	R	General function prediction only	Tfu_1510	Tfu_1510 phosphoglycolate phosphatase						
COG	R	General function prediction only	Tfu_1514	Tfu_1514 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	R	General function prediction only	Tfu_1526	Tfu_1526 ribonuclease Z					18.58	
COG	R	General function prediction only	Tfu_1535	Tfu_1535 ankyrin					15.79	
COG	R	General function prediction only	Tfu_1540	Tfu_1540 putative hydrolase					17.37	
COG	R	General function prediction only	Tfu_1578	Tfu_1578 CRISPR-associated TM1811 family protein	18.63	17.81	16.5	16.59	21.04	1.15
COG	R	General function prediction only	Tfu_1593	Tfu_1593 cRISPR-associated helicase Cas3, core	16.53	15.75	14.94	15.67	20.59	
COG	R	General function prediction only	Tfu_1601	Tfu_1601 CRISPR-associated helicase Cas3, core					15.96	
COG	R	General function prediction only	Tfu_1625	Tfu_1625 hypothetical protein						
COG	R	General function prediction only	Tfu_1639	Tfu_1639 similar to glycosyltransferase						
COG	R	General function prediction only	Tfu_1644	Tfu_1644 hypothetical protein	20.36	20.05	18.51	17.42	23.26	
COG	R	General function prediction only	Tfu_1653	Tfu_1653 chloride peroxidase						
COG	R	General function prediction only	Tfu_1658	Tfu_1658 Tyrosine protein kinase:Serine/threonine protein kinase:Sel1-like repeat						
COG	R	General function prediction only	Tfu_1660	Tfu_1660 similar to dehydrogenase						
COG	R	General function prediction only	Tfu_1670	Tfu_1670 putative acetyltransferase					18.3	
COG	R	General function prediction only	Tfu_1672	Tfu_1672 putative oxidoreductase	17.06	17.08	17.14	17.01	21.68	1.005
COG	R	General function prediction only	Tfu_1676	Tfu_1676 MoxR-like ATPase					16.26	
COG	R	General function prediction only	Tfu_1677	Tfu_1677 hypothetical protein						
COG	R	General function prediction only	Tfu_1679	Tfu_1679 HAD-superfamily hydrolase subfamily IA, variant 3:HAD-superfamily	18.12	17.54	17.74	17.68	21.01	
COG	R	General function prediction only	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
COG	R	General function prediction only	Tfu_1685	Tfu_1685 hypothetical protein					15.46	
COG	R	General function prediction only	Tfu_1686	Tfu_1686 hypothetical protein						
COG	R	General function prediction only	Tfu_1687	Tfu_1687 2,5-didehydrogluconate reductase	19.87	19.39	15.9	16.75	21.51	0.632
COG	R	General function prediction only	Tfu_1694	Tfu_1694 hypothetical protein						
COG	R	General function prediction only	Tfu_1699	Tfu_1699 putative hydrolase						
COG	R	General function prediction only	Tfu_1700	Tfu_1700 probable 3-oxoacyl-(acyl carrier protein) reductase						
COG	R	General function prediction only	Tfu_1705	Tfu_1705 putative oxidoreductase					16.5	
COG	R	General function prediction only	Tfu_1707	Tfu_1707 putative oxidoreductase					15.46	
COG	R	General function prediction only	Tfu_1717	Tfu_1717 putative racemase						
COG	R	General function prediction only	Tfu_1721	Tfu_1721 putative oxidoreductase						
COG	R	General function prediction only	Tfu_1722	Tfu_1722 hypothetical protein					14.24	
COG	R	General function prediction only	Tfu_1725	Tfu_1725 hypothetical protein	15.42	15.92			16.84	0.698
COG	R	General function prediction only	Tfu_1727	Tfu_1727 HAD-superfamily hydrolase subfamily IIB						
COG	R	General function prediction only	Tfu_1746	Tfu_1746 hypothetical protein	15.98	16.55	16.08	16.32	21.5	1.032
COG	R	General function prediction only	Tfu_1755	Tfu_1755 alcohol dehydrogenase					19.25	
COG	R	General function prediction only	Tfu_1756	Tfu_1756 Tyrosine protein kinase:Serine/threonine protein kinase	13.69	14.76	15.42	14.85	21.48	1.016
COG	R	General function prediction only	Tfu_1758	Tfu_1758 putative transporter	16.86	16.23			17.27	
COG	R	General function prediction only	Tfu_1761	Tfu_1761 similar to Protein affecting phage T7 exclusion by the F plasmid					16.38	

COG	R	General function prediction only	Tfu_1766	Tfu_1766 Conserved hypothetical protein 147						
COG	R	General function prediction only	Tfu_1784	Tfu_1784 hypothetical protein	14.4				19.3	
COG	R	General function prediction only	Tfu_1786	Tfu_1786 mandelate racemase/muconate lactonizing enzyme family	16.66	16.7	15.07	15.62	20.33	1.311
COG	R	General function prediction only	Tfu_1792	Tfu_1792 calcium-binding EF-hand	15.41	16.91	17.31	16.86	19.29	
COG	R	General function prediction only	Tfu_1793	Tfu_1793 hypothetical protein						
COG	R	General function prediction only	Tfu_1815	Tfu_1815 hypothetical protein					16.43	
COG	R	General function prediction only	Tfu_1819	Tfu_1819 ATPase components of various ABC-type transport systems contain c	20.66	20.33	19.05	19.09	23.49	2.058
COG	R	General function prediction only	Tfu_1824	Tfu_1824 hAD-superfamily hydrolase subfamily IA, variant 3:HAD-superfamily hydrolase, subfamily IA, variant 1						
COG	R	General function prediction only	Tfu_1826	Tfu_1826 hypothetical protein						
COG	R	General function prediction only	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
COG	R	General function prediction only	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
COG	R	General function prediction only	Tfu_1844	Tfu_1844 hypothetical protein					15.96	
COG	R	General function prediction only	Tfu_1873	Tfu_1873 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase					14.76	
COG	R	General function prediction only	Tfu_1875	Tfu_1875 hypothetical protein						
COG	R	General function prediction only	Tfu_1876	Tfu_1876 putative oxidoreductase					16.53	0.896
COG	R	General function prediction only	Tfu_1880	Tfu_1880 ATPase components of ABC transporters with duplicated ATPase domains					16.74	
COG	R	General function prediction only	Tfu_1881	Tfu_1881 hypothetical protein	17.96	18.27		16.35	21.12	0.846
COG	R	General function prediction only	Tfu_1884	Tfu_1884 hypothetical protein						
COG	R	General function prediction only	Tfu_1911	Tfu_1911 hypothetical protein						
COG	R	General function prediction only	Tfu_1912	Tfu_1912 hypothetical protein					18.28	
COG	R	General function prediction only	Tfu_1914	Tfu_1914 similar to metalloprotease						
COG	R	General function prediction only	Tfu_1915	Tfu_1915 ferredoxin/ferredoxin--NADP reductase, putative		13.93			20	
COG	R	General function prediction only	Tfu_1931	Tfu_1931 hypothetical protein						
COG	R	General function prediction only	Tfu_1950	Tfu_1950 hypothetical protein					20.19	1.345
COG	R	General function prediction only	Tfu_1954	Tfu_1954 similar to Zn-ribbon protein possibly nucleic acid-binding	18.07	16.4	18.15	17.67	22.45	0.894
COG	R	General function prediction only	Tfu_1960	Tfu_1960 hypothetical protein						
COG	R	General function prediction only	Tfu_1970	Tfu_1970 hypothetical protein						
COG	R	General function prediction only	Tfu_1981	Tfu_1981 hypothetical protein						
COG	R	General function prediction only	Tfu_1985	Tfu_1985 putative dioxygenase					17.16	
COG	R	General function prediction only	Tfu_1994	Tfu_1994 putative integral membrane protein						
COG	R	General function prediction only	Tfu_2020	Tfu_2020 hypothetical protein					18.72	1.016
COG	R	General function prediction only	Tfu_2027	Tfu_2027 hypothetical protein						
COG	R	General function prediction only	Tfu_2040	Tfu_2040 similar to Zn-dependent hydrolase including glyoxylases	16.2	16.28	15.24	16.07	20.58	
COG	R	General function prediction only	Tfu_2047	Tfu_2047 putative ATP/GTP-binding protein						
COG	R	General function prediction only	Tfu_2049	Tfu_2049 hypothetical protein			15.17	15.48	20.2	
COG	R	General function prediction only	Tfu_2068	Tfu_2068 putative integral membrane protein					16.18	
COG	R	General function prediction only	Tfu_2074	Tfu_2074 Tyrosine protein kinase:Serine/threonine protein kinase	18.52	18.73	17.5	17.42	22.55	0.999
COG	R	General function prediction only	Tfu_2075	Tfu_2075 Tyrosine protein kinase:Serine/threonine protein kinase	14.14				15.26	
COG	R	General function prediction only	Tfu_2087	Tfu_2087 possible hydrolase	15.2	14.79	14.34	13.62	17.81	1.028
COG	R	General function prediction only	Tfu_2105	Tfu_2105 hypothetical protein				14.7	19.77	
COG	R	General function prediction only	Tfu_2113	Tfu_2113 hypothetical protein					17.59	
COG	R	General function prediction only	Tfu_2116	Tfu_2116 YbhB and YbcL	19.38	19.18	17.34	18.02	21.84	
COG	R	General function prediction only	Tfu_2117	Tfu_2117 HAD-superfamily hydrolase subfamily IA, variant 3	15.86	16	14.36	14.56	20.08	0.869
COG	R	General function prediction only	Tfu_2125	Tfu_2125 putative hydrolase	17.23	15.72	15.82	16.54	21.15	
COG	R	General function prediction only	Tfu_2126	Tfu_2126 hypothetical protein	16.52	16.48	15.22	15.88	20.26	
COG	R	General function prediction only	Tfu_2165	Tfu_2165 hypothetical protein					17.45	
COG	R	General function prediction only	Tfu_2180	Tfu_2180 putative GTP-binding protein	16.93	16.66	17.15	17.29	21.45	0.942
COG	R	General function prediction only	Tfu_2201	Tfu_2201 hypothetical protein	16.74	15.98	18.07	17.72	22.35	
COG	R	General function prediction only	Tfu_2213	Tfu_2213 hypothetical protein						
COG	R	General function prediction only	Tfu_2215	Tfu_2215 similar to Truncated hemoglobins						
COG	R	General function prediction only	Tfu_2216	Tfu_2216 ATPase components of ABC transporters with duplicated ATPase dor	18.76	18.92	20.04	19.99	23.92	1.166
COG	R	General function prediction only	Tfu_2219	Tfu_2219 similar to GTPase	17.67	17.57	17.03	16.72	21.86	0.954
COG	R	General function prediction only	Tfu_2228	Tfu_2228 putative quinone oxidoreductase	18.91	19.37	18.34	18.58	21.72	0.952
COG	R	General function prediction only	Tfu_2229	Tfu_2229 Tyrosine protein kinase:Serine/threonine protein kinase		14.19			18.3	1.106
COG	R	General function prediction only	Tfu_2234	Tfu_2234 spermidine synthase						
COG	R	General function prediction only	Tfu_2294	Tfu_2294 phosphatase					14.18	
COG	R	General function prediction only	Tfu_2298	Tfu_2298 hypothetical protein						
COG	R	General function prediction only	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
COG	R	General function prediction only	Tfu_2314	Tfu_2314 similar to Uncharacterized conserved protein					17.71	

COG	R	General function prediction only	Tfu_2324	Tfu_2324 hypothetical protein					16.65	
COG	R	General function prediction only	Tfu_2349	Tfu_2349 peptidase S33, proline iminopeptidase 1	16.69	17.1	17.23	15.65	21	1.063
COG	R	General function prediction only	Tfu_2354	Tfu_2354 hypothetical protein						
COG	R	General function prediction only	Tfu_2361	Tfu_2361 Tyrosine protein kinase:Serine/threonine protein kinase	15.67	15.45	16.47	16.35	21.04	
COG	R	General function prediction only	Tfu_2362	Tfu_2362 putative proteinase	20.19	19.36	20.15	19.78	23.27	0.829
COG	R	General function prediction only	Tfu_2363	Tfu_2363 putative zinc proteinase	19.62	19.59	19.07	19.41	22.9	1.029
COG	R	General function prediction only	Tfu_2366	Tfu_2366 hypothetical protein	14.32		15.46		20.05	
COG	R	General function prediction only	Tfu_2370	Tfu_2370 Mov34/MPN/PAD-1	16.73	16.39	16.07	16.43	20.73	
COG	R	General function prediction only	Tfu_2375	Tfu_2375 Tyrosine protein kinase:Serine/threonine protein kinase	15.45	14.62		15.18	19.56	
COG	R	General function prediction only	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
COG	R	General function prediction only	Tfu_2397	Tfu_2397 hypothetical protein	13.95	15.51	14.43	15.4	19.9	
COG	R	General function prediction only	Tfu_2403	Tfu_2403 hypothetical protein	19.38	19.42	15.52		20.8	
COG	R	General function prediction only	Tfu_2437	Tfu_2437 peptidase M20D, amidohydrolase	19.51	19.04	18.35	17.96	22.85	0.958
COG	R	General function prediction only	Tfu_2445	Tfu_2445 hypothetical protein	15.38	14.96	17.07	16.78	20.71	
COG	R	General function prediction only	Tfu_2447	Tfu_2447 putative ATP/GTP-binding protein					16.8	
COG	R	General function prediction only	Tfu_2462	Tfu_2462 putative short chain dehydrogenase						
COG	R	General function prediction only	Tfu_2472	Tfu_2472 similar to flavoprotein						
COG	R	General function prediction only	Tfu_2482	Tfu_2482 similar to phosphatase	14.68				19.7	0.731
COG	R	General function prediction only	Tfu_2484	Tfu_2484 HAD-superfamily hydrolase subfamily IA, variant 3					18.76	
COG	R	General function prediction only	Tfu_2488	Tfu_2488 HAD-superfamily hydrolase subfamily IA, variant 3						
COG	R	General function prediction only	Tfu_2493	Tfu_2493 hypothetical protein						
COG	R	General function prediction only	Tfu_2500	Tfu_2500 ATPase	18.85	18.12	18.16	18.37	22.96	1.114
COG	R	General function prediction only	Tfu_2501	Tfu_2501 hypothetical protein		14.03			18.65	
COG	R	General function prediction only	Tfu_2507	Tfu_2507 Tyrosine protein kinase:Serine/threonine protein kinase	17.36	17.16	16.35	15.91	21.06	1.521
COG	R	General function prediction only	Tfu_2514	Tfu_2514 hypothetical protein	16.39	15.72		14.38	20.83	
COG	R	General function prediction only	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
COG	R	General function prediction only	Tfu_2531	Tfu_2531 putative glycosyltransferase					17.26	
COG	R	General function prediction only	Tfu_2545	Tfu_2545 hypothetical protein					16.2	
COG	R	General function prediction only	Tfu_2551	Tfu_2551 putative hydrolase						
COG	R	General function prediction only	Tfu_2564	Tfu_2564 peptidase M20D, amidohydrolase					20.11	
COG	R	General function prediction only	Tfu_2578	Tfu_2578 hypothetical protein						
COG	R	General function prediction only	Tfu_2592	Tfu_2592 putative phosphatase	13.93	15.27	14.31		19.57	
COG	R	General function prediction only	Tfu_2603	Tfu_2603 Ribosomal-protein-alanine acetyltransferase		13.04		14.23	19.75	
COG	R	General function prediction only	Tfu_2605	Tfu_2605 hypothetical protein	15.88	14.89			20.13	0.501
COG	R	General function prediction only	Tfu_2679	Tfu_2679 RarD protein						
COG	R	General function prediction only	Tfu_2713	Tfu_2713 hypothetical protein	16.32	15.94	18.45	18.08	22.26	
COG	R	General function prediction only	Tfu_2734	Tfu_2734 redox-sensing transcriptional repressor Rex	14.12	13.27			19.29	
COG	R	General function prediction only	Tfu_2739	Tfu_2739 putative acetyltransferase	18.06	18.1	17.74	17.44	21.61	
COG	R	General function prediction only	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
COG	R	General function prediction only	Tfu_2804	Tfu_2804 putative ATP/GTP-binding protein					20.54	
COG	R	General function prediction only	Tfu_2806	Tfu_2806 hypothetical protein						
COG	R	General function prediction only	Tfu_2814	Tfu_2814 putative dehydrogenase						
COG	R	General function prediction only	Tfu_2815	Tfu_2815 similar to hydrolase or acyltransferase (alpha/beta hydrolase superfamily)						
COG	R	General function prediction only	Tfu_2826	Tfu_2826 intracellular protease/amidase, putative	18.2	17.6	19.21	19.3	22.74	0.43
COG	R	General function prediction only	Tfu_2828	Tfu_2828 peptidase C56, PfpI						0.636
COG	R	General function prediction only	Tfu_2829	Tfu_2829 hypothetical protein						
COG	R	General function prediction only	Tfu_2845	Tfu_2845 Tyrosine protein kinase:Serine/threonine protein kinase		13.26		14.27	19.42	
COG	R	General function prediction only	Tfu_2852	Tfu_2852 putative integral membrane protein						
COG	R	General function prediction only	Tfu_2860	Tfu_2860 hypothetical protein	15.96	15.38			17.68	
COG	R	General function prediction only	Tfu_2862	Tfu_2862 Na+/solute symporter	19.41	18.76	19.51	19.24	22.62	
COG	R	General function prediction only	Tfu_2873	Tfu_2873 hypothetical protein	15.56	15.93	15.48	14.46	19.94	0.92
COG	R	General function prediction only	Tfu_2919	Tfu_2919 similar to metalloprotease						
COG	R	General function prediction only	Tfu_2920	Tfu_2920 hypothetical protein						
COG	R	General function prediction only	Tfu_2924	Tfu_2924 hypothetical protein	19.4	18.27	16.95	18.42	20.78	
COG	R	General function prediction only	Tfu_2931	Tfu_2931 hypothetical protein						
COG	R	General function prediction only	Tfu_2951	Tfu_2951 hypothetical protein				15.59	20.29	
COG	R	General function prediction only	Tfu_2997	Tfu_2997 hypothetical protein	15.4	15.6	15.36	15.19	20.52	1.169
COG	R	General function prediction only	Tfu_3025	Tfu_3025 putative alcohol dehydrogenase	18.7	19.04	16.64	17.19	21.72	
COG	R	General function prediction only	Tfu_3026	Tfu_3026 hypothetical protein					16.15	

COG	R	General function prediction only	Tfu_3027	Tfu_3027 putative reductase						
COG	R	General function prediction only	Tfu_3033	Tfu_3033 helix-turn-helix motif		14.2	19.08	18.85	22.95	1.556
COG	R	General function prediction only	Tfu_3043	Tfu_3043 HAD-superfamily hydrolase subfamily IA, variant 3:Beta-phosphoglucomutase hydrol			16.87	17.03	21.89	1.866
COG	R	General function prediction only	Tfu_3065	Tfu_3065 Tyrosine protein kinase:Serine/threonine protein kinase					18.02	
COG	R	General function prediction only	Tfu_3066	Tfu_3066 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA	19.07	19.31	18.37	17.91	22.14	0.98
COG	R	General function prediction only	Tfu_3068	Tfu_3068 Rhomboid family protein						
COG	R	General function prediction only	Tfu_3077	Tfu_3077 putative methylesterase						
COG	R	General function prediction only	Tfu_3080	Tfu_3080 similar to Uncharacterized protein SCO1/SenC/PrrC involved in biogenesis of respira			15.54	15.25	20.16	
COG	R	General function prediction only	Tfu_3084	Tfu_3084 hypothetical protein						
COG	R	General function prediction only	Tfu_3085	Tfu_3085 Rhodanese-like protein						
COG	R	General function prediction only	Tfu_3104	Tfu_3104 virulence factor MVIN-like	14.65	15.12	15.38	15.13	19.22	
COG	R	General function prediction only	Tfu_3113	Tfu_3113 single-stranded nucleic acid binding R3H	15.43	15.14	17.7		21.28	
COG	G	Carbohydrate transport and metabolism	Tfu_0003	Tfu_0003 6-phosphogluconate dehydrogenase	20.18	20.31	19.92	19.72	23.9	0.655
COG	G	Carbohydrate transport and metabolism	Tfu_0016	Tfu_0016 mannose-6-phosphate isomerase, type I						
COG	G	Carbohydrate transport and metabolism	Tfu_0046	Tfu_0046 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_0153	Tfu_0153 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_0169	Tfu_0169 nucleoside-diphosphate-sugar epimerase (UDP-glucose 4-epimerase	14.49	16.6	18.84	18.16	22.51	0.845
COG	G	Carbohydrate transport and metabolism	Tfu_0188	Tfu_0188 2-dehydro-3-deoxyphosphogluconate aldolase / 4-hydroxy-2-oxoglu	14.36				15.14	
COG	G	Carbohydrate transport and metabolism	Tfu_0189	Tfu_0189 putative PfkB-family carbohydrate kinase						
COG	G	Carbohydrate transport and metabolism	Tfu_0224	Tfu_0224 trehalose-phosphatase:HAD-superfamily hydrolase subfamily IIB	14.64	15.78	17.3	17.76	22.74	0.78
COG	G	Carbohydrate transport and metabolism	Tfu_0225	Tfu_0225 alpha,alpha-trehalose-phosphate synthase (UDP-forming)	19.68	19.62	20.81	20.85	24.46	1.199
COG	G	Carbohydrate transport and metabolism	Tfu_0242	Tfu_0242 putative integral membrane efflux protein						
COG	G	Carbohydrate transport and metabolism	Tfu_0259	Tfu_0259 ribokinase, bacterial					17.88	
COG	G	Carbohydrate transport and metabolism	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
COG	G	Carbohydrate transport and metabolism	Tfu_0341	Tfu_0341 citryl-CoA lyase	17.85	17.79	17.74	17.05	21.43	
COG	G	Carbohydrate transport and metabolism	Tfu_0367	Tfu_0367 putative transporter						
COG	G	Carbohydrate transport and metabolism	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
COG	G	Carbohydrate transport and metabolism	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
COG	G	Carbohydrate transport and metabolism	Tfu_0537	Tfu_0537 hypothetical protein					17.68	
COG	G	Carbohydrate transport and metabolism	Tfu_0542	Tfu_0542 histidinol-phosphate phosphatase, putative, inositol monophosphata	18.79	18.37	16.97	17.19	21.21	
COG	G	Carbohydrate transport and metabolism	Tfu_0580	Tfu_0580 chitinase II	17.05	17.75	15.71	15.95	21.45	
COG	G	Carbohydrate transport and metabolism	Tfu_0582	Tfu_0582 1,4-alpha-glucan branching enzyme					16.55	
COG	G	Carbohydrate transport and metabolism	Tfu_0583	Tfu_0583 putative pep2 protein						
COG	G	Carbohydrate transport and metabolism	Tfu_0584	Tfu_0584 alpha amylase, catalytic subdomain						
COG	G	Carbohydrate transport and metabolism	Tfu_0585	Tfu_0585 alpha amylase, catalytic subdomain						
COG	G	Carbohydrate transport and metabolism	Tfu_0586	Tfu_0586 alpha-glucan phosphorylase					15.86	
COG	G	Carbohydrate transport and metabolism	Tfu_0620	Tfu_0620 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_0624	Tfu_0624 hypothetical protein	14.9				17.67	
COG	G	Carbohydrate transport and metabolism	Tfu_0696	Tfu_0696 putative 6-phosphofructokinase : 1-phosphofructokinase						
COG	G	Carbohydrate transport and metabolism	Tfu_0753	Tfu_0753 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_0830	Tfu_0830 hypothetical protein					15.17	
COG	G	Carbohydrate transport and metabolism	Tfu_0831	Tfu_0831 multiple sugar transport system permease protein					15.83	
COG	G	Carbohydrate transport and metabolism	Tfu_0832	Tfu_0832 hypothetical protein	18.27	18.49	16.35	16.47	22.2	
COG	G	Carbohydrate transport and metabolism	Tfu_0833	Tfu_0833 alpha amylase, catalytic subdomain	15.71	15.55	14.92	15.54	20.77	0.845
COG	G	Carbohydrate transport and metabolism	Tfu_0843	Tfu_0843 putative protein kinase C inhibitor (HIT family	16.7	16.41		15.7	19.5	0.726
COG	G	Carbohydrate transport and metabolism	Tfu_0863	Tfu_0863 pyruvate phosphate dikinase	17.84	17.11	21.38	21.45	25.04	1.455
COG	G	Carbohydrate transport and metabolism	Tfu_0868	Tfu_0868 hypothetical protein					16.11	
COG	G	Carbohydrate transport and metabolism	Tfu_0901	Tfu_0901 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_0907	Tfu_0907 regulatory protein, DeoR					19.63	
COG	G	Carbohydrate transport and metabolism	Tfu_0915	Tfu_0915 beta-mannosidase	16.19	15.87	19.77	19.48	24.11	
COG	G	Carbohydrate transport and metabolism	Tfu_0928	Tfu_0928 fructokinase	18.37	17.96	18.63	18.42	22.16	0.898
COG	G	Carbohydrate transport and metabolism	Tfu_0934	Tfu_0934 hypothetical protein	22.95	22.9	23.76	23.39	26.25	2.077
COG	G	Carbohydrate transport and metabolism	Tfu_0935	Tfu_0935 multiple sugar transport system permease protein	16.27		17.74	17.07	21.52	0.973
COG	G	Carbohydrate transport and metabolism	Tfu_0936	Tfu_0936 multiple sugar transport system permease protein	12.91	13.62	17.29	16.44	20.46	1.159
COG	G	Carbohydrate transport and metabolism	Tfu_0937	Tfu_0937 beta-glucosidase	16.92	16.79	21.22	20.91	23.7	2.426
COG	G	Carbohydrate transport and metabolism	Tfu_0985	Tfu_0985 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1010	Tfu_1010 glycerate kinase			14.48		20.4	
COG	G	Carbohydrate transport and metabolism	Tfu_1012	Tfu_1012 putative carbohydrate kinase				14.19	20.45	
COG	G	Carbohydrate transport and metabolism	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	

COG	G	Carbohydrate transport and metabolism	Tfu_1037	Tfu_1037 phosphofructokinase	21.14	20.73	24.02	23.83	26.57	0.842
COG	G	Carbohydrate transport and metabolism	Tfu_1047	Tfu_1047 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1074	Tfu_1074 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
COG	G	Carbohydrate transport and metabolism	Tfu_1083	Tfu_1083 putative aldose-1-epimerase					18.23	
COG	G	Carbohydrate transport and metabolism	Tfu_1140	Tfu_1140 hypothetical protein					15.82	
COG	G	Carbohydrate transport and metabolism	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
COG	G	Carbohydrate transport and metabolism	Tfu_1212	Tfu_1212 archaeal fructose-1 6-bisphosphatase and related enzyme of inositol	14.95	15.73	15.51	15.72	20.15	0.894
COG	G	Carbohydrate transport and metabolism	Tfu_1233	Tfu_1233 putative transmembrane efflux protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1235	Tfu_1235 hypothetical protein			13.59	13.63	16.15	
COG	G	Carbohydrate transport and metabolism	Tfu_1285	Tfu_1285 citryl-CoA lyase						
COG	G	Carbohydrate transport and metabolism	Tfu_1295	Tfu_1295 putative membrane transport protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1313	Tfu_1313 putative citrate lyase beta subunit	20.71	20.33	20.94	21.03	24.43	1.292
COG	G	Carbohydrate transport and metabolism	Tfu_1345	Tfu_1345 hypothetical protein	14.93	14.98	18.11	17.98	22.45	1.156
COG	G	Carbohydrate transport and metabolism	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / phosphomannomutase	19.06	18.82	21.97	21.81	25.49	1.131
COG	G	Carbohydrate transport and metabolism	Tfu_1475	Tfu_1475 hypothetical protein	14.97	15.39			16.91	
COG	G	Carbohydrate transport and metabolism	Tfu_1476	Tfu_1476 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1477	Tfu_1477 TrapT family, DctM subunit, C4-dicarboxylate transport						
COG	G	Carbohydrate transport and metabolism	Tfu_1486	Tfu_1486 hypothetical protein					16.44	
COG	G	Carbohydrate transport and metabolism	Tfu_1575	Tfu_1575 putative sugar kinase protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1603	Tfu_1603 xylose isomerase	19.44	19.38	19.81	20.12	23.3	1.128
COG	G	Carbohydrate transport and metabolism	Tfu_1604	Tfu_1604 xylulokinase	16.69	16.85	17.01	17.12	22.06	
COG	G	Carbohydrate transport and metabolism	Tfu_1605	Tfu_1605 putative xylose repressor					15.44	
COG	G	Carbohydrate transport and metabolism	Tfu_1607	Tfu_1607 beta-glucosidase						
COG	G	Carbohydrate transport and metabolism	Tfu_1608	Tfu_1608 putative xylose repressor				12.13		
COG	G	Carbohydrate transport and metabolism	Tfu_1609	Tfu_1609 hypothetical protein					18.29	
COG	G	Carbohydrate transport and metabolism	Tfu_1610	Tfu_1610 putative transport system integral membrane protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1611	Tfu_1611 putative transport system integral membrane protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1612	Tfu_1612 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1613	Tfu_1613 putative alpha-glucosidase						
COG	G	Carbohydrate transport and metabolism	Tfu_1615	Tfu_1615 beta-galactosidase					16.26	
COG	G	Carbohydrate transport and metabolism	Tfu_1616	Tfu_1616 alpha-L-arabinofuranosidase	18.6	18.38			20.92	1.664
COG	G	Carbohydrate transport and metabolism	Tfu_1617	Tfu_1617 putative binding-protein-dependent transport protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1618	Tfu_1618 hypothetical protein					15.44	
COG	G	Carbohydrate transport and metabolism	Tfu_1619	Tfu_1619 hypothetical protein	22.73	22.95	21.17	20.85	24.52	1.352
COG	G	Carbohydrate transport and metabolism	Tfu_1621	Tfu_1621 hypothetical protein					16.91	
COG	G	Carbohydrate transport and metabolism	Tfu_1622	Tfu_1622 UDP-glucose 4-epimerase						
COG	G	Carbohydrate transport and metabolism	Tfu_1627	Tfu_1627 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1629	Tfu_1629 beta-glucosidase	20.15	19.64	19.92	19.43	23.45	1.12
COG	G	Carbohydrate transport and metabolism	Tfu_1652	Tfu_1652 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1668	Tfu_1668 sugar transporter						
COG	G	Carbohydrate transport and metabolism	Tfu_1702	Tfu_1702 hypothetical protein	20.15	19.13	18.05	17.45	22.1	
COG	G	Carbohydrate transport and metabolism	Tfu_1703	Tfu_1703 putative transport system permease ABC transporter protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1704	Tfu_1704 putative transport system permease ABC transporter protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1709	Tfu_1709 UDP-glucose-4-epimerase					17.2	
COG	G	Carbohydrate transport and metabolism	Tfu_1716	Tfu_1716 glycerone kinase	16	15.49	13.71		18.65	
COG	G	Carbohydrate transport and metabolism	Tfu_1719	Tfu_1719 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1728	Tfu_1728 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1734	Tfu_1734 drug resistance transporter Bcr/CflA subfamily						
COG	G	Carbohydrate transport and metabolism	Tfu_1736	Tfu_1736 hypothetical protein	15.35	15.73	14.87		19.98	1.067
COG	G	Carbohydrate transport and metabolism	Tfu_1750	Tfu_1750 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1760	Tfu_1760 HAD-superfamily hydrolase, subfamily IIA	21.89	21.93	21.45	21.86	24.86	1.072
COG	G	Carbohydrate transport and metabolism	Tfu_1763	Tfu_1763 ABC-type sugar transport systems ATPase components	22.15	21.91	22.51	21.98	25.88	1.102
COG	G	Carbohydrate transport and metabolism	Tfu_1794	Tfu_1794 major facilitator family transporter					15.82	
COG	G	Carbohydrate transport and metabolism	Tfu_1811	Tfu_1811 polyphosphate glucokinase/transcriptional regulator						
COG	G	Carbohydrate transport and metabolism	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
COG	G	Carbohydrate transport and metabolism	Tfu_1851	Tfu_1851 regulatory protein, DeoR	16.78	16.82	15.92		19.28	0.924
COG	G	Carbohydrate transport and metabolism	Tfu_1853	Tfu_1853 putative transporter						
COG	G	Carbohydrate transport and metabolism	Tfu_1854	Tfu_1854 regulatory protein, DeoR			15.82	15.05	20.7	

COG	G	Carbohydrate transport and metabolism	Tfu_1861	Tfu_1861 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1885	Tfu_1885 putative integral membrane protein					17.93	
COG	G	Carbohydrate transport and metabolism	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
COG	G	Carbohydrate transport and metabolism	Tfu_1911	Tfu_1911 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1920	Tfu_1920 putative ABC transporter transmembrane transport protein	15.44	16.24	17	17.75	21.57	1.079
COG	G	Carbohydrate transport and metabolism	Tfu_1921	Tfu_1921 ABC-type sugar transport system ATPase component	16.87	16.94	19.92	20.01	23.32	0.871
COG	G	Carbohydrate transport and metabolism	Tfu_1922	Tfu_1922 hypothetical protein	23.01	22.64	23.83	23.66	26.57	0.607
COG	G	Carbohydrate transport and metabolism	Tfu_1923	Tfu_1923 putative transcriptional repressor protein						
COG	G	Carbohydrate transport and metabolism	Tfu_1943	Tfu_1943 inositol-1(or 4)-monophosphatase	16.16	15.99			19.17	0.652
COG	G	Carbohydrate transport and metabolism	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
COG	G	Carbohydrate transport and metabolism	Tfu_1959	Tfu_1959 hypothetical protein					15.56	
COG	G	Carbohydrate transport and metabolism	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
COG	G	Carbohydrate transport and metabolism	Tfu_2003	Tfu_2003 transaldolase	20.04	20.08	21.54	21.1	24.47	1.211
COG	G	Carbohydrate transport and metabolism	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
COG	G	Carbohydrate transport and metabolism	Tfu_2005	Tfu_2005 glucose-6-phosphate 1-dehydrogenase	16.6	15.74	16.81	16.27	21.46	
COG	G	Carbohydrate transport and metabolism	Tfu_2006	Tfu_2006 hypothetical protein	17.33	16.81	17.2	17.26	21.54	0.522
COG	G	Carbohydrate transport and metabolism	Tfu_2007	Tfu_2007 6-phosphogluconolactonase	18.7	19.13	18.21	17.98	22.37	0.913
COG	G	Carbohydrate transport and metabolism	Tfu_2009	Tfu_2009 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
COG	G	Carbohydrate transport and metabolism	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
COG	G	Carbohydrate transport and metabolism	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, type I	23.03	22.77	25.37	25.33	28.17	1.113
COG	G	Carbohydrate transport and metabolism	Tfu_2033	Tfu_2033 inorganic polyphosphate/ATP-NAD kinase	16.3	16.08	15.21	15.52	19.8	
COG	G	Carbohydrate transport and metabolism	Tfu_2038	Tfu_2038 HAD-superfamily hydrolase, subfamily IIA					15.24	
COG	G	Carbohydrate transport and metabolism	Tfu_2105	Tfu_2105 hypothetical protein				14.7	19.77	
COG	G	Carbohydrate transport and metabolism	Tfu_2114	Tfu_2114 carbohydrate kinase, thermoresistant glucokinase	15.34		15.45	14.87	18.89	
COG	G	Carbohydrate transport and metabolism	Tfu_2129	Tfu_2129 putative sugar kinase					18.28	
COG	G	Carbohydrate transport and metabolism	Tfu_2168	Tfu_2168 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
COG	G	Carbohydrate transport and metabolism	Tfu_2176	Tfu_2176 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
COG	G	Carbohydrate transport and metabolism	Tfu_2205	Tfu_2205 glycoside hydrolase, family 77					15.25	
COG	G	Carbohydrate transport and metabolism	Tfu_2206	Tfu_2206 putative transporter					18.14	
COG	G	Carbohydrate transport and metabolism	Tfu_2209	Tfu_2209 dihydroxy-acid dehydratase	14.66	14.56	15.67	16.08	21.64	
COG	G	Carbohydrate transport and metabolism	Tfu_2214	Tfu_2214 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2315	Tfu_2315 putative secreted protein	15.45	17	16.7	16.18	20.62	1.02
COG	G	Carbohydrate transport and metabolism	Tfu_2320	Tfu_2320 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2322	Tfu_2322 similar to N-acetylglucosamine kinase						
COG	G	Carbohydrate transport and metabolism	Tfu_2337	Tfu_2337 hypothetical protein	24.16	24.05	23.56	23.37	26.53	0.944
COG	G	Carbohydrate transport and metabolism	Tfu_2338	Tfu_2338 ABC-type glucosylglycerol transport system permease protein	19.81	19.69	17.52	14.17	21.74	
COG	G	Carbohydrate transport and metabolism	Tfu_2339	Tfu_2339 ABC-type glucosylglycerol transport system permease protein	19.46	18.37	17.61	16.97	21.61	
COG	G	Carbohydrate transport and metabolism	Tfu_2340	Tfu_2340 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2473	Tfu_2473 n-acetylglucosamine-6-phosphate deacetylase	14.21				17.55	
COG	G	Carbohydrate transport and metabolism	Tfu_2486	Tfu_2486 hypothetical protein	16.26	16.75		15.08	20.28	
COG	G	Carbohydrate transport and metabolism	Tfu_2487	Tfu_2487 phosphoryl transfer system, HPr						
COG	G	Carbohydrate transport and metabolism	Tfu_2489	Tfu_2489 putative phosphoenolpyruvate-dependent sugar phosphotransferase					16.36	
COG	G	Carbohydrate transport and metabolism	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
COG	G	Carbohydrate transport and metabolism	Tfu_2537	Tfu_2537 ABC-type polysaccharide/polyol phosphate transport system ATPase	18.53	18.3	17.74	17.74	21.66	1.185
COG	G	Carbohydrate transport and metabolism	Tfu_2538	Tfu_2538 lipopolysaccharide exporter	17.08	16.98	17	16.55	20.46	0.958
COG	G	Carbohydrate transport and metabolism	Tfu_2566	Tfu_2566 galactokinase						
COG	G	Carbohydrate transport and metabolism	Tfu_2608	Tfu_2608 hypothetical protein	17.11	16.36	17.72	18.27	23.18	1.081
COG	G	Carbohydrate transport and metabolism	Tfu_2612	Tfu_2612 phosphoglucosamine mutase		12.2	15.38	14.97	20.13	0.827
COG	G	Carbohydrate transport and metabolism	Tfu_2676	Tfu_2676 hypothetical protein	19.55	19.14	19.58	19.66	23.65	0.938
COG	G	Carbohydrate transport and metabolism	Tfu_2709	Tfu_2709 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2712	Tfu_2712 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2723	Tfu_2723 putative epimerase						
COG	G	Carbohydrate transport and metabolism	Tfu_2725	Tfu_2725 putative phosphoglycerate mutase					19.92	
COG	G	Carbohydrate transport and metabolism	Tfu_2765	Tfu_2765 Phosphoenolpyruvate-protein phosphotransferase	14.84	14.48			19.67	
COG	G	Carbohydrate transport and metabolism	Tfu_2767	Tfu_2767 putative carbohydrate kinase					15.62	
COG	G	Carbohydrate transport and metabolism	Tfu_2768	Tfu_2768 6-phospho-beta-glucosidase	16.59	15.79	14.95	14.18	20.38	0.664

COG	G	Carbohydrate transport and metabolism	Tfu_2788	Tfu_2788 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2789	Tfu_2789 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2791	Tfu_2791 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2827	Tfu_2827 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2831	Tfu_2831 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2854	Tfu_2854 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2905	Tfu_2905 putative transmembrane transport protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
COG	G	Carbohydrate transport and metabolism	Tfu_2923	Tfu_2923 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2970	Tfu_2970 putative phosphoketolase						
COG	G	Carbohydrate transport and metabolism	Tfu_2979	Tfu_2979 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2988	Tfu_2988 hypothetical protein					16.78	
COG	G	Carbohydrate transport and metabolism	Tfu_2990	Tfu_2990 hypothetical protein						
COG	G	Carbohydrate transport and metabolism	Tfu_2994	Tfu_2994 putative transport protein						
COG	G	Carbohydrate transport and metabolism	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
COG	G	Carbohydrate transport and metabolism	Tfu_3044	Tfu_3044 trehalose 6-phosphate phosphorylase	18.07	17.65	19.63	19.25	23.3	1.354
COG	K	Transcription	Tfu_0017	Tfu_0017 cell envelope-related transcriptional attenuator						
COG	K	Transcription	Tfu_0029	Tfu_0029 putative LysR-family transcriptional regulator						
COG	K	Transcription	Tfu_0030	Tfu_0030 hypothetical protein						
COG	K	Transcription	Tfu_0033	Tfu_0033 regulatory protein GntR, HTH						
COG	K	Transcription	Tfu_0090	Tfu_0090 helix-turn-helix motif		14.74		13.88	16.54	
COG	K	Transcription	Tfu_0100	Tfu_0100 RNA binding S1:Resolvase, RNase H-like fold	14.79		14.44	14.35	21.25	
COG	K	Transcription	Tfu_0102	Tfu_0102 regulatory protein, MerR					16.67	
COG	K	Transcription	Tfu_0106	Tfu_0106 PAS protein phosphatase 2C-like						
COG	K	Transcription	Tfu_0143	Tfu_0143 similar to Transcriptional regulator					17.85	
COG	K	Transcription	Tfu_0163	Tfu_0163 Tyrosine protein kinase:Serine/threonine protein kinase	15.1	14.83	14.91	14.78	20.69	
COG	K	Transcription	Tfu_0179	Tfu_0179 RNA polymerase sigma-70 factor						
COG	K	Transcription	Tfu_0199	Tfu_0199 regulatory protein, MerR						
COG	K	Transcription	Tfu_0234	Tfu_0234 Cold shock protein		16.45	17.26	16.97	20.99	0.925
COG	K	Transcription	Tfu_0241	Tfu_0241 regulatory protein, MarR					19.52	
COG	K	Transcription	Tfu_0249	Tfu_0249 iron dependent repressor	20.66	20.23	19.81	18.78	23.34	1.163
COG	K	Transcription	Tfu_0250	Tfu_0250 PAS containing protein phosphatase 2C-like	16.84	15.81	16.62	16.02	21.84	1.175
COG	K	Transcription	Tfu_0257	Tfu_0257 response regulator receiver	18.04	17.73	16.32	14.36	21.79	
COG	K	Transcription	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
COG	K	Transcription	Tfu_0285	Tfu_0285 response regulator receiver	16.67	17.18	15.83	15.19	20.47	1.057
COG	K	Transcription	Tfu_0286	Tfu_0286 signal transduction histidine kinase	15.2	15.58	16.33	16.5	21.3	
COG	K	Transcription	Tfu_0287	Tfu_0287 Protein phosphatase 2C-like, withe GAF domain	15.09	14.85	14.53		19.25	
COG	K	Transcription	Tfu_0288	Tfu_0288 regulatory protein, LuxR:Response regulator receiver						
COG	K	Transcription	Tfu_0330	Tfu_0330 regulatory protein, LuxR:Response regulator receiver						
COG	K	Transcription	Tfu_0343	Tfu_0343 response regulator receiver	16.6	15.97	16.58	16.78	21.5	
COG	K	Transcription	Tfu_0351	Tfu_0351 helix-turn-helix, Fis-type					16.27	
COG	K	Transcription	Tfu_0384	Tfu_0384 Cold shock protein						
COG	K	Transcription	Tfu_0406	Tfu_0406 Tyrosine protein kinase:Serine/threonine protein kinase	15.36	16.04			20.09	0.675
COG	K	Transcription	Tfu_0408	Tfu_0408 redox-sensitive transcriptional activator SoxR						
COG	K	Transcription	Tfu_0411	Tfu_0411 regulatory protein, MarR	15.81	15.1		14.74	20.34	0.916
COG	K	Transcription	Tfu_0412	Tfu_0412 putative TetR-family transcriptional regulator					18.56	
COG	K	Transcription	Tfu_0422	Tfu_0422 hypothetical protein						
COG	K	Transcription	Tfu_0424	Tfu_0424 transcription-repair coupling factor					18.09	
COG	K	Transcription	Tfu_0447	Tfu_0447 prokaryotic transcription elongation factor GreA	20.37	20.1	19.06	19.15	22.34	
COG	K	Transcription	Tfu_0454	Tfu_0454 Tyrosine protein kinase:Serine/threonine protein kinase					16.34	
COG	K	Transcription	Tfu_0455	Tfu_0455 sigma subunit sigma24 -like protein	13.77	13.34	14.43		19.26	
COG	K	Transcription	Tfu_0465	Tfu_0465 hypothetical protein	15.65			14.42	19.11	
COG	K	Transcription	Tfu_0482	Tfu_0482 regulatory protein GntR, HTH	14.54	14.94			18.91	
COG	K	Transcription	Tfu_0500	Tfu_0500 Tyrosine protein kinase:Serine/threonine protein kinase	16.56	16			20.28	
COG	K	Transcription	Tfu_0504	Tfu_0504 RNA polymerase sigma-70 factor						
COG	K	Transcription	Tfu_0514	Tfu_0514 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal						
COG	K	Transcription	Tfu_0518	Tfu_0518 putative TetR-family transcriptional regulator	17.61	17.47	17.01	16.87	22.03	0.864
COG	K	Transcription	Tfu_0548	Tfu_0548 RNA polymerase sigma-70 factor	16.17	15.59	16.71	16.3	20.89	1
COG	K	Transcription	Tfu_0551	Tfu_0551 putative lipoprotein						

COG	K	Transcription	Tfu_0554	Tfu_0554 regulatory protein GntR, HTH					17.19	
COG	K	Transcription	Tfu_0559	Tfu_0559 RNA polymerase sigma factor		15.21	16.04	13.89	20.66	
COG	K	Transcription	Tfu_0563	Tfu_0563 similar to transcriptional regulators	17.42	16.55	16.98	16.09	21.06	0.869
COG	K	Transcription	Tfu_0567	Tfu_0567 possible regulator						
COG	K	Transcription	Tfu_0574	Tfu_0574 similar to DNA-directed RNA polymerase specialized sigma subunit sigma24 -like protein						
COG	K	Transcription	Tfu_0592	Tfu_0592 Tyrosine protein kinase:Serine/threonine protein kinase	18.18	17.59	17.18	17.09	21.25	
COG	K	Transcription	Tfu_0601	Tfu_0601 serine/threonine protein kinase	14.82	14.92	15.29		19.56	
COG	K	Transcription	Tfu_0625	Tfu_0625 regulatory proteins, IclR						
COG	K	Transcription	Tfu_0642	Tfu_0642 hypothetical protein	18.69	18.41	14.84		20.43	
COG	K	Transcription	Tfu_0646	Tfu_0646 ATP-dependent DNA helicase RecG					20.26	
COG	K	Transcription	Tfu_0651	Tfu_0651 ribonuclease III	19.19	19.06	19.23	19.28	23.05	0.694
COG	K	Transcription	Tfu_0684	Tfu_0684 regulatory proteins, AsnC/Lrp	16.46	16.01	15.66	14.3	18.49	
COG	K	Transcription	Tfu_0685	Tfu_0685 putative regulatory protein					16.23	
COG	K	Transcription	Tfu_0701	Tfu_0701 Tyrosine protein kinase:Serine/threonine protein kinase	18.86	18.29	16.43	15.99	22.51	0.6
COG	K	Transcription	Tfu_0725	Tfu_0725 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal					18.1	
COG	K	Transcription	Tfu_0734	Tfu_0734 regulatory protein, MerR						
COG	K	Transcription	Tfu_0757	Tfu_0757 regulatory protein, LuxR:TPR repeat						
COG	K	Transcription	Tfu_0758	Tfu_0758 regulatory protein, LuxR						
COG	K	Transcription	Tfu_0767	Tfu_0767 regulatory protein, LuxR:Response regulator receiver						
COG	K	Transcription	Tfu_0776	Tfu_0776 transcription elongation factor NusA	19.07	18.99	19.06	18.67	23.33	0.875
COG	K	Transcription	Tfu_0777	Tfu_0777 similar to nucleic-acid-binding protein implicated in transcription termination					15.41	
COG	K	Transcription	Tfu_0800	Tfu_0800 hypothetical protein	17.47	15.53	16.86	17.23	21.89	1.014
COG	K	Transcription	Tfu_0834	Tfu_0834 regulatory protein, LacI						
COG	K	Transcription	Tfu_0838	Tfu_0838 heat-inducible transcription repressor						
COG	K	Transcription	Tfu_0842	Tfu_0842 putative RNA polymerase ECF-subfamily sigma factor						
COG	K	Transcription	Tfu_0849	Tfu_0849 regulatory proteins, IclR					19.62	
COG	K	Transcription	Tfu_0867	Tfu_0867 sigma-70 factor						
COG	K	Transcription	Tfu_0872	Tfu_0872 regulatory protein, ArsR						
COG	K	Transcription	Tfu_0880	Tfu_0880 regulatory protein, MarR			16.09	15.45	20.1	
COG	K	Transcription	Tfu_0887	Tfu_0887 RNA polymerase sigma-B factor						
COG	K	Transcription	Tfu_0906	Tfu_0906 hypothetical protein						
COG	K	Transcription	Tfu_0907	Tfu_0907 regulatory protein, DeoR					19.63	
COG	K	Transcription	Tfu_0909	Tfu_0909 regulatory protein, LacI						
COG	K	Transcription	Tfu_0920	Tfu_0920 regulatory proteins, AsnC/Lrp						
COG	K	Transcription	Tfu_0938	Tfu_0938 regulatory protein, LacI	13.66				19.23	
COG	K	Transcription	Tfu_0949	Tfu_0949 putative TetR-family transcriptional regulator					17.44	
COG	K	Transcription	Tfu_1006	Tfu_1006 hypothetical protein	21.41	21.33	21.6	21.36	24.37	1.001
COG	K	Transcription	Tfu_1025	Tfu_1025 putative transcriptional regulator					18.74	
COG	K	Transcription	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
COG	K	Transcription	Tfu_1041	Tfu_1041 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA		13.51			20.01	
COG	K	Transcription	Tfu_1063	Tfu_1063 DNA-directed RNA polymerase omega subunit						
COG	K	Transcription	Tfu_1076	Tfu_1076 putative RNA-binding Sun protein					19.48	0.765
COG	K	Transcription	Tfu_1084	Tfu_1084 serine/threonine protein kinase	14.81				19.13	
COG	K	Transcription	Tfu_1087	Tfu_1087 regulatory protein, MarR	14.75	14.71	14.03	14.31	19.11	
COG	K	Transcription	Tfu_1094	Tfu_1094 transcription antitermination protein NusB			14.45		20.21	0.614
COG	K	Transcription	Tfu_1141	Tfu_1141 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	K	Transcription	Tfu_1147	Tfu_1147 putative transcriptional regulator						
COG	K	Transcription	Tfu_1205	Tfu_1205 Prokaryotic chromosome segregation and condensation protein ScpB					16.35	
COG	K	Transcription	Tfu_1232	Tfu_1232 hypothetical protein		14.51	15.68	16.11	21.29	
COG	K	Transcription	Tfu_1238	Tfu_1238 response regulator receiver						
COG	K	Transcription	Tfu_1262	Tfu_1262 hypothetical protein						
COG	K	Transcription	Tfu_1266	Tfu_1266 helix-turn-helix, AraC type						
COG	K	Transcription	Tfu_1271	Tfu_1271 PAS:Protein phosphatase 2C-like:GAF					14.7	
COG	K	Transcription	Tfu_1277	Tfu_1277 regulatory protein GntR, HTH	13.41		15.77	13.73	19.43	
COG	K	Transcription	Tfu_1289	Tfu_1289 regulatory protein GntR, HTH	18.46	18.6	16.94	17.06	22.2	
COG	K	Transcription	Tfu_1330	Tfu_1330 response regulator receiver						
COG	K	Transcription	Tfu_1334	Tfu_1334 RNA polymerase sigma factor						
COG	K	Transcription	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
COG	K	Transcription	Tfu_1342	Tfu_1342 Tyrosine protein kinase:Serine/threonine protein kinase						

COG	K	Transcription	Tfu_1372	Tfu_1372 cell envelope-related transcriptional attenuator						
COG	K	Transcription	Tfu_1373	Tfu_1373 regulatory proteins, AsnC/Lrp					15.36	
COG	K	Transcription	Tfu_1374	Tfu_1374 regulatory protein GntR, HTH		13.23			17.85	
COG	K	Transcription	Tfu_1383	Tfu_1383 putative transcriptional regulatory protein						
COG	K	Transcription	Tfu_1384	Tfu_1384 regulatory protein, MerR						
COG	K	Transcription	Tfu_1397	Tfu_1397 regulatory protein, MerR						
COG	K	Transcription	Tfu_1403	Tfu_1403 regulatory protein, LuxR:Response regulator receiver						
COG	K	Transcription	Tfu_1406	Tfu_1406 regulatory protein GntR, HTH					17.42	
COG	K	Transcription	Tfu_1407	Tfu_1407 RNA polymerase sigma factor					15.98	
COG	K	Transcription	Tfu_1422	Tfu_1422 putative LysR-family transcriptional regulator						0.719
COG	K	Transcription	Tfu_1423	Tfu_1423 putative transcriptional regulator					16.82	
COG	K	Transcription	Tfu_1440	Tfu_1440 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal			11.04		19.52	
COG	K	Transcription	Tfu_1446	Tfu_1446 putative transcriptional regulator	16.59	16			19.63	1.402
COG	K	Transcription	Tfu_1467	Tfu_1467 hypothetical protein						
COG	K	Transcription	Tfu_1501	Tfu_1501 similar to Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain						
COG	K	Transcription	Tfu_1506	Tfu_1506 similar to DNA-directed RNA polymerase specialized sigma subunit s	14.91		13.38	15.58	20.73	0.618
COG	K	Transcription	Tfu_1511	Tfu_1511 hypothetical protein					17.23	
COG	K	Transcription	Tfu_1514	Tfu_1514 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	K	Transcription	Tfu_1552	Tfu_1552 PAS:Protein phosphatase 2C-like:GAF						
COG	K	Transcription	Tfu_1556	Tfu_1556 regulatory protein, ArsR						
COG	K	Transcription	Tfu_1568	Tfu_1568 regulatory protein, ArsR						
COG	K	Transcription	Tfu_1605	Tfu_1605 putative xylose repressor					15.44	
COG	K	Transcription	Tfu_1608	Tfu_1608 putative xylose repressor				12.13		
COG	K	Transcription	Tfu_1620	Tfu_1620 regulatory protein, LacI						
COG	K	Transcription	Tfu_1626	Tfu_1626 regulatory protein GntR, HTH					13.59	
COG	K	Transcription	Tfu_1641	Tfu_1641 valine-pyruvate aminotransferase						
COG	K	Transcription	Tfu_1646	Tfu_1646 putative TetR-family transcriptional regulator					17.58	
COG	K	Transcription	Tfu_1658	Tfu_1658 Tyrosine protein kinase:Serine/threonine protein kinase:Sel1-like repeat						
COG	K	Transcription	Tfu_1664	Tfu_1664 iron dependent repressor	13.38				20.06	0.756
COG	K	Transcription	Tfu_1667	Tfu_1667 regulatory protein, MerR					13.97	
COG	K	Transcription	Tfu_1710	Tfu_1710 regulatory protein, LacI	13.61	14.65			18.21	
COG	K	Transcription	Tfu_1711	Tfu_1711 regulatory protein GntR, HTH					14.67	
COG	K	Transcription	Tfu_1739	Tfu_1739 PAS/Protein phosphatase 2C-like					17.4	
COG	K	Transcription	Tfu_1740	Tfu_1740 putative LysR-family transcriptional regulator					15.5	
COG	K	Transcription	Tfu_1752	Tfu_1752 Protein phosphatase 2C-like	13.17	14.44	15.59	15.39	21.23	
COG	K	Transcription	Tfu_1756	Tfu_1756 Tyrosine protein kinase:Serine/threonine protein kinase	13.69	14.76	15.42	14.85	21.48	1.016
COG	K	Transcription	Tfu_1771	Tfu_1771 similar to transcriptional regulator					17.57	
COG	K	Transcription	Tfu_1778	Tfu_1778 regulatory protein, LuxR						
COG	K	Transcription	Tfu_1785	Tfu_1785 regulatory protein GntR, HTH					16.43	
COG	K	Transcription	Tfu_1787	Tfu_1787 regulatory protein GntR, HTH	15.81	15.99	14.48		18.66	
COG	K	Transcription	Tfu_1811	Tfu_1811 polyphosphate glucokinase/transcriptional regulator						
COG	K	Transcription	Tfu_1817	Tfu_1817 regulatory protein, LuxR:Response regulator receiver						
COG	K	Transcription	Tfu_1845	Tfu_1845 regulatory protein, LuxR:Response regulator receiver					18.22	
COG	K	Transcription	Tfu_1851	Tfu_1851 regulatory protein, DeoR	16.78	16.82	15.92		19.28	0.924
COG	K	Transcription	Tfu_1854	Tfu_1854 regulatory protein, DeoR			15.82	15.05	20.7	
COG	K	Transcription	Tfu_1906	Tfu_1906 helix-turn-helix motif						
COG	K	Transcription	Tfu_1913	Tfu_1913 putative transcriptional regulator						
COG	K	Transcription	Tfu_1923	Tfu_1923 putative transcriptional repressor protein						
COG	K	Transcription	Tfu_1941	Tfu_1941 response regulator receiver	12.77	13.53	16.39	16.69	21.04	0.971
COG	K	Transcription	Tfu_1988	Tfu_1988 putative DNA-binding protein						
COG	K	Transcription	Tfu_2053	Tfu_2053 arginine repressor					20.35	
COG	K	Transcription	Tfu_2059	Tfu_2059 regulatory protein, MarR				14.01	18.84	0.829
COG	K	Transcription	Tfu_2074	Tfu_2074 Tyrosine protein kinase:Serine/threonine protein kinase	18.52	18.73	17.5	17.42	22.55	0.999
COG	K	Transcription	Tfu_2075	Tfu_2075 Tyrosine protein kinase:Serine/threonine protein kinase	14.14				15.26	
COG	K	Transcription	Tfu_2083	Tfu_2083 PAS/Protein phosphatase 2C-like						
COG	K	Transcription	Tfu_2090	Tfu_2090 RelA/SpoT protein	12.76			12.64	18.41	
COG	K	Transcription	Tfu_2121	Tfu_2121 hypothetical protein						
COG	K	Transcription	Tfu_2139	Tfu_2139 RNA polymerase sigma factor	14.43	14.75	14.91	14.59	21.19	
COG	K	Transcription	Tfu_2140	Tfu_2140 PAS/Protein phosphatase 2C-like	15.89	15.23	15.09	14.48	20.89	

COG	K	Transcription	Tfu_2150	Tfu_2150 hypothetical protein	15.5			15.65	20.05	
COG	K	Transcription	Tfu_2152	Tfu_2152 peptidase S24, LexA repressor	16.53	15.15	15.32		20.68	
COG	K	Transcription	Tfu_2167	Tfu_2167 helicase c2:DEAD/DEAH box helicase, N-terminal						
COG	K	Transcription	Tfu_2200	Tfu_2200 hypothetical protein					17.5	
COG	K	Transcription	Tfu_2229	Tfu_2229 Tyrosine protein kinase:Serine/threonine protein kinase		14.19			18.3	1.106
COG	K	Transcription	Tfu_2233	Tfu_2233 regulatory protein, LuxR:Response regulator receiver					15.4	
COG	K	Transcription	Tfu_2240	Tfu_2240 helix-turn-helix, Fis-type	16.32	14.63	14.48	15.9	20.91	1.381
COG	K	Transcription	Tfu_2254	Tfu_2254 putative LysR-family transcriptional regulator						
COG	K	Transcription	Tfu_2278	Tfu_2278 regulatory protein, LuxR:Response regulator receiver						
COG	K	Transcription	Tfu_2297	Tfu_2297 regulatory protein, MarR	14.21				19.89	
COG	K	Transcription	Tfu_2299	Tfu_2299 regulatory protein, ArsR						
COG	K	Transcription	Tfu_2323	Tfu_2323 putative transcriptional regulator	21.33	20.86	20.51	19.97	23.71	1.03
COG	K	Transcription	Tfu_2333	Tfu_2333 regulatory protein, MerR	15.44				18.43	
COG	K	Transcription	Tfu_2342	Tfu_2342 response regulator receiver			13.66		18.57	
COG	K	Transcription	Tfu_2344	Tfu_2344 response regulator receiver:Protein phosphatase 2C-like		14.15		13.7	18.85	
COG	K	Transcription	Tfu_2346	Tfu_2346 hypothetical protein		13.8			18.04	
COG	K	Transcription	Tfu_2361	Tfu_2361 Tyrosine protein kinase:Serine/threonine protein kinase	15.67	15.45	16.47	16.35	21.04	
COG	K	Transcription	Tfu_2375	Tfu_2375 Tyrosine protein kinase:Serine/threonine protein kinase	15.45	14.62		15.18	19.56	
COG	K	Transcription	Tfu_2381	Tfu_2381 ATPaseDEAD/DEAH box helicase, N-terminal					16.14	
COG	K	Transcription	Tfu_2389	Tfu_2389 hypothetical protein						
COG	K	Transcription	Tfu_2393	Tfu_2393 regulatory protein, MarR					18.23	0.733
COG	K	Transcription	Tfu_2421	Tfu_2421 transcription termination factor Rho	20.19	19.89	19.67	19.61	23.48	1.37
COG	K	Transcription	Tfu_2450	Tfu_2450 DEAD/DEAH box helicase, N-terminal	14.55	14.97			20.05	1.063
COG	K	Transcription	Tfu_2454	Tfu_2454 putative lysR-family transcriptional regulator					18.19	1.329
COG	K	Transcription	Tfu_2491	Tfu_2491 regulatory protein, LuxR:Response regulator receiver			16.65	15.34	21.33	
COG	K	Transcription	Tfu_2496	Tfu_2496 response regulator receiver	18.2	17.46	19.26	18.65	23.51	0.942
COG	K	Transcription	Tfu_2507	Tfu_2507 Tyrosine protein kinase:Serine/threonine protein kinase	17.36	17.16	16.35	15.91	21.06	1.521
COG	K	Transcription	Tfu_2526	Tfu_2526 hypothetical protein						
COG	K	Transcription	Tfu_2542	Tfu_2542 cell envelope-related transcriptional attenuator						
COG	K	Transcription	Tfu_2549	Tfu_2549 response regulator receiver						
COG	K	Transcription	Tfu_2567	Tfu_2567 cell envelope-related transcriptional attenuator					18.36	
COG	K	Transcription	Tfu_2582	Tfu_2582 regulatory protein, LuxR:Response regulator receiver	17.73	17.94	17.3	17.21	21.46	
COG	K	Transcription	Tfu_2583	Tfu_2583 putative two-component system sensor kinase						
COG	K	Transcription	Tfu_2597	Tfu_2597 RNA polymerase sigma-70 factor						
COG	K	Transcription	Tfu_2618	Tfu_2618 DNA-directed RNA polymerase alpha subunit	20.3	20.33	21.62	21.41	24.58	1.11
COG	K	Transcription	Tfu_2653	Tfu_2653 DNA-directed RNA polymerase beta' subunit	20.69	20.49	21.52	21.3	25.54	1.261
COG	K	Transcription	Tfu_2654	Tfu_2654 DNA-directed RNA polymerase beta subunit	20.88	20.63	21.68	21.31	25.36	1.169
COG	K	Transcription	Tfu_2659	Tfu_2659 transcription antitermination protein NusG	18.54	18.96	18.82	18.89	23.15	0.605
COG	K	Transcription	Tfu_2716	Tfu_2716 alanine-rich protein						
COG	K	Transcription	Tfu_2737	Tfu_2737 transcriptional regulatory protein						
COG	K	Transcription	Tfu_2755	Tfu_2755 putative TetR-family transcriptional regulator	15.26	14.54	15.65		19.87	
COG	K	Transcription	Tfu_2778	Tfu_2778 helix-turn-helix motif	15.45	15.22		13.44	19.61	
COG	K	Transcription	Tfu_2790	Tfu_2790 regulatory protein, LacI						
COG	K	Transcription	Tfu_2793	Tfu_2793 regulatory protein, ArsR						
COG	K	Transcription	Tfu_2796	Tfu_2796 Protein phosphatase 2C-like					15.05	
COG	K	Transcription	Tfu_2799	Tfu_2799 TetR/AcrR family transcriptional regulator	14.45		16.22	14.99	19.6	
COG	K	Transcription	Tfu_2809	Tfu_2809 regulatory protein, LuxR						
COG	K	Transcription	Tfu_2816	Tfu_2816 hypothetical protein	12.88				17.67	
COG	K	Transcription	Tfu_2825	Tfu_2825 putative LysR-family transcriptional regulator				13.26	18.78	
COG	K	Transcription	Tfu_2845	Tfu_2845 Tyrosine protein kinase:Serine/threonine protein kinase		13.26		14.27	19.42	
COG	K	Transcription	Tfu_2855	Tfu_2855 similar to Putative stress-responsive transcriptional regulator						
COG	K	Transcription	Tfu_2858	Tfu_2858 response regulator receiver	17.19	15.96		14.41	20.77	
COG	K	Transcription	Tfu_2880	Tfu_2880 regulatory protein, LuxR						
COG	K	Transcription	Tfu_2882	Tfu_2882 Bvg accessory factor	15.79	15.26	16.09	15.65	20.23	
COG	K	Transcription	Tfu_2907	Tfu_2907 putative CarD-like transcriptional regulator	16.71	16.93	15.75	17.35	21.57	
COG	K	Transcription	Tfu_2910	Tfu_2910 response regulator receiver	16.38	16.03	17	17.51	21.88	1.079
COG	K	Transcription	Tfu_2916	Tfu_2916 similar to transcriptional regulator					17.12	
COG	K	Transcription	Tfu_2941	Tfu_2941 regulatory protein GntR, HTH					20.46	
COG	K	Transcription	Tfu_2943	Tfu_2943 regulatory protein GntR, HTH	15.1	14.09			18.49	

COG	K	Transcription	Tfu_2950	Tfu_2950 regulatory protein, LuxR:Response regulator receiver		14.43	18.83	18.71	22.94	2.366
COG	K	Transcription	Tfu_2953	Tfu_2953 putative transcriptional regulator	15.38	15.61	16.42	14.9	19.48	1.394
COG	K	Transcription	Tfu_2956	Tfu_2956 cell envelope-related transcriptional attenuator						
COG	K	Transcription	Tfu_2959	Tfu_2959 regulatory protein, LuxR:Response regulator receiver					15.74	
COG	K	Transcription	Tfu_3022	Tfu_3022 putative RNA polymerase sigma factor						
COG	K	Transcription	Tfu_3028	Tfu_3028 regulatory protein, MarR					15.63	
COG	K	Transcription	Tfu_3035	Tfu_3035 regulatory protein, LuxR:Response regulator receiver		14.57	17.43	17.54	21.22	0.687
COG	K	Transcription	Tfu_3038	Tfu_3038 hypothetical protein						
COG	K	Transcription	Tfu_3048	Tfu_3048 regulatory protein GntR, HTH						
COG	K	Transcription	Tfu_3065	Tfu_3065 Tyrosine protein kinase:Serine/threonine protein kinase					18.02	
COG	K	Transcription	Tfu_3066	Tfu_3066 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA	19.07	19.31	18.37	17.91	22.14	0.98
COG	K	Transcription	Tfu_3098	Tfu_3098 hypothetical protein						
COG	K	Transcription	Tfu_3106	Tfu_3106 RNA polymerase sigma-70 factor					18.22	
COG	K	Transcription	Tfu_3110	Tfu_3110 ParB-like partition protein			15.48	14.69	20.32	
COG	E	Amino acid transport and metabolism	Tfu_0028	Tfu_0028 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1 related	18.57	18.71	20.61	20.33	23.82	0.982
COG	E	Amino acid transport and metabolism	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
COG	E	Amino acid transport and metabolism	Tfu_0058	Tfu_0058 putative agmatinase	15.19	15.1			18.15	1.47
COG	E	Amino acid transport and metabolism	Tfu_0074	Tfu_0074 hypothetical protein	22.9	22.75	20.91	20.91	24.27	0.895
COG	E	Amino acid transport and metabolism	Tfu_0075	Tfu_0075 ABC-type branched-chain amino acid transport systems ATPase com	18.61	18.36	16.71	15.78	20.43	
COG	E	Amino acid transport and metabolism	Tfu_0076	Tfu_0076 ABC-type branched-chain amino acid transport systems ATPase com	20.12	19.67	17.26	16.94	22.02	
COG	E	Amino acid transport and metabolism	Tfu_0077	Tfu_0077 branched-chain amino acid ABC transporter permease protein						
COG	E	Amino acid transport and metabolism	Tfu_0078	Tfu_0078 branched-chain amino acid ABC transporter permease protein	19.29	19.14	15.68	16.2	20.45	0.777
COG	E	Amino acid transport and metabolism	Tfu_0136	Tfu_0136 phosphoserine phosphatase SerB:HAD-superfamily hydrolase subfamily IB, PSPase-like					16.25	
COG	E	Amino acid transport and metabolism	Tfu_0142	Tfu_0142 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_0173	Tfu_0173 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_0174	Tfu_0174 ATP phosphoribosyltransferase	19.33	18.84	19.91	18.99	23.24	1.037
COG	E	Amino acid transport and metabolism	Tfu_0175	Tfu_0175 phosphoribosyl-ATP pyrophosphatase	17.66	17.21	14.18	15.95	21.68	0.868
COG	E	Amino acid transport and metabolism	Tfu_0191	Tfu_0191 similar to N-acetylglutamate synthase and related acetyltransferase	17.01	17	15.47		18.31	1.108
COG	E	Amino acid transport and metabolism	Tfu_0226	Tfu_0226 threonine synthase	15.9	15.94	18.57	18.65	22.91	1.385
COG	E	Amino acid transport and metabolism	Tfu_0246	Tfu_0246 phosphoserine aminotransferase	19.59	19.46	22.48	21.91	25.76	1.096
COG	E	Amino acid transport and metabolism	Tfu_0272	Tfu_0272 DUF160	17.82	17.78	20.43	19.91	24.03	1.174
COG	E	Amino acid transport and metabolism	Tfu_0280	Tfu_0280 spermidine/putrescine ABC transporter ATP-binding subunit	16.15	16.84	16.09	16.49	21.27	
COG	E	Amino acid transport and metabolism	Tfu_0281	Tfu_0281 hypothetical protein	18.47	18.78	17.46	17.13	21.33	1.121
COG	E	Amino acid transport and metabolism	Tfu_0282	Tfu_0282 polyamine ABC-transporter, inner membrane subunit					17.78	
COG	E	Amino acid transport and metabolism	Tfu_0283	Tfu_0283 polyamine ABC-transporter, inner membrane subunit						
COG	E	Amino acid transport and metabolism	Tfu_0284	Tfu_0284 putative oxidoreductase	16.6	15.38	15.46		20.66	
COG	E	Amino acid transport and metabolism	Tfu_0301	Tfu_0301 diaminobutyrate--2-oxoglutarate aminotransferase						
COG	E	Amino acid transport and metabolism	Tfu_0303	Tfu_0303 hypothetical protein	14.25		14.59	14.35	18.3	
COG	E	Amino acid transport and metabolism	Tfu_0304	Tfu_0304 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_0305	Tfu_0305 amino acid ABC transporter, inner membrane subunit						
COG	E	Amino acid transport and metabolism	Tfu_0306	Tfu_0306 ABC-type polar amino acid transport system ATPase component					16.25	
COG	E	Amino acid transport and metabolism	Tfu_0326	Tfu_0326 ABC-type spermidine/putrescine transport systems ATPase components						
COG	E	Amino acid transport and metabolism	Tfu_0415	Tfu_0415 ribose-phosphate pyrophosphokinase	18.35	17.7	20.22	20.21	23.7	1.099
COG	E	Amino acid transport and metabolism	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
COG	E	Amino acid transport and metabolism	Tfu_0434	Tfu_0434 proline dehydrogenase	18.28	18.4	17.73	16.85	22.15	1.304
COG	E	Amino acid transport and metabolism	Tfu_0437	Tfu_0437 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_0438	Tfu_0438 cystathionine beta-synthase	13		14.49	12.98	20.18	
COG	E	Amino acid transport and metabolism	Tfu_0440	Tfu_0440 cystathionine gamma-synthase					17.4	
COG	E	Amino acid transport and metabolism	Tfu_0485	Tfu_0485 putative peptidase	17.73	17.6	18.42	18.1	22.9	0.789
COG	E	Amino acid transport and metabolism	Tfu_0492	Tfu_0492 hypothetical protein				14.66	20.29	0.928
COG	E	Amino acid transport and metabolism	Tfu_0494	Tfu_0494 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	20.98	20.36	20.57	20.17	24.7	0.791
COG	E	Amino acid transport and metabolism	Tfu_0495	Tfu_0495 succinyl-diaminopimelate desuccinylase	16.35	16.43	16.49	16.87	20.83	0.501
COG	E	Amino acid transport and metabolism	Tfu_0503	Tfu_0503 leucyl aminopeptidase	19.88	19.54	19.89	19.71	24.09	0.912
COG	E	Amino acid transport and metabolism	Tfu_0526	Tfu_0526 putative peptidase	15.83	16.02	17.91	17.02	21.95	1.067
COG	E	Amino acid transport and metabolism	Tfu_0544	Tfu_0544 3-phosphoshikimate 1-carboxyvinyltransferase						
COG	E	Amino acid transport and metabolism	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
COG	E	Amino acid transport and metabolism	Tfu_0568	Tfu_0568 hypothetical protein					18.2	
COG	E	Amino acid transport and metabolism	Tfu_0595	Tfu_0595 putative pyridoxal-phosphate-dependent aminotransferase					16.06	

COG	E	Amino acid transport and metabolism	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	
COG	E	Amino acid transport and metabolism	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
COG	E	Amino acid transport and metabolism	Tfu_0613	Tfu_0613 ketol-acid reductoisomerase	19.9	19.77	19.96	19.71	23.42	0.799
COG	E	Amino acid transport and metabolism	Tfu_0614	Tfu_0614 D-3-phosphoglycerate dehydrogenase	20.25	20.04	22.34	22.29	25.26	1.066
COG	E	Amino acid transport and metabolism	Tfu_0615	Tfu_0615 3-isopropylmalate dehydrogenase	19.78	19.7	19.64	19.42	23.35	1.025
COG	E	Amino acid transport and metabolism	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
COG	E	Amino acid transport and metabolism	Tfu_0617	Tfu_0617 2-isopropylmalate synthase	16.51	16.22	15.8	13.84	20.9	
COG	E	Amino acid transport and metabolism	Tfu_0626	Tfu_0626 isopropylmalate isomerase large subunit			15.08	14.46	19.36	
COG	E	Amino acid transport and metabolism	Tfu_0627	Tfu_0627 isopropylmalate isomerase small subunit	13.33				18.83	
COG	E	Amino acid transport and metabolism	Tfu_0632	Tfu_0632 cystathionine gamma-synthase					15.55	0.471
COG	E	Amino acid transport and metabolism	Tfu_0634	Tfu_0634 putative integral membrane protein					15.37	0.851
COG	E	Amino acid transport and metabolism	Tfu_0686	Tfu_0686 putative aminotransferase	15.88	15.52	17.94	18.09	22.23	0.999
COG	E	Amino acid transport and metabolism	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
COG	E	Amino acid transport and metabolism	Tfu_0745	Tfu_0745 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_0771	Tfu_0771 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_0786	Tfu_0786 dihydrodipicolinate reductase	18.87	17.45	19.64	18.4	23.22	0.825
COG	E	Amino acid transport and metabolism	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844
COG	E	Amino acid transport and metabolism	Tfu_0806	Tfu_0806 putative acyl-peptide hydrolase	20.06	19.46	18.88	19.07	23.81	1.011
COG	E	Amino acid transport and metabolism	Tfu_0807	Tfu_0807 amino acid ABC transporter, permease protein, 3-TM region, His/Glu	18.54	17.53	15.99	15.66	20.16	0.846
COG	E	Amino acid transport and metabolism	Tfu_0808	Tfu_0808 amino acid ABC transporter, permease protein, 3-TM region, His/Glu	20.17	18.67	18.21	18.6	21.97	1.222
COG	E	Amino acid transport and metabolism	Tfu_0809	Tfu_0809 hypothetical protein	23.78	23.37	21.95	21.85	24.44	0.831
COG	E	Amino acid transport and metabolism	Tfu_0810	Tfu_0810 ABC-type polar amino acid transport system ATPase component	20.65	20.47	19.17	19	22.36	1.163
COG	E	Amino acid transport and metabolism	Tfu_0816	Tfu_0816 diaminopimelate epimerase					18.06	
COG	E	Amino acid transport and metabolism	Tfu_0817	Tfu_0817 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_0818	Tfu_0818 hypothetical protein	17.3	17.04	15.39	15.33	20.85	
COG	E	Amino acid transport and metabolism	Tfu_0850	Tfu_0850 2-isopropylmalate synthase	16.67	16.9	16.57	16.17	21.98	
COG	E	Amino acid transport and metabolism	Tfu_0854	Tfu_0854 hypothetical protein					17.58	
COG	E	Amino acid transport and metabolism	Tfu_0855	Tfu_0855 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_0885	Tfu_0885 putative glutathione-dependent aldehyde dehydrogenase						
COG	E	Amino acid transport and metabolism	Tfu_0899	Tfu_0899 similar to V8-like Glu-specific endopeptidase						
COG	E	Amino acid transport and metabolism	Tfu_0908	Tfu_0908 hypothetical protein					16.23	
COG	E	Amino acid transport and metabolism	Tfu_0910	Tfu_0910 hypothetical protein	23.09	23.21	22.87	22.38	25.97	1.94
COG	E	Amino acid transport and metabolism	Tfu_0911	Tfu_0911 ABC-type dipeptide/oligopeptide/nickel transport systems, permease components			15.01		17.95	
COG	E	Amino acid transport and metabolism	Tfu_0912	Tfu_0912 ABC-type dipeptide/oligopeptide/nickel transport systems, permease components				14.07	19.4	
COG	E	Amino acid transport and metabolism	Tfu_0913	Tfu_0913 oligopeptide/dipeptide ABC transporter, ATP-binding protein	17.06	17.13	17.75	18.6	22.63	
COG	E	Amino acid transport and metabolism	Tfu_0914	Tfu_0914 ABC-type oligopeptide transport system ATPase component	16.1	16.25	18.3	17.89	22.26	2.047
COG	E	Amino acid transport and metabolism	Tfu_0921	Tfu_0921 putative tryptophan 2,3-dioxygenase	13.54	14.16			17.35	
COG	E	Amino acid transport and metabolism	Tfu_0922	Tfu_0922 kynureninase	16.91	15.34	13.9	14.63	19.53	1.172
COG	E	Amino acid transport and metabolism	Tfu_0961	Tfu_0961 alanine dehydrogenase and pyridine nucleotide transhydrogenase			19.5	19.59	23.05	1.544
COG	E	Amino acid transport and metabolism	Tfu_0982	Tfu_0982 glutamine synthetase type I	16.36	15.34	14.3	15.33	20.84	1.147
COG	E	Amino acid transport and metabolism	Tfu_0988	Tfu_0988 glutamine synthetase type I		16.24	19.93	19.87	23.49	1.247
COG	E	Amino acid transport and metabolism	Tfu_0995	Tfu_0995 leucyl aminopeptidase	22.3	22.22	21.93	22.33	25.29	1.048
COG	E	Amino acid transport and metabolism	Tfu_1024	Tfu_1024 anthranilate phosphoribosyltransferase						
COG	E	Amino acid transport and metabolism	Tfu_1039	Tfu_1039 phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 2						
COG	E	Amino acid transport and metabolism	Tfu_1044	Tfu_1044 thiamine biosynthesis oxidoreductase ThiO	14.05				17.56	0.833
COG	E	Amino acid transport and metabolism	Tfu_1050	Tfu_1050 5,10-methylenetetrahydrofolate reductase						
COG	E	Amino acid transport and metabolism	Tfu_1056	Tfu_1056 carbamoyl-phosphate synthase, small subunit		15.52	17.25	17.26	22.56	0.884
COG	E	Amino acid transport and metabolism	Tfu_1057	Tfu_1057 carbamoyl-phosphate synthase, large subunit, glutamine-dependent	16.53	16.24	19.8	19.69	24.13	0.99
COG	E	Amino acid transport and metabolism	Tfu_1090	Tfu_1090 chorismate synthase	19.19	18.56	19.76	19.46	23.47	
COG	E	Amino acid transport and metabolism	Tfu_1091	Tfu_1091 shikimate kinase					19.23	
COG	E	Amino acid transport and metabolism	Tfu_1092	Tfu_1092 3-dehydroquinate synthase	18.86	18.36	19.22	18.34	23.14	1.077
COG	E	Amino acid transport and metabolism	Tfu_1098	Tfu_1098 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_1138	Tfu_1138 hypothetical protein		12.77		13.45		
COG	E	Amino acid transport and metabolism	Tfu_1145	Tfu_1145 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_1150	Tfu_1150 histidinol dehydrogenase	19.66	19.37	19.47	19.89	23.27	0.966
COG	E	Amino acid transport and metabolism	Tfu_1151	Tfu_1151 histidinol-phosphate aminotransferase					19.66	1.354
COG	E	Amino acid transport and metabolism	Tfu_1152	Tfu_1152 imidazoleglycerol-phosphate dehydratase					17.24	
COG	E	Amino acid transport and metabolism	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
COG	E	Amino acid transport and metabolism	Tfu_1155	Tfu_1155 1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole-4-c			15.7	16.67	21.72	

COG	E	Amino acid transport and metabolism	Tfu_1156	Tfu_1156 histidine biosynthesis protein HisF	14.6	14.45	14.77	14.57	20.69	
COG	E	Amino acid transport and metabolism	Tfu_1159	Tfu_1159 phosphoribosyl-AMP cyclohydrolase					16.88	
COG	E	Amino acid transport and metabolism	Tfu_1164	Tfu_1164 indole-3-glycerol-phosphate synthase					20.46	1.072
COG	E	Amino acid transport and metabolism	Tfu_1165	Tfu_1165 tryptophan synthase, beta chain					18.55	
COG	E	Amino acid transport and metabolism	Tfu_1166	Tfu_1166 tryptophan synthase subunit alpha					18.24	
COG	E	Amino acid transport and metabolism	Tfu_1173	Tfu_1173 glutamate synthase (ferredoxin)					19.09	
COG	E	Amino acid transport and metabolism	Tfu_1174	Tfu_1174 glutamate synthase, NADH/NADPH, small subunit 1						
COG	E	Amino acid transport and metabolism	Tfu_1182	Tfu_1182 hypothetical protein	18.55	17.76	17.76	17.69	21.61	1.107
COG	E	Amino acid transport and metabolism	Tfu_1183	Tfu_1183 branched-chain amino acid transport system permease protein	15.85	13.37		13.2	19.42	
COG	E	Amino acid transport and metabolism	Tfu_1184	Tfu_1184 branched-chain amino acid transport system ATP-binding protein	19.81	19.69	19.88	20.05	23.28	0.869
COG	E	Amino acid transport and metabolism	Tfu_1185	Tfu_1185 ABC-type branched-chain amino acid transport systems ATPase com	20.76	20.17	19.92	19.93	23.52	0.915
COG	E	Amino acid transport and metabolism	Tfu_1186	Tfu_1186 hypothetical protein	23.7	23.37	23.34	22.75	25.45	0.832
COG	E	Amino acid transport and metabolism	Tfu_1207	Tfu_1207 chorismate mutase of the AroH class						
COG	E	Amino acid transport and metabolism	Tfu_1208	Tfu_1208 prephenate dehydrogenase						
COG	E	Amino acid transport and metabolism	Tfu_1290	Tfu_1290 hypothetical protein					17	
COG	E	Amino acid transport and metabolism	Tfu_1291	Tfu_1291 probable amino-acid transmembrane lipoprotein ABC transporter						
COG	E	Amino acid transport and metabolism	Tfu_1292	Tfu_1292 similar to ABC-type branched-chain amino acid transport system permease component						
COG	E	Amino acid transport and metabolism	Tfu_1293	Tfu_1293 ABC-type branched-chain amino acid transport systems ATPase component						
COG	E	Amino acid transport and metabolism	Tfu_1294	Tfu_1294 ABC-type branched-chain amino acid transport systems ATPase component						
COG	E	Amino acid transport and metabolism	Tfu_1308	Tfu_1308 ABC-type spermidine/putrescine transport systems ATPase components						
COG	E	Amino acid transport and metabolism	Tfu_1365	Tfu_1365 putative acetyltransferase						
COG	E	Amino acid transport and metabolism	Tfu_1371	Tfu_1371 glutamate dehydrogenase	13.87		17.06	16.78	21.17	1.233
COG	E	Amino acid transport and metabolism	Tfu_1386	Tfu_1386 glutamine amidotransferase of anthranilate synthase:Anthranilate sy	14.29	15.3	14.48	14.83	21.47	1.207
COG	E	Amino acid transport and metabolism	Tfu_1398	Tfu_1398 glycine dehydrogenase	19.26	19.25	19.62	19.33	23.73	1.358
COG	E	Amino acid transport and metabolism	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
COG	E	Amino acid transport and metabolism	Tfu_1630	Tfu_1630 oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terr	15.55	15.84			18.2	
COG	E	Amino acid transport and metabolism	Tfu_1631	Tfu_1631 ABC transporter, permease protein						
COG	E	Amino acid transport and metabolism	Tfu_1632	Tfu_1632 hypothetical protein	14.9				16.2	
COG	E	Amino acid transport and metabolism	Tfu_1633	Tfu_1633 hypothetical protein	21.04	20.99	19.85	19.66	23.61	0.589
COG	E	Amino acid transport and metabolism	Tfu_1635	Tfu_1635 dehydroquinase, class II					16.28	
COG	E	Amino acid transport and metabolism	Tfu_1641	Tfu_1641 valine-pyruvate aminotransferase						
COG	E	Amino acid transport and metabolism	Tfu_1666	Tfu_1666 para-aminobenzoate synthase, component I:Glutamine amidotransferase of anthranilate synthase						
COG	E	Amino acid transport and metabolism	Tfu_1681	Tfu_1681 probable conserved integral membrane protein						
COG	E	Amino acid transport and metabolism	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
COG	E	Amino acid transport and metabolism	Tfu_1718	Tfu_1718 putative 5-dehydro-4-deoxyglucarate dehydratase						
COG	E	Amino acid transport and metabolism	Tfu_1741	Tfu_1741 threonine dehydratase					16.86	
COG	E	Amino acid transport and metabolism	Tfu_1744	Tfu_1744 xaa-Pro aminopeptidase	17.01	17.42	17.27	18.16	22.27	1.008
COG	E	Amino acid transport and metabolism	Tfu_1755	Tfu_1755 alcohol dehydrogenase					19.25	
COG	E	Amino acid transport and metabolism	Tfu_1779	Tfu_1779 hypothetical protein	18.86	18.42			20.09	
COG	E	Amino acid transport and metabolism	Tfu_1780	Tfu_1780 ABC transporter permease protein						
COG	E	Amino acid transport and metabolism	Tfu_1781	Tfu_1781 possible ABC transporter, permease protein						
COG	E	Amino acid transport and metabolism	Tfu_1782	Tfu_1782 ABC-type branched-chain amino acid transport systems ATPase component						
COG	E	Amino acid transport and metabolism	Tfu_1783	Tfu_1783 ABC-type branched-chain amino acid transport systems ATPase component						
COG	E	Amino acid transport and metabolism	Tfu_1820	Tfu_1820 hypothetical protein	17.64	16.81			19.82	
COG	E	Amino acid transport and metabolism	Tfu_1821	Tfu_1821 hypothetical protein	24.51	24.26	23.96	23.7	26.74	1.154
COG	E	Amino acid transport and metabolism	Tfu_1822	Tfu_1822 oligopeptide transport integral membrane protein	16.87		16.15	15.61	21	
COG	E	Amino acid transport and metabolism	Tfu_1825	Tfu_1825 5-methyltetrahydrofolate--homocysteine methyltransferase					15.39	
COG	E	Amino acid transport and metabolism	Tfu_1856	Tfu_1856 prolyl oligopeptidase					19.55	
COG	E	Amino acid transport and metabolism	Tfu_1889	Tfu_1889 phosphoadenosine phosphosulfate reductase						
COG	E	Amino acid transport and metabolism	Tfu_1915	Tfu_1915 ferredoxin/ferredoxin--NADP reductase, putative		13.93			20	
COG	E	Amino acid transport and metabolism	Tfu_1968	Tfu_1968 allophanate hydrolase subunit 2						
COG	E	Amino acid transport and metabolism	Tfu_1969	Tfu_1969 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_1978	Tfu_1978 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_1983	Tfu_1983 cysteine desulphurases, SufS	14.11			13.91	18.52	0.647
COG	E	Amino acid transport and metabolism	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
COG	E	Amino acid transport and metabolism	Tfu_1993	Tfu_1993 arginine deiminase	17.46	16.86	15.61	15.61	20.88	1.353
COG	E	Amino acid transport and metabolism	Tfu_2011	Tfu_2011 putative cationic amino acid transporter						
COG	E	Amino acid transport and metabolism	Tfu_2012	Tfu_2012 N-carbamoyl-L-amino acid amidohydrolase	13.88	14.26	13.69	13.1	19.27	
COG	E	Amino acid transport and metabolism	Tfu_2051	Tfu_2051 argininosuccinate lyase	15.68	16.51	18.68	18.9	22.79	

COG	E	Amino acid transport and metabolism	Tfu_2052	Tfu_2052 argininosuccinate synthase	13.3		18.49	17.16	22.53	
COG	E	Amino acid transport and metabolism	Tfu_2054	Tfu_2054 acetylornithine and succinylornithine aminotransferase	16.33	18.16	18.68	18.83	22.2	1.056
COG	E	Amino acid transport and metabolism	Tfu_2055	Tfu_2055 acetylglutamate kinase		13.89	16.85	16.6	21.88	1.485
COG	E	Amino acid transport and metabolism	Tfu_2056	Tfu_2056 bifunctional ornithine acetyltransferase/N-acetylglutamate synthase	17.05	16.43	18.49	17.65	22.7	
COG	E	Amino acid transport and metabolism	Tfu_2057	Tfu_2057 N-acetyl-gamma-glutamyl-phosphate reductase					20.33	
COG	E	Amino acid transport and metabolism	Tfu_2058	Tfu_2058 hypothetical protein	18.62	18.51	16.78	15.69	21.52	
COG	E	Amino acid transport and metabolism	Tfu_2067	Tfu_2067 shikimate 5-dehydrogenase					17.29	
COG	E	Amino acid transport and metabolism	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
COG	E	Amino acid transport and metabolism	Tfu_2175	Tfu_2175 gamma-glutamyl phosphate reductase GPR	16.65	16.53	17.82	17.26	21.71	
COG	E	Amino acid transport and metabolism	Tfu_2179	Tfu_2179 gamma-glutamyl kinase					17.69	
COG	E	Amino acid transport and metabolism	Tfu_2204	Tfu_2204 peptidase M, neutral zinc metallopeptidase, zinc-binding site	19.26	19.22	19.6	18.89	23.54	1.255
COG	E	Amino acid transport and metabolism	Tfu_2209	Tfu_2209 dihydroxy-acid dehydratase	14.66	14.56	15.67	16.08	21.64	
COG	E	Amino acid transport and metabolism	Tfu_2212	Tfu_2212 prolyl oligopeptidase						
COG	E	Amino acid transport and metabolism	Tfu_2223	Tfu_2223 putative aminotransferase					16.25	
COG	E	Amino acid transport and metabolism	Tfu_2246	Tfu_2246 hypothetical protein					15.5	
COG	E	Amino acid transport and metabolism	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
COG	E	Amino acid transport and metabolism	Tfu_2251	Tfu_2251 sodium:alanine symporter	22.26	21.56	20.84	20.34	23.61	0.815
COG	E	Amino acid transport and metabolism	Tfu_2253	Tfu_2253 hypothetical protein					17.71	
COG	E	Amino acid transport and metabolism	Tfu_2255	Tfu_2255 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_2259	Tfu_2259 similar to Phosphoglycerate dehydrogenase and related dehydrogenase						
COG	E	Amino acid transport and metabolism	Tfu_2263	Tfu_2263 putative dehydrogenase	15.9	15.27			19.69	
COG	E	Amino acid transport and metabolism	Tfu_2291	Tfu_2291 oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal						
COG	E	Amino acid transport and metabolism	Tfu_2292	Tfu_2292 putative peptide ABC transporter permease protein						
COG	E	Amino acid transport and metabolism	Tfu_2332	Tfu_2332 putative cholesterol oxidase					14.87	
COG	E	Amino acid transport and metabolism	Tfu_2350	Tfu_2350 phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1			14.88	13.66	19.21	
COG	E	Amino acid transport and metabolism	Tfu_2351	Tfu_2351 aminomethyltransferase	17.24	17.22	16.2	16.08	20.82	0.867
COG	E	Amino acid transport and metabolism	Tfu_2352	Tfu_2352 Glycine cleavage H-protein		14.52			17.57	0.666
COG	E	Amino acid transport and metabolism	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
COG	E	Amino acid transport and metabolism	Tfu_2357	Tfu_2357 hypothetical protein	19.02	18.48			19.77	
COG	E	Amino acid transport and metabolism	Tfu_2368	Tfu_2368 cysteine synthase K/M		14.5	14.44		19.69	
COG	E	Amino acid transport and metabolism	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
COG	E	Amino acid transport and metabolism	Tfu_2422	Tfu_2422 homoserine kinase					19.33	0.823
COG	E	Amino acid transport and metabolism	Tfu_2423	Tfu_2423 threonine synthase	13.86				17.31	
COG	E	Amino acid transport and metabolism	Tfu_2424	Tfu_2424 homoserine dehydrogenase					18.67	1.062
COG	E	Amino acid transport and metabolism	Tfu_2425	Tfu_2425 diaminopimelate decarboxylase					18.01	
COG	E	Amino acid transport and metabolism	Tfu_2435	Tfu_2435 putative hydrolase						
COG	E	Amino acid transport and metabolism	Tfu_2470	Tfu_2470 fibronectin, type III						
COG	E	Amino acid transport and metabolism	Tfu_2481	Tfu_2481 putative NAD-glutamate dehydrogenase	20.96	20.83	21.88	21.73	25.49	1.153
COG	E	Amino acid transport and metabolism	Tfu_2661	Tfu_2661 aspartate aminotransferase	21.82	21.22	23.56	23.2	26.43	1.189
COG	E	Amino acid transport and metabolism	Tfu_2708	Tfu_2708 delta 1-pyrroline-5-carboxylate reductase	17.73	17.16	18.03	17.57	21.11	
COG	E	Amino acid transport and metabolism	Tfu_2722	Tfu_2722 HAD-superfamily hydrolase subfamily IB, PSPase-like:HAD-superfamily subfamily IB, PSPase-like						
COG	E	Amino acid transport and metabolism	Tfu_2763	Tfu_2763 arginine/ornithine transport system ATPase	16.2	15.51	14.39	14.55	18.73	
COG	E	Amino acid transport and metabolism	Tfu_2779	Tfu_2779 hypothetical protein						
COG	E	Amino acid transport and metabolism	Tfu_2787	Tfu_2787 hypothetical protein	18.92	18.83	18.07	18.59	22.23	1.1
COG	E	Amino acid transport and metabolism	Tfu_2797	Tfu_2797 d-amino-acid dehydrogenase	19.11	19.07	21.99	22	24.93	1.927
COG	E	Amino acid transport and metabolism	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
COG	E	Amino acid transport and metabolism	Tfu_2814	Tfu_2814 putative dehydrogenase						
COG	E	Amino acid transport and metabolism	Tfu_2822	Tfu_2822 homoserine O-acetyltransferase	15.5	15.63		15.19	19.08	
COG	E	Amino acid transport and metabolism	Tfu_2823	Tfu_2823 O-acetylhomoserine sulfhydrylase	22.33	21.67	21.43	21.62	25.14	0.779
COG	E	Amino acid transport and metabolism	Tfu_2879	Tfu_2879 hypothetical protein	13.85	13.58			19.82	
COG	E	Amino acid transport and metabolism	Tfu_2928	Tfu_2928 hypothetical protein	20.69	21.33	20.08	19.7	23	0.829
COG	E	Amino acid transport and metabolism	Tfu_2929	Tfu_2929 similar to ABC-type proline/glycine betaine transport system permease component					18.2	
COG	E	Amino acid transport and metabolism	Tfu_2930	Tfu_2930 glycine betaine/L-proline transport ATP-binding subunit			14.84		19.59	
COG	E	Amino acid transport and metabolism	Tfu_3018	Tfu_3018 putative aminotransferase					19.29	1.473
COG	E	Amino acid transport and metabolism	Tfu_3025	Tfu_3025 putative alcohol dehydrogenase	18.7	19.04	16.64	17.19	21.72	
COG	E	Amino acid transport and metabolism	Tfu_3053	Tfu_3053 prephenate dehydratase					16.06	
COG	L	Replication, recombination and repair	Tfu_0001	Tfu_0001 bacterial chromosomal replication initiator protein, DnaA					16.48	
COG	L	Replication, recombination and repair	Tfu_0002	Tfu_0002 DNA polymerase III subunit beta			14.09		20.64	
COG	L	Replication, recombination and repair	Tfu_0004	Tfu_0004 recombination protein F	16.84				21.06	

COG	L	Replication, recombination and repair	Tfu_0006	Tfu_0006 DNA topoisomerase IV subunit B	17.12	17.69	18.92	18.55	22.87	1.181
COG	L	Replication, recombination and repair	Tfu_0007	Tfu_0007 DNA gyrase, subunit A	19.16	19.14	20.72	20.43	24.43	1.156
COG	L	Replication, recombination and repair	Tfu_0019	Tfu_0019 DnaB helicase					15.82	
COG	L	Replication, recombination and repair	Tfu_0044	Tfu_0044 recombination protein RecR					17.72	
COG	L	Replication, recombination and repair	Tfu_0047	Tfu_0047 DNA polymerase III subunit alpha					14.78	
COG	L	Replication, recombination and repair	Tfu_0051	Tfu_0051 DNA polymerase III subunits gamma and tau					16.27	
COG	L	Replication, recombination and repair	Tfu_0064	Tfu_0064 putative DNA helicase	14.96	16.02			20.03	
COG	L	Replication, recombination and repair	Tfu_0086	Tfu_0086 DNA polymerase III subunit beta	14.58			14.38	19.46	
COG	L	Replication, recombination and repair	Tfu_0118	Tfu_0118 hypothetical protein					16.68	
COG	L	Replication, recombination and repair	Tfu_0163	Tfu_0163 Tyrosine protein kinase:Serine/threonine protein kinase	15.1	14.83	14.91	14.78	20.69	
COG	L	Replication, recombination and repair	Tfu_0183	Tfu_0183 DNA polymerase III subunit epsilon					16.34	
COG	L	Replication, recombination and repair	Tfu_0214	Tfu_0214 similar to Site-specific recombinase XerD					14.34	
COG	L	Replication, recombination and repair	Tfu_0258	Tfu_0258 AP endonuclease, family 1:Exodeoxyribonuclease III xth		15.38	17.28	16.99	20.99	
COG	L	Replication, recombination and repair	Tfu_0366	Tfu_0366 methylated-DNA (protein)-cysteine S-methyltransferase						
COG	L	Replication, recombination and repair	Tfu_0398	Tfu_0398 TatD-related deoxyribonuclease					18.88	
COG	L	Replication, recombination and repair	Tfu_0406	Tfu_0406 Tyrosine protein kinase:Serine/threonine protein kinase	15.36	16.04			20.09	0.675
COG	L	Replication, recombination and repair	Tfu_0424	Tfu_0424 transcription-repair coupling factor					18.09	
COG	L	Replication, recombination and repair	Tfu_0454	Tfu_0454 Tyrosine protein kinase:Serine/threonine protein kinase					16.34	
COG	L	Replication, recombination and repair	Tfu_0467	Tfu_0467 exodeoxyribonuclease VII small subunit	15.19	15.36			16.56	
COG	L	Replication, recombination and repair	Tfu_0468	Tfu_0468 exodeoxyribonuclease VII large subunit	16.38	16.62		14.75	20.3	
COG	L	Replication, recombination and repair	Tfu_0498	Tfu_0498 DNA-3-methyladenine glycosylase I					15.85	
COG	L	Replication, recombination and repair	Tfu_0500	Tfu_0500 Tyrosine protein kinase:Serine/threonine protein kinase	16.56	16			20.28	
COG	L	Replication, recombination and repair	Tfu_0514	Tfu_0514 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal						
COG	L	Replication, recombination and repair	Tfu_0522	Tfu_0522 hypothetical protein						
COG	L	Replication, recombination and repair	Tfu_0523	Tfu_0523 putative ATP-dependent DNA helicase					17.89	
COG	L	Replication, recombination and repair	Tfu_0524	Tfu_0524 putative DNA helicase					16.97	
COG	L	Replication, recombination and repair	Tfu_0527	Tfu_0527 hypothetical protein					16.28	
COG	L	Replication, recombination and repair	Tfu_0530	Tfu_0530 superfamily I DNA and RNA helicases						
COG	L	Replication, recombination and repair	Tfu_0534	Tfu_0534 deoxyribodipyrimidine photolyase						
COG	L	Replication, recombination and repair	Tfu_0535	Tfu_0535 hypothetical protein						
COG	L	Replication, recombination and repair	Tfu_0592	Tfu_0592 Tyrosine protein kinase:Serine/threonine protein kinase	18.18	17.59	17.18	17.09	21.25	
COG	L	Replication, recombination and repair	Tfu_0601	Tfu_0601 serine/threonine protein kinase	14.82	14.92	15.29		19.56	
COG	L	Replication, recombination and repair	Tfu_0603	Tfu_0603 DNA ligase	17.51	17.99	18.58	17.99	22.94	
COG	L	Replication, recombination and repair	Tfu_0628	Tfu_0628 Histone-like bacterial DNA-binding protein						
COG	L	Replication, recombination and repair	Tfu_0646	Tfu_0646 ATP-dependent DNA helicase RecG					20.26	
COG	L	Replication, recombination and repair	Tfu_0647	Tfu_0647 Conserved hypothetical protein 95					19.34	
COG	L	Replication, recombination and repair	Tfu_0652	Tfu_0652 formamidopyrimidine-DNA glycosylase						
COG	L	Replication, recombination and repair	Tfu_0669	Tfu_0669 hypothetical protein						
COG	L	Replication, recombination and repair	Tfu_0671	Tfu_0671 SMF protein						
COG	L	Replication, recombination and repair	Tfu_0674	Tfu_0674 tyrosine recombinase						
COG	L	Replication, recombination and repair	Tfu_0693	Tfu_0693 similar to Superfamily I DNA and RNA helicases and helicase subunits					15.37	
COG	L	Replication, recombination and repair	Tfu_0694	Tfu_0694 putative DNA repair hydrolase						
COG	L	Replication, recombination and repair	Tfu_0701	Tfu_0701 Tyrosine protein kinase:Serine/threonine protein kinase	18.86	18.29	16.43	15.99	22.51	0.6
COG	L	Replication, recombination and repair	Tfu_0703	Tfu_0703 transposase, IS605 OrfB					16.09	
COG	L	Replication, recombination and repair	Tfu_0714	Tfu_0714 exonuclease	20.07	19.91	16.25	15.46	21.16	1.005
COG	L	Replication, recombination and repair	Tfu_0715	Tfu_0715 similar to Rossmann fold nucleotide-binding protein involved in DNA uptake						
COG	L	Replication, recombination and repair	Tfu_0720	Tfu_0720 similar to Superfamily I DNA and RNA helicases and helicase subunits					18.48	
COG	L	Replication, recombination and repair	Tfu_0725	Tfu_0725 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal					18.1	
COG	L	Replication, recombination and repair	Tfu_0803	Tfu_0803 intein	19.36	19.4	18.02	18.02	22.28	1.189
COG	L	Replication, recombination and repair	Tfu_0823	Tfu_0823 DNA polymerase III, delta subunit					18.6	
COG	L	Replication, recombination and repair	Tfu_0826	Tfu_0826 helix-hairpin-helix DNA-binding, class 1						
COG	L	Replication, recombination and repair	Tfu_0852	Tfu_0852 DNA repair protein RecO						
COG	L	Replication, recombination and repair	Tfu_0866	Tfu_0866 DNA primase					16.49	
COG	L	Replication, recombination and repair	Tfu_0878	Tfu_0878 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal	15.05	15.84	15.93	16.16	20.97	0.767
COG	L	Replication, recombination and repair	Tfu_0902	Tfu_0902 DNA polymerase III, epsilon subunit						
COG	L	Replication, recombination and repair	Tfu_1000	Tfu_1000 probable phosphoesterase YhaO-putative DNA repair exonuclease						
COG	L	Replication, recombination and repair	Tfu_1027	Tfu_1027 hypothetical protein						
COG	L	Replication, recombination and repair	Tfu_1041	Tfu_1041 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA		13.51			20.01	
COG	L	Replication, recombination and repair	Tfu_1073	Tfu_1073 primosome assembly protein PriA					16.49	0.882

COG	L	Replication, recombination and repair	Tfu_1084	Tfu_1084 serine/threonine protein kinase	14.81				19.13	
COG	L	Replication, recombination and repair	Tfu_1096	Tfu_1096 DNA-directed DNA polymerase						
COG	L	Replication, recombination and repair	Tfu_1133	Tfu_1133 transposase, IS605 OrfB						
COG	L	Replication, recombination and repair	Tfu_1134	Tfu_1134 transposase-related protein						
COG	L	Replication, recombination and repair	Tfu_1141	Tfu_1141 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	L	Replication, recombination and repair	Tfu_1189	Tfu_1189 DNA polymerase I	20.07	19.68	19.65	19.77	23.74	0.917
COG	L	Replication, recombination and repair	Tfu_1196	Tfu_1196 excinuclease ABC subunit B	15.43	14.4	16.74	17.22	21.51	1.302
COG	L	Replication, recombination and repair	Tfu_1200	Tfu_1200 hypothetical protein			14.4	14.71	20.54	
COG	L	Replication, recombination and repair	Tfu_1201	Tfu_1201 tyrosine recombinase						
COG	L	Replication, recombination and repair	Tfu_1323	Tfu_1323 transposase-related protein						
COG	L	Replication, recombination and repair	Tfu_1324	Tfu_1324 transposase, IS605 OrfB						
COG	L	Replication, recombination and repair	Tfu_1341	Tfu_1341 uracil-DNA glycosylase	17.73	18.1	16.87	17.48	21.34	0.623
COG	L	Replication, recombination and repair	Tfu_1342	Tfu_1342 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	L	Replication, recombination and repair	Tfu_1400	Tfu_1400 putative endonuclease						
COG	L	Replication, recombination and repair	Tfu_1427	Tfu_1427 putative DNA repair protein						
COG	L	Replication, recombination and repair	Tfu_1440	Tfu_1440 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal			11.04		19.52	
COG	L	Replication, recombination and repair	Tfu_1507	Tfu_1507 Methylated-DNA-(protein)-cysteine S-methyltransferase			15.09	15.77	19.75	0.755
COG	L	Replication, recombination and repair	Tfu_1514	Tfu_1514 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	L	Replication, recombination and repair	Tfu_1529	Tfu_1529 hypothetical protein						
COG	L	Replication, recombination and repair	Tfu_1541	Tfu_1541 AP endonuclease, family 1:Exodeoxyribonuclease III xth					16.85	
COG	L	Replication, recombination and repair	Tfu_1553	Tfu_1553 putative integrase/recombinase						
COG	L	Replication, recombination and repair	Tfu_1559	Tfu_1559 putative uvrA-like protein						
COG	L	Replication, recombination and repair	Tfu_1560	Tfu_1560 putative excision nuclease ABC subunit						
COG	L	Replication, recombination and repair	Tfu_1561	Tfu_1561 uvrA-like protein						
COG	L	Replication, recombination and repair	Tfu_1579	Tfu_1579 similar to Uncharacterized protein predicted to be involved in DNA repair (RAMP superfamily)					18.59	
COG	L	Replication, recombination and repair	Tfu_1580	Tfu_1580 Protein of unknown function DUF324	19.7	19.12	18.49	18.33	22.9	0.99
COG	L	Replication, recombination and repair	Tfu_1582	Tfu_1582 CRISPR-associated TM1791 family protein	16.2	17.31	14.77	16.18	19.95	
COG	L	Replication, recombination and repair	Tfu_1583	Tfu_1583 CRISPR-associated TM1795 family protein	17.39	17.18	15.44	13.94	20.79	1.201
COG	L	Replication, recombination and repair	Tfu_1587	Tfu_1587 Protein of unknown function DUF48						
COG	L	Replication, recombination and repair	Tfu_1658	Tfu_1658 Tyrosine protein kinase:Serine/threonine protein kinase:Sel1-like repeat						
COG	L	Replication, recombination and repair	Tfu_1753	Tfu_1753 helicase RecD/TraA					15.31	
COG	L	Replication, recombination and repair	Tfu_1756	Tfu_1756 Tyrosine protein kinase:Serine/threonine protein kinase	13.69	14.76	15.42	14.85	21.48	1.016
COG	L	Replication, recombination and repair	Tfu_1765	Tfu_1765 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal	14.16		17.46	17.45	22.14	0.919
COG	L	Replication, recombination and repair	Tfu_1816	Tfu_1816 hypothetical protein						
COG	L	Replication, recombination and repair	Tfu_1840	Tfu_1840 hypothetical protein					19.33	
COG	L	Replication, recombination and repair	Tfu_1918	Tfu_1918 putative DNA glycosylase						
COG	L	Replication, recombination and repair	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
COG	L	Replication, recombination and repair	Tfu_1956	Tfu_1956 AP endonuclease, family 2			12.75	12.58	17.8	
COG	L	Replication, recombination and repair	Tfu_2021	Tfu_2021 excinuclease ABC subunit C			13.35		19.94	
COG	L	Replication, recombination and repair	Tfu_2024	Tfu_2024 excinuclease ABC subunit A			14.49	13.44	21.02	1.418
COG	L	Replication, recombination and repair	Tfu_2032	Tfu_2032 DNA repair protein RecN	15.14		15.66	15.33	21.25	
COG	L	Replication, recombination and repair	Tfu_2039	Tfu_2039 hypothetical protein						
COG	L	Replication, recombination and repair	Tfu_2069	Tfu_2069 Holliday junction resolvase YqgF					17.3	
COG	L	Replication, recombination and repair	Tfu_2074	Tfu_2074 Tyrosine protein kinase:Serine/threonine protein kinase	18.52	18.73	17.5	17.42	22.55	0.999
COG	L	Replication, recombination and repair	Tfu_2075	Tfu_2075 Tyrosine protein kinase:Serine/threonine protein kinase	14.14				15.26	
COG	L	Replication, recombination and repair	Tfu_2081	Tfu_2081 ATPase related to the helicase subunit of the Holliday junction resolvase					18.55	
COG	L	Replication, recombination and repair	Tfu_2093	Tfu_2093 Holliday junction DNA helicase RuvB						
COG	L	Replication, recombination and repair	Tfu_2094	Tfu_2094 DNA recombination protein, RuvA					18.24	
COG	L	Replication, recombination and repair	Tfu_2095	Tfu_2095 Holliday junction resolvase						
COG	L	Replication, recombination and repair	Tfu_2131	Tfu_2131 DNA gyrase subunit A			14.33		20.22	
COG	L	Replication, recombination and repair	Tfu_2134	Tfu_2134 DNA gyrase subunit B		13.06			19.19	
COG	L	Replication, recombination and repair	Tfu_2145	Tfu_2145 ribonuclease HII						
COG	L	Replication, recombination and repair	Tfu_2167	Tfu_2167 helicase c2:DEAD/DEAH box helicase, N-terminal						
COG	L	Replication, recombination and repair	Tfu_2229	Tfu_2229 Tyrosine protein kinase:Serine/threonine protein kinase		14.19			18.3	1.106
COG	L	Replication, recombination and repair	Tfu_2317	Tfu_2317 ATP-dependent helicase HrpA					19.03	
COG	L	Replication, recombination and repair	Tfu_2326	Tfu_2326 putative DNA helicase					17.64	
COG	L	Replication, recombination and repair	Tfu_2329	Tfu_2329 similar to Superfamily I DNA and RNA helicases	20.12	20.02	20.35	20.24	24.1	1.249
COG	L	Replication, recombination and repair	Tfu_2347	Tfu_2347 exonuclease					16.03	
COG	L	Replication, recombination and repair	Tfu_2361	Tfu_2361 Tyrosine protein kinase:Serine/threonine protein kinase	15.67	15.45	16.47	16.35	21.04	

COG	L	Replication, recombination and repair	Tfu_2375	Tfu_2375 Tyrosine protein kinase:Serine/threonine protein kinase	15.45	14.62		15.18	19.56	
COG	L	Replication, recombination and repair	Tfu_2381	Tfu_2381 ATPaseDEAD/DEAH box helicase, N-terminal					16.14	
COG	L	Replication, recombination and repair	Tfu_2401	Tfu_2401 hypothetical protein	15.24	13.88			20.8	
COG	L	Replication, recombination and repair	Tfu_2450	Tfu_2450 DEAD/DEAH box helicase, N-terminal	14.55	14.97			20.05	1.063
COG	L	Replication, recombination and repair	Tfu_2507	Tfu_2507 Tyrosine protein kinase:Serine/threonine protein kinase	17.36	17.16	16.35	15.91	21.06	1.521
COG	L	Replication, recombination and repair	Tfu_2580	Tfu_2580 ATP-dependent DNA helicase PcrA					19.8	
COG	L	Replication, recombination and repair	Tfu_2668	Tfu_2668 hypothetical protein	14.3	15.26	14.26	14.47	20.69	0.884
COG	L	Replication, recombination and repair	Tfu_2699	Tfu_2699 excisionase/Xis, DNA-binding						
COG	L	Replication, recombination and repair	Tfu_2751	Tfu_2751 excisionase/Xis, DNA-binding						
COG	L	Replication, recombination and repair	Tfu_2782	Tfu_2782 DNA polymerase III delta prime subunit					15.08	
COG	L	Replication, recombination and repair	Tfu_2784	Tfu_2784 bacterial DNA topoisomerase I	18.89	18.47	19.13	18.7	23.17	1.366
COG	L	Replication, recombination and repair	Tfu_2824	Tfu_2824 hypothetical protein						
COG	L	Replication, recombination and repair	Tfu_2845	Tfu_2845 Tyrosine protein kinase:Serine/threonine protein kinase		13.26		14.27	19.42	
COG	L	Replication, recombination and repair	Tfu_2875	Tfu_2875 HhH-GPD:Iron-sulfur cluster loop						
COG	L	Replication, recombination and repair	Tfu_2878	Tfu_2878 DNA and RNA helicase	13.84		14.52		21.11	
COG	L	Replication, recombination and repair	Tfu_3065	Tfu_3065 Tyrosine protein kinase:Serine/threonine protein kinase					18.02	
COG	L	Replication, recombination and repair	Tfu_3066	Tfu_3066 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA	19.07	19.31	18.37	17.91	22.14	0.98
COG	L	Replication, recombination and repair	Tfu_3094	Tfu_3094 single-strand DNA-binding protein	18.47	18.74	19.16	18.86	21.78	1.038
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0057	Tfu_0057 putative regulatory protein						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0080	Tfu_0080 GAF domain protein	19.13	18.7	16.8	16.58	21.11	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0081	Tfu_0081 3-hydroxybutyrate dehydrogenase	21.11	21.46	19.94	20.31	23.95	1.187
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0082	Tfu_0082 hypothetical protein		13.31			15.38	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0085	Tfu_0085 hypothetical protein					17.54	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0275	Tfu_0275 putative short chain dehydrogenase	19.38	19.27	18.64	18.26	23.3	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0621	Tfu_0621 5-carboxymethyl-2-hydroxymuconate delta-isomerase		15.03	16.15	16.99	20.92	0.813
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0691	Tfu_0691 helix-turn-helix, Fis-type					18.97	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0756	Tfu_0756 similar to Acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0821	Tfu_0821 imidazolonepropionase					17.2	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_0883	Tfu_0883 hypothetical protein						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1139	Tfu_1139 hypothetical protein						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1188	Tfu_1188 Phenylacetic acid degradation-related protein				15.85	20.42	1.083
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1221	Tfu_1221 hypothetical protein						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1224	Tfu_1224 putative 3-oxoacyl-(acyl-carrier protein) reductase						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1225	Tfu_1225 putative cytochrome P450						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1231	Tfu_1231 modular polyketide synthase					14.31	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1242	Tfu_1242 short chain dehydrogenase					18.48	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1257	Tfu_1257 cytochrome P450 monooxygenase	18.3	17.85	18.66	17.53	22.31	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1267	Tfu_1267 frnE protein					16.17	0.636
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1274	Tfu_1274 hypothetical protein					18.59	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1279	Tfu_1279 short chain dehydrogenase					16.87	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1283	Tfu_1283 probable short-chain type dehydrogenase/reductase						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1298	Tfu_1298 2-deoxy-D-gluconate 3-dehydrogenase	15.48	14.84		13.51	17.6	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly related to diterpenoid m	16.49	15.45			20.78	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1408	Tfu_1408 putative ortho-succinylbenzoate-CoA synthetase						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1413	Tfu_1413 isochorismate synthase						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1462	Tfu_1462 similar to Acetyl esterase (deacetylase)	17.67	15.79	15.84	16.11	21.76	0.85
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1466	Tfu_1466 short-chain alcohol dehydrogenase						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1472	Tfu_1472 short-chain dehydrogenase/reductase (SDR) family protein						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1474	Tfu_1474 short chain dehydrogenase						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1478	Tfu_1478 hypothetical protein					15.15	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1747	Tfu_1747 putative cytochrome P450	14.01	13.89	16.95	16.88	21.61	0.961
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1748	Tfu_1748 cytochrome P450-family protein	21.07	20.88	21.08	21.02	24.29	0.744
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1784	Tfu_1784 hypothetical protein	14.4				19.3	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1795	Tfu_1795 helix-turn-helix, Fis-type					14.89	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118

COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1848	Tfu_1848 hypothetical protein					13.81	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1865	Tfu_1865 amino acid adenylation				14.72	20.83	0.97
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1866	Tfu_1866 amino acid adenylation			13.74		19.3	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1867	Tfu_1867 non-ribosomal peptide synthase:Amino acid adenylation			16.51	15.91	21.64	0.777
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1868	Tfu_1868 isochorismatase					16.81	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1869	Tfu_1869 putative peptide monooxygenase					18.53	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1870	Tfu_1870 isochorismatase						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1871	Tfu_1871 2,3-dihydroxybenzoate-AMP ligase			14.18	14.93	21.25	0.737
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1872	Tfu_1872 isochorismate synthase					17.85	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1873	Tfu_1873 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase					14.76	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1972	Tfu_1972 hypothetical protein			14.16		19.27	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1975	Tfu_1975 acyl carrier protein	20.19	20.71	21.15	20.99	23.95	0.341
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1976	Tfu_1976 putative 3-oxoacyl-ACP synthase II	18.39	18.02	19.63	19.4	22.79	0.718
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2316	Tfu_2316 thioesterase II						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2707	Tfu_2707 putative acetoin utilization protein			16.17	15.33	21.16	1.239
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2794	Tfu_2794 hypothetical protein						
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2798	Tfu_2798 putative DNA-binding protein					15.73	
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2802	Tfu_2802 putative cytochrome P450	22.14	21.99	22.82	22.52	25.75	1.258
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2803	Tfu_2803 putative cytochrome P450-family protein	16.68	17.52	15.1	15.06	21.3	0.807
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2975	Tfu_2975 putative cytochrome P450	14.88	15.08	13.71		19.36	0.862
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_2976	Tfu_2976 cytochrome P450-family protein	17.8	17.66	17.44	17.56	21.48	0.739
COG	Q	Secondary metabolites biosynthesis, transport and catabolism	Tfu_3075	Tfu_3075 putative phytoene desaturase						
COG	H	Coenzyme transport and metabolism	Tfu_0055	Tfu_0055 hypothetical protein						
COG	H	Coenzyme transport and metabolism	Tfu_0150	Tfu_0150 hypothetical protein					18.27	
COG	H	Coenzyme transport and metabolism	Tfu_0206	Tfu_0206 aminotransferase, class III						
COG	H	Coenzyme transport and metabolism	Tfu_0227	Tfu_0227 hypothetical protein	18.67	18.07	17.48	17.67	21.55	0.839
COG	H	Coenzyme transport and metabolism	Tfu_0246	Tfu_0246 phosphoserine aminotransferase	19.59	19.46	22.48	21.91	25.76	1.096
COG	H	Coenzyme transport and metabolism	Tfu_0248	Tfu_0248 pyridoxamine 5'-phosphate oxidase	15.34	14.98		14.89	18.71	
COG	H	Coenzyme transport and metabolism	Tfu_0278	Tfu_0278 hypothetical protein	16.59	16.92	17.63	17.14	21.84	0.729
COG	H	Coenzyme transport and metabolism	Tfu_0309	Tfu_0309 cobyric acid synthase					19.41	
COG	H	Coenzyme transport and metabolism	Tfu_0310	Tfu_0310 precorrin-6x reductase CbiJ/CobK					14.55	
COG	H	Coenzyme transport and metabolism	Tfu_0311	Tfu_0311 cobyrinic acid a,c-diamide synthase CbiA					16.36	
COG	H	Coenzyme transport and metabolism	Tfu_0312	Tfu_0312 cob(I)yrinic acid a,c-diamide adenosyltransferase					16.96	
COG	H	Coenzyme transport and metabolism	Tfu_0313	Tfu_0313 Mg-chelatase subunit ChlI	16.96	16.73	17.38	16.55	20.43	
COG	H	Coenzyme transport and metabolism	Tfu_0314	Tfu_0314 SAM (and some other nucleotide) binding motif						
COG	H	Coenzyme transport and metabolism	Tfu_0315	Tfu_0315 precorrin-4 C11-methyltransferase region					19.46	0.814
COG	H	Coenzyme transport and metabolism	Tfu_0316	Tfu_0316 precorrin-3B C17-methyltransferase region:Precorrin-2 C20-methyltransferase						
COG	H	Coenzyme transport and metabolism	Tfu_0317	Tfu_0317 precorrin-8X methylmutase						
COG	H	Coenzyme transport and metabolism	Tfu_0319	Tfu_0319 cobaltochelatase	18.14	17.88	19.25	19.28	23.66	1.195
COG	H	Coenzyme transport and metabolism	Tfu_0320	Tfu_0320 putative cobF protein, precorrin-6A synthase						
COG	H	Coenzyme transport and metabolism	Tfu_0336	Tfu_0336 ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components					15.18	
COG	H	Coenzyme transport and metabolism	Tfu_0372	Tfu_0372 hypothetical protein						
COG	H	Coenzyme transport and metabolism	Tfu_0374	Tfu_0374 molybdopterin binding domain						
COG	H	Coenzyme transport and metabolism	Tfu_0375	Tfu_0375 molybdenum cofactor biosynthesis protein C						
COG	H	Coenzyme transport and metabolism	Tfu_0376	Tfu_0376 molybdopterin binding domain					15.3	
COG	H	Coenzyme transport and metabolism	Tfu_0396	Tfu_0396 hypothetical protein	15.1	14.77		15.42	19.51	
COG	H	Coenzyme transport and metabolism	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
COG	H	Coenzyme transport and metabolism	Tfu_0443	Tfu_0443 magnesium chelatase subunit ChlI					17.16	
COG	H	Coenzyme transport and metabolism	Tfu_0520	Tfu_0520 molybdopterin biosynthesis protein MoeB	17.59	17.14	18.26	18.38	22.64	0.841
COG	H	Coenzyme transport and metabolism	Tfu_0538	Tfu_0538 molybdenum cofactor biosynthesis protein E					15.59	
COG	H	Coenzyme transport and metabolism	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
COG	H	Coenzyme transport and metabolism	Tfu_0572	Tfu_0572 hypothetical protein					16.37	
COG	H	Coenzyme transport and metabolism	Tfu_0575	Tfu_0575 quinolinate synthetase						
COG	H	Coenzyme transport and metabolism	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	

COG	H	Coenzyme transport and metabolism	Tfu_0613	Tfu_0613 ketol-acid reductoisomerase	19.9	19.77	19.96	19.71	23.42	0.799
COG	H	Coenzyme transport and metabolism	Tfu_0614	Tfu_0614 D-3-phosphoglycerate dehydrogenase	20.25	20.04	22.34	22.29	25.26	1.066
COG	H	Coenzyme transport and metabolism	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
COG	H	Coenzyme transport and metabolism	Tfu_0643	Tfu_0643 thiamine monophosphate kinase					14.5	
COG	H	Coenzyme transport and metabolism	Tfu_0648	Tfu_0648 coenzyme A biosynthesis protein:Cytidyltransferase-related	18.01	16.72	17.97	17.55	22.5	1.132
COG	H	Coenzyme transport and metabolism	Tfu_0735	Tfu_0735 ubiquinone/menaquinone biosynthesis methyltransferase						
COG	H	Coenzyme transport and metabolism	Tfu_0737	Tfu_0737 hypothetical protein						
COG	H	Coenzyme transport and metabolism	Tfu_0739	Tfu_0739 coproporphyrinogen III oxidase						
COG	H	Coenzyme transport and metabolism	Tfu_0782	Tfu_0782 Cytidyltransferase-related		13.35	14.92	14.18	20.03	
COG	H	Coenzyme transport and metabolism	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
COG	H	Coenzyme transport and metabolism	Tfu_0835	Tfu_0835 putative oxygen-independent coproporphyrinogen III oxidase						
COG	H	Coenzyme transport and metabolism	Tfu_0876	Tfu_0876 5-amino-6-(5-phosphoribosylamino)uracil reductase					18.52	
COG	H	Coenzyme transport and metabolism	Tfu_0877	Tfu_0877 hypothetical protein					17.13	
COG	H	Coenzyme transport and metabolism	Tfu_0944	Tfu_0944 similar to 2-polyprenyl-3-methyl-5-hydroxy-6-metoxy-1 4-benzoquinol methylase						
COG	H	Coenzyme transport and metabolism	Tfu_0981	Tfu_0981 3-methyl-2-oxobutanoate hydroxymethyltransferase	18.23	17.36	19.12	19.31	23.68	0.787
COG	H	Coenzyme transport and metabolism	Tfu_0983	Tfu_0983 NAD+ synthase	16.91	16.85	17.72	17.22	22.21	0.82
COG	H	Coenzyme transport and metabolism	Tfu_0991	Tfu_0991 lipoyl synthase					17.9	1.46
COG	H	Coenzyme transport and metabolism	Tfu_0992	Tfu_0992 lipoyltransferase					18.24	
COG	H	Coenzyme transport and metabolism	Tfu_0996	Tfu_0996 putative cobalamin (5'-phosphate) synthase : adenosylcobinamide-GDP ribazoletransferase						
COG	H	Coenzyme transport and metabolism	Tfu_0997	Tfu_0997 adenosylcobinamide kinase / adenosylcobinamide-phosphate guanylyltransf		15.35		15.47	20.21	
COG	H	Coenzyme transport and metabolism	Tfu_1038	Tfu_1038 thiamine biosynthesis protein	11.78	11.81	13.56	13.9	19.3	
COG	H	Coenzyme transport and metabolism	Tfu_1042	Tfu_1042 thiazole synthase	15.18	14.95	16.52	16.29	21.36	0.853
COG	H	Coenzyme transport and metabolism	Tfu_1043	Tfu_1043 ThiS, thiamine-biosynthesis						
COG	H	Coenzyme transport and metabolism	Tfu_1046	Tfu_1046 thiamine-phosphate pyrophosphorylase		14.35			19.31	
COG	H	Coenzyme transport and metabolism	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
COG	H	Coenzyme transport and metabolism	Tfu_1058	Tfu_1058 dihydroorotate dehydrogenase electron transfer subunit						
COG	H	Coenzyme transport and metabolism	Tfu_1064	Tfu_1064 phosphopantothenoylcysteine synthase/decarboxylase	18.49	18.47	18.49	18.95	22.74	1.103
COG	H	Coenzyme transport and metabolism	Tfu_1065	Tfu_1065 S-adenosylmethionine synthetase	15.28	15.32	15.74	16.4	20.99	0.962
COG	H	Coenzyme transport and metabolism	Tfu_1078	Tfu_1078 Lumazine-binding protein		13.92	16.4	17.05	20.31	
COG	H	Coenzyme transport and metabolism	Tfu_1079	Tfu_1079 nicotinamide mononucleotide transporter PnuC						
COG	H	Coenzyme transport and metabolism	Tfu_1080	Tfu_1080 bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein						
COG	H	Coenzyme transport and metabolism	Tfu_1081	Tfu_1081 6,7-dimethyl-8-ribityllumazine synthase	15.97	15.69	16.33	16.62	21.62	
COG	H	Coenzyme transport and metabolism	Tfu_1095	Tfu_1095 putative methyltransferase	18.7	18.18	17.65	17.39	22.37	0.9
COG	H	Coenzyme transport and metabolism	Tfu_1192	Tfu_1192 dephospho-CoA kinase	17.51	17.36	16.73	16.92	20.12	
COG	H	Coenzyme transport and metabolism	Tfu_1216	Tfu_1216 hypothetical protein						
COG	H	Coenzyme transport and metabolism	Tfu_1223	Tfu_1223 hypothetical protein					15.45	
COG	H	Coenzyme transport and metabolism	Tfu_1258	Tfu_1258 hypothetical protein					16.44	
COG	H	Coenzyme transport and metabolism	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
COG	H	Coenzyme transport and metabolism	Tfu_1314	Tfu_1314 dihydropteroate synthase	16.71	16.84	17.22	16.91	22.57	1.071
COG	H	Coenzyme transport and metabolism	Tfu_1316	Tfu_1316 hypothetical protein	16.83	16.57	17.51	16.59	22.22	
COG	H	Coenzyme transport and metabolism	Tfu_1348	Tfu_1348 molybdenum cofactor biosynthesis protein A						
COG	H	Coenzyme transport and metabolism	Tfu_1366	Tfu_1366 hypothetical protein						
COG	H	Coenzyme transport and metabolism	Tfu_1386	Tfu_1386 glutamine amidotransferase of anthranilate synthase:Anthranilate sy	14.29	15.3	14.48	14.83	21.47	1.207
COG	H	Coenzyme transport and metabolism	Tfu_1409	Tfu_1409 naphthoate synthase	16.03	15.45	18.71	18.23	22.53	
COG	H	Coenzyme transport and metabolism	Tfu_1411	Tfu_1411 Menaquinone biosynthesis protein					16.81	
COG	H	Coenzyme transport and metabolism	Tfu_1413	Tfu_1413 isochorismate synthase						
COG	H	Coenzyme transport and metabolism	Tfu_1494	Tfu_1494 ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components						
COG	H	Coenzyme transport and metabolism	Tfu_1547	Tfu_1547 pterin-4-alpha-carbinolamine dehydratase						
COG	H	Coenzyme transport and metabolism	Tfu_1565	Tfu_1565 hypothetical protein					18.32	
COG	H	Coenzyme transport and metabolism	Tfu_1634	Tfu_1634 putative ribosomal RNA methyltransferase						
COG	H	Coenzyme transport and metabolism	Tfu_1666	Tfu_1666 para-aminobenzoate synthase, component I:Glutamine amidotransferase of anthranilate synthase						
COG	H	Coenzyme transport and metabolism	Tfu_1671	Tfu_1671 s-adenosylmethionine (SAM)-dependent methyltransferase						
COG	H	Coenzyme transport and metabolism	Tfu_1678	Tfu_1678 von Willebrand factor, type A						
COG	H	Coenzyme transport and metabolism	Tfu_1751	Tfu_1751 putative methyltransferase					16.95	
COG	H	Coenzyme transport and metabolism	Tfu_1806	Tfu_1806 hypothetical protein						
COG	H	Coenzyme transport and metabolism	Tfu_1855	Tfu_1855 4'-phosphopantetheinyl transferase						
COG	H	Coenzyme transport and metabolism	Tfu_1862	Tfu_1862 aspartate 1-decarboxylase precursor			14.98		19.99	
COG	H	Coenzyme transport and metabolism	Tfu_1872	Tfu_1872 isochorismate synthase					17.85	
COG	H	Coenzyme transport and metabolism	Tfu_1889	Tfu_1889 phosphoadenosine phosphosulfate reductase						

COG	H	Coenzyme transport and metabolism	Tfu_1897	Tfu_1897 protoporphyrinogen oxidase			14.61		20.74	1.244
COG	H	Coenzyme transport and metabolism	Tfu_1899	Tfu_1899 uroporphyrinogen decarboxylase HemE		14.37	15.41	15.99	20.69	0.856
COG	H	Coenzyme transport and metabolism	Tfu_1909	Tfu_1909 hypothetical protein						
COG	H	Coenzyme transport and metabolism	Tfu_1917	Tfu_1917 1-deoxy-D-xylulose-5-phosphate synthase					16.98	
COG	H	Coenzyme transport and metabolism	Tfu_1945	Tfu_1945 ferrochelatase		13.87	18.69	18.79	22.82	1.023
COG	H	Coenzyme transport and metabolism	Tfu_2000	Tfu_2000 hypothetical protein						
COG	H	Coenzyme transport and metabolism	Tfu_2097	Tfu_2097 putative glutamine amidotransferase					15.71	
COG	H	Coenzyme transport and metabolism	Tfu_2099	Tfu_2099 pyridoxine biosynthesis protein	20.72	20.99	21.71	21.88	24.97	0.901
COG	H	Coenzyme transport and metabolism	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
COG	H	Coenzyme transport and metabolism	Tfu_2115	Tfu_2115 putative molybdopterin biosynthesis protein					17.63	
COG	H	Coenzyme transport and metabolism	Tfu_2171	Tfu_2171 nicotinic acid mononucleotide adenyltransferase					18.95	
COG	H	Coenzyme transport and metabolism	Tfu_2190	Tfu_2190 folylpolyglutamate synthetase					19.35	
COG	H	Coenzyme transport and metabolism	Tfu_2221	Tfu_2221 uroporphyrin-III C-methyltransferase, C-terminal:Siroheme synthase	17.11	16.52	17.24	16.23	21.37	0.99
COG	H	Coenzyme transport and metabolism	Tfu_2222	Tfu_2222 nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransfe	15.06		15.97	15.99	20.79	0.7
COG	H	Coenzyme transport and metabolism	Tfu_2224	Tfu_2224 cobalamin biosynthesis protein						
COG	H	Coenzyme transport and metabolism	Tfu_2250	Tfu_2250 phosphomethylpyrimidine kinase	16.07	16.41	14.97		19.92	1.225
COG	H	Coenzyme transport and metabolism	Tfu_2259	Tfu_2259 similar to Phosphoglycerate dehydrogenase and related dehydrogenase						
COG	H	Coenzyme transport and metabolism	Tfu_2263	Tfu_2263 putative dehydrogenase	15.9	15.27			19.69	
COG	H	Coenzyme transport and metabolism	Tfu_2369	Tfu_2369 hypothetical protein	19.04	18.72	19.19	18.66	21.95	
COG	H	Coenzyme transport and metabolism	Tfu_2373	Tfu_2373 nicotinate phosphoribosyltransferase	14.96		15.9	12.14	20.35	
COG	H	Coenzyme transport and metabolism	Tfu_2441	Tfu_2441 hypothetical protein						
COG	H	Coenzyme transport and metabolism	Tfu_2455	Tfu_2455 putative monooxygenase (putative secreted protein)	13.91				19.65	
COG	H	Coenzyme transport and metabolism	Tfu_2460	Tfu_2460 hypothetical protein						
COG	H	Coenzyme transport and metabolism	Tfu_2464	Tfu_2464 similar to Methylase involved in ubiquinone/menaquinone biosynthesis						
COG	H	Coenzyme transport and metabolism	Tfu_2465	Tfu_2465 hypothetical protein	15.06	15.27			18.08	
COG	H	Coenzyme transport and metabolism	Tfu_2505	Tfu_2505 S-adenosyl-L-homocysteine hydrolase	18.66	19.01	19.8	19.23	23.56	1.126
COG	H	Coenzyme transport and metabolism	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
COG	H	Coenzyme transport and metabolism	Tfu_2520	Tfu_2520 similar to Methylase involved in ubiquinone/menaquinone biosynthesis					14.68	
COG	H	Coenzyme transport and metabolism	Tfu_2553	Tfu_2553 biotin--acetyl-CoA-carboxylase ligase						
COG	H	Coenzyme transport and metabolism	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
COG	H	Coenzyme transport and metabolism	Tfu_2610	Tfu_2610 pantothenate kinase			14.28		19	
COG	H	Coenzyme transport and metabolism	Tfu_2681	Tfu_2681 trans-hexaprenyltranstransferase					20.84	0.581
COG	H	Coenzyme transport and metabolism	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
COG	H	Coenzyme transport and metabolism	Tfu_2726	Tfu_2726 glutamate-1-semialdehyde aminotransferase	17.89	17.41	18.76	18.54	22.7	
COG	H	Coenzyme transport and metabolism	Tfu_2727	Tfu_2727 ribonuclease activity regulator protein RraA					16.96	
COG	H	Coenzyme transport and metabolism	Tfu_2730	Tfu_2730 porphobilinogen synthase					18.56	
COG	H	Coenzyme transport and metabolism	Tfu_2731	Tfu_2731 putative uroporphyrin-III C-methyltransferase/uroporphyrinogen-II	19.75	19.58	19.91	19.51	24.15	1.231
COG	H	Coenzyme transport and metabolism	Tfu_2732	Tfu_2732 porphobilinogen deaminase	13.44				19.8	
COG	H	Coenzyme transport and metabolism	Tfu_2733	Tfu_2733 glutamyl-tRNA reductase						
COG	H	Coenzyme transport and metabolism	Tfu_2841	Tfu_2841 putative rifampin monooxygenase					17.42	
COG	H	Coenzyme transport and metabolism	Tfu_2883	Tfu_2883 L-aspartate oxidase			15.62	16.95	20.84	
COG	H	Coenzyme transport and metabolism	Tfu_2884	Tfu_2884 pantoate-beta-alanine ligase	18.94	18.13	19.39	18.92	22.68	1.137
COG	H	Coenzyme transport and metabolism	Tfu_2890	Tfu_2890 7, 8-Dihydro-6-hydroxymethylpterin-pyrophosphokinase, HPPK					15.52	
COG	H	Coenzyme transport and metabolism	Tfu_2891	Tfu_2891 dihydroneopterin aldolase family:Dihydroneopterin aldolase	14.95	14.62	16	15.74	20.08	
COG	H	Coenzyme transport and metabolism	Tfu_2893	Tfu_2893 dihydropteroate synthase	18.01	17.46	18.35	17.82	21.56	1.133
COG	H	Coenzyme transport and metabolism	Tfu_2894	Tfu_2894 GTP cyclohydrolase I		15.85	17.62	17.38	21.27	0.628
COG	H	Coenzyme transport and metabolism	Tfu_3023	Tfu_3023 similar to Flavodoxin						
COG	H	Coenzyme transport and metabolism	Tfu_3089	Tfu_3089 putative methyltransferase						
COG	N	Cell motility	Tfu_1089	Tfu_1089 hypothetical protein						
COG	N	Cell motility	Tfu_2276	Tfu_2276 putative integral membrane protein						
COG	A	RNA processing and modification	Tfu_2269	Tfu_2269 oligoribonuclease	16.91	16.6	17.83	17.13	21.66	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0009	Tfu_0009 putative transferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0010	Tfu_0010 n-acetylneuraminate synthase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0011	Tfu_0011 putative glycosyltransferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0109	Tfu_0109 hypothetical protein					16.97	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0144	Tfu_0144 hypothetical protein	20	19.55		14.9	20.44	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0166	Tfu_0166 similar to Glycosyltransferase probably involved in cell wall biogenesis					19.49	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0169	Tfu_0169 nucleoside-diphosphate-sugar epimerase (UDP-glucose 4-epimerase	14.49	16.6	18.84	18.16	22.51	0.845
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0184	Tfu_0184 BCCT transporter						

COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0190	Tfu_0190 similar to Cell wall-associated hydrolase (invasion-associated proteins)							
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0295	Tfu_0295 hypothetical protein							
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0368	Tfu_0368 hypothetical protein							
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase, bacterial and archaea	16.85	15	17.24	17.46	22.15	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0414	Tfu_0414 UDP-N-acetylglucosamine pyrophosphorylase	19.4	19.37	19.9	19.97	23.72	1.114
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0471	Tfu_0471 4-hydroxy-3-methylbut-2-enyl diphosphate reductase					19.27	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0480	Tfu_0480 similar to Cell wall-associated hydrolase (invasion-associated proteins)						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0537	Tfu_0537 hypothetical protein					17.68	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0561	Tfu_0561 putative acetyltransferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0570	Tfu_0570 similar to Membrane carboxypeptidase (penicillin-binding protein)	16.79	17.66	15.52	15.8	21.54	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0573	Tfu_0573 putative glycosyl transferase					12.58	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0633	Tfu_0633 D-alanylalanine synthetase	15.85	14.68	13.91		19.95	0.685
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0675	Tfu_0675 hypothetical protein						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0742	Tfu_0742 similar to Outer membrane protein and related peptidoglycan-associated (lipo)proteins						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0748	Tfu_0748 PDZ/DHR/GLGF					17.99	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0829	Tfu_0829 GTP-binding protein LepA		14.01	16.31	15.88	21.87	0.739
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0894	Tfu_0894 putative glycosyltransferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0897	Tfu_0897 similar to ADP-heptose:LPS heptosyltransferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0898	Tfu_0898 hypothetical protein						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0916	Tfu_0916 hypothetical protein						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_0960	Tfu_0960 n-acylamino acid racemase : O-succinylbenzoate-CoA synthase					19.49	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1029	Tfu_1029 hypothetical protein						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1030	Tfu_1030 hypothetical protein					15.74	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1047	Tfu_1047 hypothetical protein						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1102	Tfu_1102 bacterial methyltransferase	16.91	16.77	14.4		20.21	0.758
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1104	Tfu_1104 peptidoglycan glycosyltransferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1105	Tfu_1105 UDP-N-acetylmuramyl-tripeptide synthetase	15.32	14.97	16.06	15.77	20.43	0.647
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1106	Tfu_1106 UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-a		13.98	15.35	14.44	21.31	0.824
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1107	Tfu_1107 phospho-N-acetylmuramoyl-pentapeptide- transferase					17.98	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1108	Tfu_1108 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase					18.55	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1110	Tfu_1110 N-acetylglucosaminyl transferase	19.15	18.71	18.79	18.53	22.9	0.735
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1111	Tfu_1111 UDP-N-acetylmuramate--alanine ligase			14.68	15.53	20.38	1.128
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1112	Tfu_1112 cell division protein FtsQ						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1122	Tfu_1122 signal peptidase II					18.28	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1140	Tfu_1140 hypothetical protein					15.82	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1169	Tfu_1169 prolipoprotein diacylglyceryl transferase	15.48	14.97		15.1	19.56	1.033
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1235	Tfu_1235 hypothetical protein			13.59	13.63	16.15	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / phosphomannomutase	19.06	18.82	21.97	21.81	25.49	1.131
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1410	Tfu_1410 O-succinylbenzoate synthase					15.48	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1416	Tfu_1416 putative secreted penicillin binding protein	14.67	14.74			19.25	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1527	Tfu_1527 rare lipoprotein A						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1564	Tfu_1564 hypothetical protein	14.75		14.55	14.11	20.48	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1622	Tfu_1622 UDP-glucose 4-epimerase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1640	Tfu_1640 D-alanine--D-alanine ligase					15.9	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1652	Tfu_1652 hypothetical protein						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1709	Tfu_1709 UDP-glucose-4-epimerase					17.2	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1717	Tfu_1717 putative racemase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1718	Tfu_1718 putative 5-dehydro-4-deoxyglucarate dehydratase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1730	Tfu_1730 hypothetical protein						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1732	Tfu_1732 hypothetical protein						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1742	Tfu_1742 probable glycosyltransferase					17.3	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1786	Tfu_1786 mandelate racemase/muconate lactonizing enzyme family	16.66	16.7	15.07	15.62	20.33	1.311
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_1850	Tfu_1850 dolichyl-phosphate beta-D-mannosyltransferase	17.8	17.7	16.81	17.93	21.31	0.842
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2022	Tfu_2022 similar to Small-conductance mechanosensitive channel	17.67	17.89	18.36	18.91	23.51	1.543
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2026	Tfu_2026 putative glycosyl transferase						

COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2101	Tfu_2101 phosphatidyl-myo-inositol alpha-mannosyltransferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2130	Tfu_2130 hypothetical protein						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2143	Tfu_2143 putative guanyltransferase					17.31	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2160	Tfu_2160 putative cyclopropane fatty acid synthase	20.23	19.76	18.57	18.29	22.69	1.518
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2162	Tfu_2162 glutamate racemase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2173	Tfu_2173 similar to Glycosyltransferase involved in cell wall biogenesis					15.79	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2177	Tfu_2177 putative glycosyl transferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2178	Tfu_2178 similar to Putative glycosyl/glycerophosphate transferase involved in teichoic acid biosynthesis TagF/TagB/EpsJ/Rod(						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2196	Tfu_2196 cytidyltransferase-related					16.26	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2257	Tfu_2257 glucosyltransferase		14.56			17.53	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2262	Tfu_2262 similar to Cell wall-associated hydrolase (invasion-associated proteins)						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2281	Tfu_2281 hypothetical protein						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2283	Tfu_2283 similar to Cell wall-associated hydrolase (invasion-associated proteins)						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2383	Tfu_2383 peptidase C60, sortase A and B					17.58	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2416	Tfu_2416 hypothetical protein					14.97	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2468	Tfu_2468 putative glycosyltransferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2475	Tfu_2475 hypothetical protein	18.12	17.36	18.05	17.73	22.7	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2522	Tfu_2522 glycosyl transferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2523	Tfu_2523 dolichol-phosphate mannosyltransferase, fused to C-terminal uncharacterized domain						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2527	Tfu_2527 similar to Glycosyltransferase	17.2	15.48	15.03		20.79	0.632
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2529	Tfu_2529 putative UDP-glucose/GDP-mannose dehydrogenase					16.47	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2534	Tfu_2534 putative nucleotide sugar-1-phosphate transferase	15.2	16.47	18.2	17.93	22.17	0.6
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2537	Tfu_2537 ABC-type polysaccharide/polyol phosphate transport system ATPase	18.53	18.3	17.74	17.74	21.66	1.185
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2538	Tfu_2538 lipopolysaccharide exporter	17.08	16.98	17	16.55	20.46	0.958
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2541	Tfu_2541 putative glycosyl transferase	16.76	16.14	17.62	17.31	21.79	1.357
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2591	Tfu_2591 UDP-glucose 4-epimerase					14.83	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2594	Tfu_2594 similar to Membrane-bound lytic murein transglycosylase B						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2606	Tfu_2606 alanine racemase region	16.31	14.93	16.54	16.55	20.86	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2611	Tfu_2611 D-fructose-6-phosphate amidotransferase	16.46	16.09	18.53	18.54	22.75	1.101
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2664	Tfu_2664 UDP-N-acetylenolpyruvoylglucosamine reductase	13.88				20.85	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2676	Tfu_2676 hypothetical protein	19.55	19.14	19.58	19.66	23.65	0.938
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2714	Tfu_2714 putative ligase	17.3	16.32	17.84	18.37	21.97	1.077
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2723	Tfu_2723 putative epimerase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2753	Tfu_2753 cell wall hydrolase/autolysin						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2903	Tfu_2903 hypothetical protein					17.09	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2913	Tfu_2913 putative glycosyltransferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_2978	Tfu_2978 putative glycosyltransferase						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_3016	Tfu_3016 UDP-N-acetylglucosamine 1-carboxyvinyltransferase		14.48	17.9	17.73	22.19	1.204
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_3054	Tfu_3054 glycosyltransferase involved in cell wall biogenesis						
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_3064	Tfu_3064 hypothetical protein	17.05	16.02	15.7	15.59	20.75	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_3097	Tfu_3097 putative penicillin-binding protein	14.56	13.16		15.73	19.18	
COG	M	Cell wall/membrane/envelope biogenesis	Tfu_3112	Tfu_3112 glucose-inhibited division protein B					18.58	
COG	Z	Cytoskeleton	Tfu_1792	Tfu_1792 calcium-binding EF-hand	15.41	16.91	17.31	16.86	19.29	
COG	F	Nucleotide transport and metabolism	Tfu_0027	Tfu_0027 putative deaminase					17.96	0.99
COG	F	Nucleotide transport and metabolism	Tfu_0059	Tfu_0059 putative transporter						
COG	F	Nucleotide transport and metabolism	Tfu_0097	Tfu_0097 hypothetical protein						
COG	F	Nucleotide transport and metabolism	Tfu_0156	Tfu_0156 phosphoribosylformylglycinamidine synthase I			15.57	15.14	21.14	0.902
COG	F	Nucleotide transport and metabolism	Tfu_0158	Tfu_0158 phosphoribosylformylglycinamidine synthase subunit II	13.89	15.06	17.93	18.1	22.88	0.924
COG	F	Nucleotide transport and metabolism	Tfu_0178	Tfu_0178 phosphoribosylformylglycinamidine synthase					17.74	
COG	F	Nucleotide transport and metabolism	Tfu_0229	Tfu_0229 putative MutT family protein						
COG	F	Nucleotide transport and metabolism	Tfu_0415	Tfu_0415 ribose-phosphate pyrophosphokinase	18.35	17.7	20.22	20.21	23.7	1.099
COG	F	Nucleotide transport and metabolism	Tfu_0431	Tfu_0431 putative hydrolase					20.26	
COG	F	Nucleotide transport and metabolism	Tfu_0576	Tfu_0576 hypothetical protein					17.31	
COG	F	Nucleotide transport and metabolism	Tfu_0678	Tfu_0678 uridylate kinase	18.09	18.05	17.82	18.33	22.01	1.02
COG	F	Nucleotide transport and metabolism	Tfu_0843	Tfu_0843 putative protein kinase C inhibitor (HIT family	16.7	16.41		15.7	19.5	0.726
COG	F	Nucleotide transport and metabolism	Tfu_0865	Tfu_0865 deoxyguanosinetriphosphate triphosphohydrolase-like protein	15.92	16.87			18.37	
COG	F	Nucleotide transport and metabolism	Tfu_0927	Tfu_0927 dihydroorotate dehydrogenase	17.12	17.21	17.52	17.43	21.74	

COG	F	Nucleotide transport and metabolism	Tfu_0962	Tfu_0962 allantoinase						
COG	F	Nucleotide transport and metabolism	Tfu_1053	Tfu_1053 pyrimidine regulatory protein PyrR	17.14	17.38	18.18	18.29	22.2	0.824
COG	F	Nucleotide transport and metabolism	Tfu_1054	Tfu_1054 aspartate carbamoyltransferase catalytic subunit					19.72	1.183
COG	F	Nucleotide transport and metabolism	Tfu_1055	Tfu_1055 dihydroorotase	13.79		18.6	18.17	22.62	
COG	F	Nucleotide transport and metabolism	Tfu_1056	Tfu_1056 carbamoyl-phosphate synthase, small subunit		15.52	17.25	17.26	22.56	0.884
COG	F	Nucleotide transport and metabolism	Tfu_1057	Tfu_1057 carbamoyl-phosphate synthase, large subunit, glutamine-dependent	16.53	16.24	19.8	19.69	24.13	0.99
COG	F	Nucleotide transport and metabolism	Tfu_1059	Tfu_1059 dihydroorotate dehydrogenase 1						
COG	F	Nucleotide transport and metabolism	Tfu_1060	Tfu_1060 orotidine 5'-phosphate decarboxylase	17.31	17.43	16.58	16.96	22.37	0.988
COG	F	Nucleotide transport and metabolism	Tfu_1062	Tfu_1062 guanylate kinase			14.95	15.22	19.61	
COG	F	Nucleotide transport and metabolism	Tfu_1199	Tfu_1199 CTP synthetase	15.21	15.76	18.58	17.89	22.8	1.201
COG	F	Nucleotide transport and metabolism	Tfu_1209	Tfu_1209 cytidylate kinase	15.69	15.43		14.19	19.62	
COG	F	Nucleotide transport and metabolism	Tfu_1355	Tfu_1355 putative MutT-family protein						
COG	F	Nucleotide transport and metabolism	Tfu_1387	Tfu_1387 thymidylate synthase complementing protein ThyX			16.01	15.73	20.7	0.764
COG	F	Nucleotide transport and metabolism	Tfu_1518	Tfu_1518 xanthine/uracil permease	16.42	16.08	14.78	14.62	20.06	
COG	F	Nucleotide transport and metabolism	Tfu_1537	Tfu_1537 hypothetical protein						
COG	F	Nucleotide transport and metabolism	Tfu_1680	Tfu_1680 hypothetical protein						
COG	F	Nucleotide transport and metabolism	Tfu_1723	Tfu_1723 hypothetical protein	16.31	16.16			20.65	
COG	F	Nucleotide transport and metabolism	Tfu_1911	Tfu_1911 hypothetical protein						
COG	F	Nucleotide transport and metabolism	Tfu_1924	Tfu_1924 hypothetical protein						
COG	F	Nucleotide transport and metabolism	Tfu_1935	Tfu_1935 deoxyUTP pyrophosphatase subfamily 1					16.91	
COG	F	Nucleotide transport and metabolism	Tfu_2041	Tfu_2041 hypothetical protein						
COG	F	Nucleotide transport and metabolism	Tfu_2091	Tfu_2091 adenine phosphoribosyltransferase		14.26			19.51	0.761
COG	F	Nucleotide transport and metabolism	Tfu_2105	Tfu_2105 hypothetical protein				14.7	19.77	
COG	F	Nucleotide transport and metabolism	Tfu_2149	Tfu_2149 ribonucleotide-diphosphate reductase alpha subunit	14.41		17.19	15.02	21.83	0.68
COG	F	Nucleotide transport and metabolism	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
COG	F	Nucleotide transport and metabolism	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
COG	F	Nucleotide transport and metabolism	Tfu_2356	Tfu_2356 formyltetrahydrofolate deformylase					15.81	
COG	F	Nucleotide transport and metabolism	Tfu_2364	Tfu_2364 Ham1-like protein	17.27	15.22	18.89	17.92	22.35	0.853
COG	F	Nucleotide transport and metabolism	Tfu_2440	Tfu_2440 inositol-5-monophosphate dehydrogenase	19.82	19.85	19.51	19.28	23.25	1.113
COG	F	Nucleotide transport and metabolism	Tfu_2457	Tfu_2457 putative mutT-like protein						
COG	F	Nucleotide transport and metabolism	Tfu_2546	Tfu_2546 1-(5-Phosphoribosyl)-5-amino-4-imidazole- carboxylate (AIR) carbo	17.46	17.22	17.98	17.21	21.62	
COG	F	Nucleotide transport and metabolism	Tfu_2547	Tfu_2547 phosphoribosylaminoimidazole carboxylase, ATPase subunit					18.27	
COG	F	Nucleotide transport and metabolism	Tfu_2563	Tfu_2563 adenosine deaminase					16.67	
COG	F	Nucleotide transport and metabolism	Tfu_2572	Tfu_2572 bifunctional phosphoribosylaminoimidazolecarboxamide formyltran	19.86	19.04	20.76	20.79	24.53	0.912
COG	F	Nucleotide transport and metabolism	Tfu_2573	Tfu_2573 phosphoribosylglycinamide formyltransferase	14.49	14.7	17.07	16.78	21.38	
COG	F	Nucleotide transport and metabolism	Tfu_2581	Tfu_2581 inosine-uridine preferring nucleoside hydrolase	16.93	16.72	16.96	15.37	21.32	
COG	F	Nucleotide transport and metabolism	Tfu_2589	Tfu_2589 bifunctional GMP synthase/glutamine amidotransferase protein	14.94		18.4	18.53	23.34	1.278
COG	F	Nucleotide transport and metabolism	Tfu_2595	Tfu_2595 inositol-5-monophosphate dehydrogenase	18.6	18.73	20.9	20.27	24.94	0.944
COG	F	Nucleotide transport and metabolism	Tfu_2596	Tfu_2596 IMP dehydrogenase	17.6	17.76	20.1	19.82	24.11	1.035
COG	F	Nucleotide transport and metabolism	Tfu_2625	Tfu_2625 adenylate kinase, subfamily	19.36	20.27	22.16	21.48	24.95	0.736
COG	F	Nucleotide transport and metabolism	Tfu_2662	Tfu_2662 adenosine deaminase				13.97	19.93	1.018
COG	F	Nucleotide transport and metabolism	Tfu_2747	Tfu_2747 amidophosphoribosyltransferase						
COG	F	Nucleotide transport and metabolism	Tfu_2748	Tfu_2748 phosphoribosylaminoimidazole synthetase	14.77		17.56	17.33	20.81	0.689
COG	F	Nucleotide transport and metabolism	Tfu_2758	Tfu_2758 putative mut-like protein					16.5	
COG	F	Nucleotide transport and metabolism	Tfu_2783	Tfu_2783 thymidylate kinase	19.41	19.13	18.67	18.47	22.51	0.962
COG	F	Nucleotide transport and metabolism	Tfu_2896	Tfu_2896 hypoxanthine phosphoribosyl transferase		16.7	16.94	16.58	21.76	0.668
COG	F	Nucleotide transport and metabolism	Tfu_2932	Tfu_2932 deoxycytidine triphosphate deaminase					19.21	
COG	F	Nucleotide transport and metabolism	Tfu_2940	Tfu_2940 mutT-like protein					16.68	1.002
COG	F	Nucleotide transport and metabolism	Tfu_2973	Tfu_2973 putative mutT-like protein					17.15	
COG	F	Nucleotide transport and metabolism	Tfu_3001	Tfu_3001 ribonucleoside-diphosphate reductase	13.73	13.7	18.55	18.52	22.84	1.196
COG	F	Nucleotide transport and metabolism	Tfu_3002	Tfu_3002 ribonucleoside-diphosphate reductase			18.75	18.62	22.88	0.758
COG	F	Nucleotide transport and metabolism	Tfu_3008	Tfu_3008 orotate phosphoribosyltransferase	17.41	17.4	17.96	17.05	22.2	0.852
COG	F	Nucleotide transport and metabolism	Tfu_3012	Tfu_3012 adenylosuccinate synthetase	15.75	15.57	18.76	18.61	22.25	0.954
COG	F	Nucleotide transport and metabolism	Tfu_3013	Tfu_3013 phosphoribosylglycinamide synthetase			17.63	17.26	21.77	
COG	F	Nucleotide transport and metabolism	Tfu_3014	Tfu_3014 adenylosuccinate lyase	18.68	18.68	20.17	19.69	23.57	0.954
COG	F	Nucleotide transport and metabolism	Tfu_3015	Tfu_3015 phosphoribosylaminoimidazole-succinocarboxamide synthase	17.2	16.06	17.97	17.67	21.89	0.805
COG	F	Nucleotide transport and metabolism	Tfu_0023	Tfu_0023						
COG	F	Nucleotide transport and metabolism	Tfu_0024	Tfu_0024						
COG	T	Signal transduction mechanisms	Tfu_0057	Tfu_0057 putative regulatory protein						

COG	T	Signal transduction mechanisms	Tfu_0080	Tfu_0080 GAF domain protein	19.13	18.7	16.8	16.58	21.11	
COG	T	Signal transduction mechanisms	Tfu_0106	Tfu_0106 PAS protein phosphatase 2C-like						
COG	T	Signal transduction mechanisms	Tfu_0117	Tfu_0117 Cyclic nucleotide-binding:Bacterial regulatory protein, Crp	23.3	23.07	23.16	22.92	25.92	0.892
COG	T	Signal transduction mechanisms	Tfu_0121	Tfu_0121 hypothetical protein	16.28	16.69	17.94	17.46	22.26	
COG	T	Signal transduction mechanisms	Tfu_0122	Tfu_0122 anti-sigma factor antagonist	21.86	22.24	22.15	21.96	24.63	0.834
COG	T	Signal transduction mechanisms	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
COG	T	Signal transduction mechanisms	Tfu_0163	Tfu_0163 Tyrosine protein kinase:Serine/threonine protein kinase	15.1	14.83	14.91	14.78	20.69	
COG	T	Signal transduction mechanisms	Tfu_0177	Tfu_0177 hypothetical protein					15.64	
COG	T	Signal transduction mechanisms	Tfu_0207	Tfu_0207 putative transcriptional regulator						
COG	T	Signal transduction mechanisms	Tfu_0250	Tfu_0250 PAS containing protein phosphatase 2C-like	16.84	15.81	16.62	16.02	21.84	1.175
COG	T	Signal transduction mechanisms	Tfu_0256	Tfu_0256 hypothetical protein	15.31	14.78			18.74	
COG	T	Signal transduction mechanisms	Tfu_0257	Tfu_0257 response regulator receiver	18.04	17.73	16.32	14.36	21.79	
COG	T	Signal transduction mechanisms	Tfu_0265	Tfu_0265 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_0285	Tfu_0285 response regulator receiver	16.67	17.18	15.83	15.19	20.47	1.057
COG	T	Signal transduction mechanisms	Tfu_0286	Tfu_0286 signal transduction histidine kinase	15.2	15.58	16.33	16.5	21.3	
COG	T	Signal transduction mechanisms	Tfu_0287	Tfu_0287 Protein phosphatase 2C-like, withe GAF domain	15.09	14.85	14.53		19.25	
COG	T	Signal transduction mechanisms	Tfu_0288	Tfu_0288 regulatory protein, LuxR:Response regulator receiver						
COG	T	Signal transduction mechanisms	Tfu_0289	Tfu_0289 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_0293	Tfu_0293 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_0294	Tfu_0294 anti-sigma factor antagonist					17.55	
COG	T	Signal transduction mechanisms	Tfu_0297	Tfu_0297 Protein phosphatase 2C-like	14.85		14.32		19.33	0.687
COG	T	Signal transduction mechanisms	Tfu_0303	Tfu_0303 hypothetical protein	14.25		14.59	14.35	18.3	
COG	T	Signal transduction mechanisms	Tfu_0324	Tfu_0324 putative MutT family protein			14.42		18.55	
COG	T	Signal transduction mechanisms	Tfu_0329	Tfu_0329 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_0330	Tfu_0330 regulatory protein, LuxR:Response regulator receiver						
COG	T	Signal transduction mechanisms	Tfu_0333	Tfu_0333 anti-sigma factor antagonist						
COG	T	Signal transduction mechanisms	Tfu_0343	Tfu_0343 response regulator receiver	16.6	15.97	16.58	16.78	21.5	
COG	T	Signal transduction mechanisms	Tfu_0344	Tfu_0344 signal transduction histidine kinase					18.04	
COG	T	Signal transduction mechanisms	Tfu_0357	Tfu_0357 hypothetical protein	21.73	21.47	23.5	23.11	26.19	1.661
COG	T	Signal transduction mechanisms	Tfu_0391	Tfu_0391 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_0406	Tfu_0406 Tyrosine protein kinase:Serine/threonine protein kinase	15.36	16.04			20.09	0.675
COG	T	Signal transduction mechanisms	Tfu_0454	Tfu_0454 Tyrosine protein kinase:Serine/threonine protein kinase					16.34	
COG	T	Signal transduction mechanisms	Tfu_0457	Tfu_0457 Nucleotide binding protein, PINc			13.39		18.31	0.921
COG	T	Signal transduction mechanisms	Tfu_0500	Tfu_0500 Tyrosine protein kinase:Serine/threonine protein kinase	16.56	16			20.28	
COG	T	Signal transduction mechanisms	Tfu_0506	Tfu_0506 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_0528	Tfu_0528 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_0539	Tfu_0539 hypothetical protein		15.88			18.17	
COG	T	Signal transduction mechanisms	Tfu_0550	Tfu_0550 metal-dependent phosphohydrolase, HD region						
COG	T	Signal transduction mechanisms	Tfu_0551	Tfu_0551 putative lipoprotein						
COG	T	Signal transduction mechanisms	Tfu_0555	Tfu_0555 signal transduction histidine kinase	17.29	17.71	15.2	14.03	20.13	0.886
COG	T	Signal transduction mechanisms	Tfu_0592	Tfu_0592 Tyrosine protein kinase:Serine/threonine protein kinase	18.18	17.59	17.18	17.09	21.25	
COG	T	Signal transduction mechanisms	Tfu_0600	Tfu_0600 hypothetical protein	16.79	16.24		15.56	20.29	1.129
COG	T	Signal transduction mechanisms	Tfu_0601	Tfu_0601 serine/threonine protein kinase	14.82	14.92	15.29		19.56	
COG	T	Signal transduction mechanisms	Tfu_0604	Tfu_0604 putative phosphodiesterase						
COG	T	Signal transduction mechanisms	Tfu_0610	Tfu_0610 hypothetical protein	16.36	16.57	15.42	16.18	20.59	
COG	T	Signal transduction mechanisms	Tfu_0685	Tfu_0685 putative regulatory protein					16.23	
COG	T	Signal transduction mechanisms	Tfu_0691	Tfu_0691 helix-turn-helix, Fis-type					18.97	
COG	T	Signal transduction mechanisms	Tfu_0701	Tfu_0701 Tyrosine protein kinase:Serine/threonine protein kinase	18.86	18.29	16.43	15.99	22.51	0.6
COG	T	Signal transduction mechanisms	Tfu_0704	Tfu_0704 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_0755	Tfu_0755 putative regulatory protein					15.75	
COG	T	Signal transduction mechanisms	Tfu_0757	Tfu_0757 regulatory protein, LuxR:TPR repeat						
COG	T	Signal transduction mechanisms	Tfu_0758	Tfu_0758 regulatory protein, LuxR						
COG	T	Signal transduction mechanisms	Tfu_0767	Tfu_0767 regulatory protein, LuxR:Response regulator receiver						
COG	T	Signal transduction mechanisms	Tfu_0768	Tfu_0768 putative two-component system sensor kinase					16.25	
COG	T	Signal transduction mechanisms	Tfu_0809	Tfu_0809 hypothetical protein	23.78	23.37	21.95	21.85	24.44	0.831
COG	T	Signal transduction mechanisms	Tfu_0844	Tfu_0844 phosphate starvation-inducible protein PhoH predicted ATPase	13.82		16.95	16.5	20.79	0.721
COG	T	Signal transduction mechanisms	Tfu_0940	Tfu_0940 signal transduction histidine kinase						
COG	T	Signal transduction mechanisms	Tfu_0945	Tfu_0945 CBS domain protein						
COG	T	Signal transduction mechanisms	Tfu_0976	Tfu_0976 hypothetical protein						

COG	T	Signal transduction mechanisms	Tfu_0986	Tfu_0986 glutamate-ammonia-ligase adenylyltransferase					18.95	
COG	T	Signal transduction mechanisms	Tfu_1006	Tfu_1006 hypothetical protein	21.41	21.33	21.6	21.36	24.37	1.001
COG	T	Signal transduction mechanisms	Tfu_1041	Tfu_1041 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA		13.51			20.01	
COG	T	Signal transduction mechanisms	Tfu_1084	Tfu_1084 serine/threonine protein kinase	14.81				19.13	
COG	T	Signal transduction mechanisms	Tfu_1141	Tfu_1141 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	T	Signal transduction mechanisms	Tfu_1181	Tfu_1181 response regulator receiver	19.27	18.83	19.35	18.45	22.85	0.711
COG	T	Signal transduction mechanisms	Tfu_1238	Tfu_1238 response regulator receiver						
COG	T	Signal transduction mechanisms	Tfu_1271	Tfu_1271 PAS:Protein phosphatase 2C-like:GAF					14.7	
COG	T	Signal transduction mechanisms	Tfu_1310	Tfu_1310 CBS			15.71	15.96	20.67	
COG	T	Signal transduction mechanisms	Tfu_1329	Tfu_1329 ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histidine kinase A, N-terminal						
COG	T	Signal transduction mechanisms	Tfu_1330	Tfu_1330 response regulator receiver						
COG	T	Signal transduction mechanisms	Tfu_1339	Tfu_1339 hypothetical protein	17.12	17.78	15.82	16.43	21.43	1.083
COG	T	Signal transduction mechanisms	Tfu_1342	Tfu_1342 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	T	Signal transduction mechanisms	Tfu_1389	Tfu_1389 carbon starvation-induced protein	21.86	21.5	19.18	19.25	23.12	0.825
COG	T	Signal transduction mechanisms	Tfu_1395	Tfu_1395 forkhead-associated	20.03	19.66	18.24	19.05	23.03	0.886
COG	T	Signal transduction mechanisms	Tfu_1402	Tfu_1402 putative two-component system sensor kinase	12.49				14.44	
COG	T	Signal transduction mechanisms	Tfu_1403	Tfu_1403 regulatory protein, LuxR:Response regulator receiver						
COG	T	Signal transduction mechanisms	Tfu_1412	Tfu_1412 hypothetical protein	15.09	15.94	15.54	16.66	21.64	
COG	T	Signal transduction mechanisms	Tfu_1429	Tfu_1429 anti-sigma factor antagonist						
COG	T	Signal transduction mechanisms	Tfu_1433	Tfu_1433 hypothetical protein	19.64	19.33	16.71	16.48	21.3	
COG	T	Signal transduction mechanisms	Tfu_1451	Tfu_1451 similar to Protein tyrosine/serine phosphatase						
COG	T	Signal transduction mechanisms	Tfu_1501	Tfu_1501 similar to Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain						
COG	T	Signal transduction mechanisms	Tfu_1514	Tfu_1514 Tyrosine protein kinase:Serine/threonine protein kinase						
COG	T	Signal transduction mechanisms	Tfu_1552	Tfu_1552 PAS:Protein phosphatase 2C-like:GAF						
COG	T	Signal transduction mechanisms	Tfu_1554	Tfu_1554 Low molecular weight phosphotyrosine protein phosphatase	12.56	12.64	14.42	12.86	16.39	
COG	T	Signal transduction mechanisms	Tfu_1658	Tfu_1658 Tyrosine protein kinase:Serine/threonine protein kinase:Sel1-like repeat						
COG	T	Signal transduction mechanisms	Tfu_1739	Tfu_1739 PAS/Protein phosphatase 2C-like					17.4	
COG	T	Signal transduction mechanisms	Tfu_1752	Tfu_1752 Protein phosphatase 2C-like	13.17	14.44	15.59	15.39	21.23	
COG	T	Signal transduction mechanisms	Tfu_1756	Tfu_1756 Tyrosine protein kinase:Serine/threonine protein kinase	13.69	14.76	15.42	14.85	21.48	1.016
COG	T	Signal transduction mechanisms	Tfu_1778	Tfu_1778 regulatory protein, LuxR						
COG	T	Signal transduction mechanisms	Tfu_1792	Tfu_1792 calcium-binding EF-hand	15.41	16.91	17.31	16.86	19.29	
COG	T	Signal transduction mechanisms	Tfu_1795	Tfu_1795 helix-turn-helix, Fis-type					14.89	
COG	T	Signal transduction mechanisms	Tfu_1805	Tfu_1805 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_1817	Tfu_1817 regulatory protein, LuxR:Response regulator receiver						
COG	T	Signal transduction mechanisms	Tfu_1845	Tfu_1845 regulatory protein, LuxR:Response regulator receiver					18.22	
COG	T	Signal transduction mechanisms	Tfu_1846	Tfu_1846 similar to Signal transduction histidine kinase						
COG	T	Signal transduction mechanisms	Tfu_1940	Tfu_1940 ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histi	15.96	14.84	14.2	14.99	19.94	
COG	T	Signal transduction mechanisms	Tfu_1941	Tfu_1941 response regulator receiver	12.77	13.53	16.39	16.69	21.04	0.971
COG	T	Signal transduction mechanisms	Tfu_1972	Tfu_1972 hypothetical protein			14.16		19.27	
COG	T	Signal transduction mechanisms	Tfu_1977	Tfu_1977 EAL domain						
COG	T	Signal transduction mechanisms	Tfu_2045	Tfu_2045 ATP-binding region, ATPase-like						
COG	T	Signal transduction mechanisms	Tfu_2050	Tfu_2050 hypothetical protein		14.35	17.11	16.19	21.74	0.875
COG	T	Signal transduction mechanisms	Tfu_2062	Tfu_2062 PAS/Putative two-component system sensor kinase					17.32	
COG	T	Signal transduction mechanisms	Tfu_2074	Tfu_2074 Tyrosine protein kinase:Serine/threonine protein kinase	18.52	18.73	17.5	17.42	22.55	0.999
COG	T	Signal transduction mechanisms	Tfu_2075	Tfu_2075 Tyrosine protein kinase:Serine/threonine protein kinase	14.14				15.26	
COG	T	Signal transduction mechanisms	Tfu_2083	Tfu_2083 PAS/Protein phosphatase 2C-like						
COG	T	Signal transduction mechanisms	Tfu_2090	Tfu_2090 RelA/SpoT protein	12.76			12.64	18.41	
COG	T	Signal transduction mechanisms	Tfu_2140	Tfu_2140 PAS/Protein phosphatase 2C-like	15.89	15.23	15.09	14.48	20.89	
COG	T	Signal transduction mechanisms	Tfu_2152	Tfu_2152 peptidase S24, LexA repressor	16.53	15.15	15.32		20.68	
COG	T	Signal transduction mechanisms	Tfu_2200	Tfu_2200 hypothetical protein					17.5	
COG	T	Signal transduction mechanisms	Tfu_2218	Tfu_2218 GGDEF						
COG	T	Signal transduction mechanisms	Tfu_2229	Tfu_2229 Tyrosine protein kinase:Serine/threonine protein kinase		14.19			18.3	1.106
COG	T	Signal transduction mechanisms	Tfu_2232	Tfu_2232 hypothetical protein					13.75	
COG	T	Signal transduction mechanisms	Tfu_2233	Tfu_2233 regulatory protein, LuxR:Response regulator receiver					15.4	
COG	T	Signal transduction mechanisms	Tfu_2277	Tfu_2277 ATP-binding region, ATPase-like						
COG	T	Signal transduction mechanisms	Tfu_2278	Tfu_2278 regulatory protein, LuxR:Response regulator receiver						
COG	T	Signal transduction mechanisms	Tfu_2295	Tfu_2295 hypothetical protein		14.23	14.96		19.4	0.952
COG	T	Signal transduction mechanisms	Tfu_2341	Tfu_2341 Protein-tyrosine-phosphatase				13.75	19	
COG	T	Signal transduction mechanisms	Tfu_2342	Tfu_2342 response regulator receiver			13.66		18.57	

COG	T	Signal transduction mechanisms	Tfu_2343	Tfu_2343 ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histi	14.21	14.2			17.81	
COG	T	Signal transduction mechanisms	Tfu_2344	Tfu_2344 response regulator receiver:Protein phosphatase 2C-like		14.15		13.7	18.85	
COG	T	Signal transduction mechanisms	Tfu_2361	Tfu_2361 Tyrosine protein kinase:Serine/threonine protein kinase	15.67	15.45	16.47	16.35	21.04	
COG	T	Signal transduction mechanisms	Tfu_2375	Tfu_2375 Tyrosine protein kinase:Serine/threonine protein kinase	15.45	14.62		15.18	19.56	
COG	T	Signal transduction mechanisms	Tfu_2444	Tfu_2444 hypothetical protein	16.62	15.98	17.95	17.31	22.26	
COG	T	Signal transduction mechanisms	Tfu_2456	Tfu_2456 Small GTP-binding protein domain:GTP-binding protein TypA	14.36		16.11	15.84	20.75	1.012
COG	T	Signal transduction mechanisms	Tfu_2491	Tfu_2491 regulatory protein, LuxR:Response regulator receiver			16.65	15.34	21.33	
COG	T	Signal transduction mechanisms	Tfu_2495	Tfu_2495 ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histidine kinase A, N-terminal					17.64	
COG	T	Signal transduction mechanisms	Tfu_2496	Tfu_2496 response regulator receiver	18.2	17.46	19.26	18.65	23.51	0.942
COG	T	Signal transduction mechanisms	Tfu_2507	Tfu_2507 Tyrosine protein kinase:Serine/threonine protein kinase	17.36	17.16	16.35	15.91	21.06	1.521
COG	T	Signal transduction mechanisms	Tfu_2549	Tfu_2549 response regulator receiver						
COG	T	Signal transduction mechanisms	Tfu_2550	Tfu_2550 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_2552	Tfu_2552 adenylyl cyclase class-3/4/guanylyl cyclase	15.46	15.87		14.57	19.3	
COG	T	Signal transduction mechanisms	Tfu_2570	Tfu_2570 forkhead-associated	16.03				16.22	0.608
COG	T	Signal transduction mechanisms	Tfu_2582	Tfu_2582 regulatory protein, LuxR:Response regulator receiver	17.73	17.94	17.3	17.21	21.46	
COG	T	Signal transduction mechanisms	Tfu_2583	Tfu_2583 putative two-component system sensor kinase						
COG	T	Signal transduction mechanisms	Tfu_2596	Tfu_2596 IMP dehydrogenase	17.6	17.76	20.1	19.82	24.11	1.035
COG	T	Signal transduction mechanisms	Tfu_2737	Tfu_2737 transcriptional regulatory protein						
COG	T	Signal transduction mechanisms	Tfu_2764	Tfu_2764 anti-sigma factor antagonist					18.06	
COG	T	Signal transduction mechanisms	Tfu_2776	Tfu_2776 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_2796	Tfu_2796 Protein phosphatase 2C-like					15.05	
COG	T	Signal transduction mechanisms	Tfu_2798	Tfu_2798 putative DNA-binding protein					15.73	
COG	T	Signal transduction mechanisms	Tfu_2807	Tfu_2807 hypothetical protein	14.76	14.48	15.55	15.17	20.5	
COG	T	Signal transduction mechanisms	Tfu_2809	Tfu_2809 regulatory protein, LuxR						
COG	T	Signal transduction mechanisms	Tfu_2845	Tfu_2845 Tyrosine protein kinase:Serine/threonine protein kinase		13.26		14.27	19.42	
COG	T	Signal transduction mechanisms	Tfu_2855	Tfu_2855 similar to Putative stress-responsive transcriptional regulator						
COG	T	Signal transduction mechanisms	Tfu_2857	Tfu_2857 ATP-binding region, ATPase-like					15.54	
COG	T	Signal transduction mechanisms	Tfu_2858	Tfu_2858 response regulator receiver	17.19	15.96		14.41	20.77	
COG	T	Signal transduction mechanisms	Tfu_2880	Tfu_2880 regulatory protein, LuxR						
COG	T	Signal transduction mechanisms	Tfu_2909	Tfu_2909 ATP-binding region, ATPase-like:Histidine kinase A, N-terminal					18.74	
COG	T	Signal transduction mechanisms	Tfu_2910	Tfu_2910 response regulator receiver	16.38	16.03	17	17.51	21.88	1.079
COG	T	Signal transduction mechanisms	Tfu_2950	Tfu_2950 regulatory protein, LuxR:Response regulator receiver		14.43	18.83	18.71	22.94	2.366
COG	T	Signal transduction mechanisms	Tfu_2959	Tfu_2959 regulatory protein, LuxR:Response regulator receiver					15.74	
COG	T	Signal transduction mechanisms	Tfu_2960	Tfu_2960 hypothetical protein	14.82				18.22	
COG	T	Signal transduction mechanisms	Tfu_2967	Tfu_2967 hypothetical protein						
COG	T	Signal transduction mechanisms	Tfu_3032	Tfu_3032 hypothetical protein			15.66		20.46	1.735
COG	T	Signal transduction mechanisms	Tfu_3034	Tfu_3034 hypothetical protein	18.02	18.18	19.17	19.03	22.58	0.969
COG	T	Signal transduction mechanisms	Tfu_3035	Tfu_3035 regulatory protein, LuxR:Response regulator receiver		14.57	17.43	17.54	21.22	0.687
COG	T	Signal transduction mechanisms	Tfu_3036	Tfu_3036 hypothetical protein			17.11	16.25	21.35	1.073
COG	T	Signal transduction mechanisms	Tfu_3041	Tfu_3041 putative stress-inducible protein	15.4	15.65	18.7	18.52	22.1	1.873
COG	T	Signal transduction mechanisms	Tfu_3042	Tfu_3042 CBS					17.45	
COG	T	Signal transduction mechanisms	Tfu_3045	Tfu_3045 hypothetical protein					16.61	1.11
COG	T	Signal transduction mechanisms	Tfu_3046	Tfu_3046 GAF:ATP-binding region, ATPase-like	15.92	15.88	16.9	16.5	21.13	
COG	T	Signal transduction mechanisms	Tfu_3055	Tfu_3055 anti-sigma factor antagonist						
COG	T	Signal transduction mechanisms	Tfu_3060	Tfu_3060 FHA domain protein	19.47	19.33	20.06	19.95	23.16	0.848
COG	T	Signal transduction mechanisms	Tfu_3061	Tfu_3061 FHA domain protein	18.37	18.51	18.17	18.12	21.74	0.985
COG	T	Signal transduction mechanisms	Tfu_3062	Tfu_3062 Protein phosphatase 2C-like	19.97	19.61	19.68	19.29	23.44	1.296
COG	T	Signal transduction mechanisms	Tfu_3065	Tfu_3065 Tyrosine protein kinase:Serine/threonine protein kinase					18.02	
COG	T	Signal transduction mechanisms	Tfu_3066	Tfu_3066 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA	19.07	19.31	18.37	17.91	22.14	0.98
COG	S	Function unknown	Tfu_0045	Tfu_0045 Conserved hypothetical protein 103	15.51				18.04	
COG	S	Function unknown	Tfu_0065	Tfu_0065 similar to Uncharacterized conserved protein	18.35	18.22	17.86	17.33	22.53	0.904
COG	S	Function unknown	Tfu_0084	Tfu_0084 hypothetical protein	20.22	19.47	18.01	17.32	22.11	0.76
COG	S	Function unknown	Tfu_0104	Tfu_0104 putative integral membrane protein						
COG	S	Function unknown	Tfu_0108	Tfu_0108 hypothetical protein	18.99	19.21	19.36	18.81	23.04	0.494
COG	S	Function unknown	Tfu_0130	Tfu_0130 hypothetical protein					17.5	
COG	S	Function unknown	Tfu_0148	Tfu_0148 hypothetical protein					16.98	
COG	S	Function unknown	Tfu_0164	Tfu_0164 hypothetical protein						
COG	S	Function unknown	Tfu_0168	Tfu_0168 conserved hypothetical protein, possibly membrane-associated					20.24	
COG	S	Function unknown	Tfu_0171	Tfu_0171 probable conserved membrane protein						

COG	S	Function unknown	Tfu_0211	Tfu_0211 hypothetical protein	16.66	15.51	14.67		18.33	
COG	S	Function unknown	Tfu_0222	Tfu_0222 hypothetical protein					19.21	0.606
COG	S	Function unknown	Tfu_0236	Tfu_0236 hypothetical protein					20.41	0.434
COG	S	Function unknown	Tfu_0251	Tfu_0251 ribonuclease BN		16.13			18.44	
COG	S	Function unknown	Tfu_0254	Tfu_0254 hypothetical protein					15.84	
COG	S	Function unknown	Tfu_0268	Tfu_0268 hypothetical protein					17.1	
COG	S	Function unknown	Tfu_0308	Tfu_0308 hypothetical protein			15.16		19.04	0.795
COG	S	Function unknown	Tfu_0358	Tfu_0358 hypothetical protein						
COG	S	Function unknown	Tfu_0371	Tfu_0371 hypothetical protein						
COG	S	Function unknown	Tfu_0430	Tfu_0430 hypothetical protein					19.35	
COG	S	Function unknown	Tfu_0435	Tfu_0435 hypothetical protein	14.74				19.68	
COG	S	Function unknown	Tfu_0444	Tfu_0444 hypothetical protein					16.64	
COG	S	Function unknown	Tfu_0445	Tfu_0445 hypothetical protein			15.91	17.2	18.84	0.643
COG	S	Function unknown	Tfu_0446	Tfu_0446 hypothetical protein					18.17	1.982
COG	S	Function unknown	Tfu_0449	Tfu_0449 hypothetical protein		14.73	16.07	16.84	21.43	
COG	S	Function unknown	Tfu_0470	Tfu_0470 hypothetical protein	22.83	22.15	21.25	20.8	24.32	
COG	S	Function unknown	Tfu_0486	Tfu_0486 hypothetical protein	15.4	16.4	16.51	15.88	21.61	0.747
COG	S	Function unknown	Tfu_0525	Tfu_0525 hypothetical protein			14.15		18.01	
COG	S	Function unknown	Tfu_0536	Tfu_0536 hypothetical protein	18.63	18.97	19.27	18.89	23.13	0.758
COG	S	Function unknown	Tfu_0541	Tfu_0541 hypothetical protein	18.4	18.23	18.56	18.03	23.47	1.141
COG	S	Function unknown	Tfu_0546	Tfu_0546 hypothetical protein						
COG	S	Function unknown	Tfu_0564	Tfu_0564 hypothetical protein	18.17	18.03	17.21	17.42	22.19	0.889
COG	S	Function unknown	Tfu_0587	Tfu_0587 ABC transporter, permease protein					15.17	1.882
COG	S	Function unknown	Tfu_0591	Tfu_0591 hypothetical protein					13.59	
COG	S	Function unknown	Tfu_0598	Tfu_0598 similar to Uncharacterized membrane-associated protein						
COG	S	Function unknown	Tfu_0622	Tfu_0622 hypothetical protein	18.62	18.1	17.41	16.97	20.92	0.668
COG	S	Function unknown	Tfu_0629	Tfu_0629 hypothetical protein						
COG	S	Function unknown	Tfu_0639	Tfu_0639 putative secreted protein					17.52	
COG	S	Function unknown	Tfu_0718	Tfu_0718 hypothetical protein					17.1	
COG	S	Function unknown	Tfu_0775	Tfu_0775 hypothetical protein	16.66	16.35	16.02	16.85	20.89	
COG	S	Function unknown	Tfu_0779	Tfu_0779 hypothetical protein						
COG	S	Function unknown	Tfu_0790	Tfu_0790 hypothetical protein						
COG	S	Function unknown	Tfu_0794	Tfu_0794 helix-turn-helix motif						
COG	S	Function unknown	Tfu_0813	Tfu_0813 hypothetical protein					16.73	
COG	S	Function unknown	Tfu_0824	Tfu_0824 hypothetical protein						
COG	S	Function unknown	Tfu_0836	Tfu_0836 hypothetical protein	17.88	18.19			19.98	
COG	S	Function unknown	Tfu_0837	Tfu_0837 hypothetical protein						
COG	S	Function unknown	Tfu_0840	Tfu_0840 Conserved hypothetical protein 46					18.56	
COG	S	Function unknown	Tfu_0851	Tfu_0851 hypothetical protein						
COG	S	Function unknown	Tfu_0864	Tfu_0864 hypothetical protein						
COG	S	Function unknown	Tfu_0905	Tfu_0905 hypothetical protein						
COG	S	Function unknown	Tfu_0918	Tfu_0918 hypothetical protein						
COG	S	Function unknown	Tfu_0952	Tfu_0952 hypothetical protein						
COG	S	Function unknown	Tfu_0963	Tfu_0963 hypothetical protein					19.77	
COG	S	Function unknown	Tfu_0999	Tfu_0999 hypothetical protein					18.23	
COG	S	Function unknown	Tfu_1011	Tfu_1011 HesB/YadR/YfhF					15.79	
COG	S	Function unknown	Tfu_1018	Tfu_1018 hypothetical protein		15.9			18.77	
COG	S	Function unknown	Tfu_1041	Tfu_1041 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA		13.51			20.01	
COG	S	Function unknown	Tfu_1048	Tfu_1048 hypothetical protein					15.24	
COG	S	Function unknown	Tfu_1066	Tfu_1066 hypothetical protein						
COG	S	Function unknown	Tfu_1086	Tfu_1086 hypothetical protein						0.777
COG	S	Function unknown	Tfu_1101	Tfu_1101 hypothetical protein	18.65	17.95	16.32	14.81	21.23	
COG	S	Function unknown	Tfu_1114	Tfu_1114 Protein of unknown function DUF152					16.58	
COG	S	Function unknown	Tfu_1116	Tfu_1116 hypothetical protein	12.22	11.86		11.92	18.9	
COG	S	Function unknown	Tfu_1204	Tfu_1204 hypothetical protein						
COG	S	Function unknown	Tfu_1211	Tfu_1211 hypothetical protein						
COG	S	Function unknown	Tfu_1266	Tfu_1266 helix-turn-helix, AraC type						
COG	S	Function unknown	Tfu_1268	Tfu_1268 hypothetical protein						
COG	S	Function unknown	Tfu_1344	Tfu_1344 hypothetical protein						

COG	S	Function unknown	Tfu_1346	Tfu_1346 hypothetical protein					16.58	2.1
COG	S	Function unknown	Tfu_1357	Tfu_1357 hypothetical protein						
COG	S	Function unknown	Tfu_1382	Tfu_1382 hypothetical protein						
COG	S	Function unknown	Tfu_1396	Tfu_1396 hypothetical protein	17.12	17.43	17.78	17.63	21.99	0.762
COG	S	Function unknown	Tfu_1414	Tfu_1414 hypothetical protein			13.67		18.64	
COG	S	Function unknown	Tfu_1438	Tfu_1438 hypothetical protein					12.15	
COG	S	Function unknown	Tfu_1452	Tfu_1452 hypothetical protein						
COG	S	Function unknown	Tfu_1455	Tfu_1455 hypothetical protein					18.15	
COG	S	Function unknown	Tfu_1515	Tfu_1515 hypothetical protein						
COG	S	Function unknown	Tfu_1519	Tfu_1519 hypothetical protein					15.93	
COG	S	Function unknown	Tfu_1542	Tfu_1542 hypothetical protein					18.25	
COG	S	Function unknown	Tfu_1562	Tfu_1562 hypothetical protein						
COG	S	Function unknown	Tfu_1576	Tfu_1576 Conserved hypothetical protein 374					16.14	
COG	S	Function unknown	Tfu_1628	Tfu_1628 hypothetical protein						
COG	S	Function unknown	Tfu_1650	Tfu_1650 conserved hypothetical membrane-anchored protein						
COG	S	Function unknown	Tfu_1665	Tfu_1665 hypothetical protein						
COG	S	Function unknown	Tfu_1689	Tfu_1689 hypothetical protein					15.48	
COG	S	Function unknown	Tfu_1712	Tfu_1712 hypothetical protein	17.46	16.63			19.24	
COG	S	Function unknown	Tfu_1714	Tfu_1714 hypothetical protein						
COG	S	Function unknown	Tfu_1818	Tfu_1818 hypothetical protein						
COG	S	Function unknown	Tfu_1833	Tfu_1833 similar to Uncharacterized conserved protein					17.36	
COG	S	Function unknown	Tfu_1857	Tfu_1857 hypothetical protein	20.22	19.96	21.16	20.88	24.49	1.187
COG	S	Function unknown	Tfu_1863	Tfu_1863 putative conserved protein MbtH						
COG	S	Function unknown	Tfu_1874	Tfu_1874 hypothetical protein						
COG	S	Function unknown	Tfu_1882	Tfu_1882 hypothetical protein			14.83		14.63	1.068
COG	S	Function unknown	Tfu_1887	Tfu_1887 similar to membrane protein					14.01	
COG	S	Function unknown	Tfu_1890	Tfu_1890 putative secreted protein					14.82	
COG	S	Function unknown	Tfu_1896	Tfu_1896 hypothetical protein	19.35	18.85	21.46	21.28	24.64	1.157
COG	S	Function unknown	Tfu_1948	Tfu_1948 hypothetical protein	15.08	14.37	14.1		18.89	
COG	S	Function unknown	Tfu_1949	Tfu_1949 hypothetical protein		15.26	14.92	15.15	19.77	
COG	S	Function unknown	Tfu_1955	Tfu_1955 Protein of unknown function DUF34	18.4	18.01	17.16	17.37	21.4	0.797
COG	S	Function unknown	Tfu_1958	Tfu_1958 hypothetical protein						
COG	S	Function unknown	Tfu_1966	Tfu_1966 hypothetical protein	17.51	17.14	16.84	16.95	20.1	
COG	S	Function unknown	Tfu_1980	Tfu_1980 hypothetical protein					14.45	
COG	S	Function unknown	Tfu_1996	Tfu_1996 putative integral membrane protein	14.61	14.71	15.91		19.94	
COG	S	Function unknown	Tfu_2018	Tfu_2018 Protein of unknown function DUF199						
COG	S	Function unknown	Tfu_2019	Tfu_2019 Conserved hypothetical protein CofD related					17.18	
COG	S	Function unknown	Tfu_2030	Tfu_2030 hypothetical protein						
COG	S	Function unknown	Tfu_2031	Tfu_2031 hypothetical protein						
COG	S	Function unknown	Tfu_2089	Tfu_2089 hypothetical protein					14.84	
COG	S	Function unknown	Tfu_2096	Tfu_2096 hypothetical protein	17.95	17.48	18.86	18.56	22.33	0.952
COG	S	Function unknown	Tfu_2100	Tfu_2100 hypothetical protein					18.19	
COG	S	Function unknown	Tfu_2104	Tfu_2104 hypothetical protein						
COG	S	Function unknown	Tfu_2107	Tfu_2107 hypothetical protein					15.74	
COG	S	Function unknown	Tfu_2123	Tfu_2123 hypothetical protein						
COG	S	Function unknown	Tfu_2136	Tfu_2136 hypothetical protein		14.36			15.97	
COG	S	Function unknown	Tfu_2170	Tfu_2170 Iojap-related protein			14.97	16	19	
COG	S	Function unknown	Tfu_2174	Tfu_2174 similar to Uncharacterized conserved protein	16.81	16.58	15.08	15.07	19.32	
COG	S	Function unknown	Tfu_2184	Tfu_2184 hypothetical protein						
COG	S	Function unknown	Tfu_2244	Tfu_2244 hypothetical protein					16.96	
COG	S	Function unknown	Tfu_2249	Tfu_2249 hypothetical protein	17.67	17.74	18.15	18.31	20.87	1.082
COG	S	Function unknown	Tfu_2325	Tfu_2325 similar to Uncharacterized membrane protein						
COG	S	Function unknown	Tfu_2336	Tfu_2336 hypothetical protein					18.91	
COG	S	Function unknown	Tfu_2372	Tfu_2372 ATP-dependent Clp protease adaptor protein ClpS						
COG	S	Function unknown	Tfu_2396	Tfu_2396 putative cellulose-binding protein	21.98	21.74	21.6	21.85	25.03	0.966
COG	S	Function unknown	Tfu_2402	Tfu_2402 hypothetical protein	18.76	18.37	18.32	17.02	21.23	1
COG	S	Function unknown	Tfu_2404	Tfu_2404 cobalamin adenosyltransferase	19.46	19.11	18.77	18.13	22.82	1.335
COG	S	Function unknown	Tfu_2414	Tfu_2414 hypothetical protein						
COG	S	Function unknown	Tfu_2502	Tfu_2502 putative integral membrane protein					17.21	

COG	S	Function unknown	Tfu_2503	Tfu_2503 possible conserved membrane protein					17.73	
COG	S	Function unknown	Tfu_2509	Tfu_2509 hypothetical protein	14.6			15.23	17.75	
COG	S	Function unknown	Tfu_2517	Tfu_2517 LPPG:Fo 2-phospho-L-lactate transferase			14.64	15.51	20.71	
COG	S	Function unknown	Tfu_2518	Tfu_2518 hypothetical protein			14.93		19.68	
COG	S	Function unknown	Tfu_2548	Tfu_2548 hypothetical protein						
COG	S	Function unknown	Tfu_2565	Tfu_2565 Enzymatic protein of unknown function	15.64	15.14	17.69	15.59	21.46	1.452
COG	S	Function unknown	Tfu_2608	Tfu_2608 hypothetical protein	17.11	16.36	17.72	18.27	23.18	1.081
COG	S	Function unknown	Tfu_2663	Tfu_2663 hypothetical protein						
COG	S	Function unknown	Tfu_2672	Tfu_2672 hypothetical protein	18.29	17.63	17.92	18.16	21.62	1.319
COG	S	Function unknown	Tfu_2680	Tfu_2680 hypothetical protein			14.56	14.4	20.18	
COG	S	Function unknown	Tfu_2752	Tfu_2752 hypothetical protein						
COG	S	Function unknown	Tfu_2757	Tfu_2757 hypothetical protein					15.08	
COG	S	Function unknown	Tfu_2775	Tfu_2775 hypothetical protein						
COG	S	Function unknown	Tfu_2777	Tfu_2777 hypothetical protein	15.29	13.94			18.96	
COG	S	Function unknown	Tfu_2781	Tfu_2781 similar to Uncharacterized protein of PSP1						
COG	S	Function unknown	Tfu_2813	Tfu_2813 similar to membrane protein					16.93	
COG	S	Function unknown	Tfu_2818	Tfu_2818 hypothetical protein	17.32	16.88	15.8	15.58	20.93	0.826
COG	S	Function unknown	Tfu_2833	Tfu_2833 putative secreted protein	20.07	19.86	18.01	18.05	22.85	1.291
COG	S	Function unknown	Tfu_2846	Tfu_2846 hypothetical protein				12.54	16.8	
COG	S	Function unknown	Tfu_2853	Tfu_2853 hypothetical protein					17.37	
COG	S	Function unknown	Tfu_2861	Tfu_2861 hypothetical protein	17.17	18.1	18.69	18.57	22.32	
COG	S	Function unknown	Tfu_2870	Tfu_2870 putative integral membrane protein						
COG	S	Function unknown	Tfu_2878	Tfu_2878 DNA and RNA helicase	13.84		14.52		21.11	
COG	S	Function unknown	Tfu_2885	Tfu_2885 hypothetical protein	15.25		15.25	15.1	19.38	
COG	S	Function unknown	Tfu_2887	Tfu_2887 similar to membrane protein					17.58	
COG	S	Function unknown	Tfu_2888	Tfu_2888 similar to Uncharacterized conserved protein					17.21	
COG	S	Function unknown	Tfu_2898	Tfu_2898 hypothetical protein	19.8	19.56	18.71	19.13	23.48	0.841
COG	S	Function unknown	Tfu_2972	Tfu_2972 hypothetical protein						
COG	S	Function unknown	Tfu_2999	Tfu_2999 similar to Uncharacterized protein conserved in bacteria	15.85				18.38	
COG	S	Function unknown	Tfu_3005	Tfu_3005 hypothetical protein		14.31			19.1	
COG	S	Function unknown	Tfu_3066	Tfu_3066 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA	19.07	19.31	18.37	17.91	22.14	0.98
COG	S	Function unknown	Tfu_3071	Tfu_3071 hypothetical protein		14.31			18.95	
COG	S	Function unknown	Tfu_3079	Tfu_3079 hypothetical protein						
COG	S	Function unknown	Tfu_3082	Tfu_3082 hypothetical protein						
COG	S	Function unknown	Tfu_3090	Tfu_3090 putative beta-carotene desaturase/methylase						
COG	S	Function unknown	Tfu_3096	Tfu_3096 putative integral membrane protein						
COG	S	Function unknown	Tfu_3115	Tfu_3115 Protein of unknown function DUF37						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0027	Tfu_0027 putative deaminase					17.96	0.99
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0031	Tfu_0031 seryl-tRNA synthetase	19.71	19.5	20.47	20.38	23.8	0.939
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0114	Tfu_0114 hypothetical protein	19.59	19.5	19.15	18.92	22.27	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0205	Tfu_0205 hypothetical protein						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0212	Tfu_0212 cysteinyl-tRNA synthetase	16.41	14.49	18.9	18.08	23.01	1.169
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0213	Tfu_0213 RNA methyltransferase TrmH, group 3	14.34	15.23	17.16	16.99	21.69	0.777
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0238	Tfu_0238 hypothetical protein	17.87	17.79	17.13	16.85	21.87	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0243	Tfu_0243 hypothetical protein					16.84	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0269	Tfu_0269 arginyl-tRNA synthetase, class Ic	17.72	17.49	20.13	19.85	24.16	1.223
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0359	Tfu_0359 peptide chain release factor 3:Small GTP-binding protein domain					14.71	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0377	Tfu_0377 ribosomal-protein-alanine N-acetyltransferase						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0389	Tfu_0389 methionyl-tRNA synthetase	18.09	18	20.33	20.35	23.82	1.106
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0405	Tfu_0405 dimethyladenosine transferase	13.75	15.29		12.82	19.01	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0416	Tfu_0416 Ribosomal protein L25	15.18	16.55	19.26	18.89	22.21	0.898
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0417	Tfu_0417 peptidyl-tRNA hydrolase	16.17	14.6	16.64	16.59	20.35	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0473	Tfu_0473 Conserved hypothetical protein 92	15.85	15.67	19.25	19.19	23.04	0.65
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0514	Tfu_0514 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0597	Tfu_0597 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0605	Tfu_0605 aspartyl/glutamyl-tRNA amidotransferase subunit C				14.86	18.24	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0606	Tfu_0606 glutamyl-tRNA amidotransferase subunit A	15.37		19.4	18.8	23.02	0.99
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0609	Tfu_0609 aspartyl/glutamyl-tRNA amidotransferase subunit B	15.46	16.45	19.76	19.56	23.81	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0623	Tfu_0623 glutamyl-tRNA synthetase bacterial/mitochondrial	18.5	17.36	18.79	19.22	23.34	0.908

COG	J	Translation, ribosomal structure and biogenesis	Tfu_0645	Tfu_0645 50S ribosomal protein L28					19.58	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0650	Tfu_0650 50S ribosomal protein L32					19.03	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0662	Tfu_0662 Ribosomal protein S16	18.39	18.66	20.07	19.55	23.34	1.197
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0664	Tfu_0664 16S rRNA processing protein RimM	14.85	15.27		15.9	20.79	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0665	Tfu_0665 tRNA (guanine-N1-)-methyltransferase					18.74	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0666	Tfu_0666 Ribosomal protein L19	18.01	16.27	19.85	18.82	23.06	1.347
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0673	Tfu_0673 hypothetical protein						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0676	Tfu_0676 30S ribosomal protein S2	19.71	20.16	22.1	21.87	25.09	1.094
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0677	Tfu_0677 elongation factor Ts	21.96	21.95	23.3	22.74	26.44	0.857
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0679	Tfu_0679 ribosome recycling factor	20.62	20.4	19.99	19.55	23.26	0.686
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0737	Tfu_0737 hypothetical protein						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0759	Tfu_0759 histidine--tRNA ligase	16.98	16.75	18.26	18.29	22.52	0.925
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0772	Tfu_0772 prolyl-tRNA synthetase	19.32	19.13	19.74	19.37	23.57	1.007
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0778	Tfu_0778 translation initiation factor IF-2	19.55	19.5	20.84	20.47	24.49	0.936
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0780	Tfu_0780 ribosome-binding factor A	18.85	18.2	18.48	17.87	22.64	0.538
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0781	Tfu_0781 tRNA pseudouridine synthase B					18.04	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0783	Tfu_0783 Ribosomal protein S15, bacterial chloroplast and mitochondrial type	15.74		17.1	16.76	20.8	1.338
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0784	Tfu_0784 polyribonucleotide nucleotidyltransferase	20.08	19.88	21.21	21.25	24.81	1.127
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0795	Tfu_0795 hypothetical protein						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0811	Tfu_0811 hypothetical protein					15.49	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0815	Tfu_0815 tRNA delta(2)-isopentenylpyrophosphate transferase					18.28	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0827	Tfu_0827 Ribosomal protein S20p	15.94	15.42	17.36	17.25	21.3	0.872
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0861	Tfu_0861 glycyl-tRNA synthetase	18.27	17.66	19.58	19.58	23.56	1.154
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0903	Tfu_0903 putative acetyltransferase	21.51	21.23	20.76	20.72	24.44	0.924
COG	J	Translation, ribosomal structure and biogenesis	Tfu_0968	Tfu_0968 methionine aminopeptidase	15.07			15	21.26	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1013	Tfu_1013 30S ribosomal protein S4	17.09	15.75	19.47	19.58	23.57	1.141
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1075	Tfu_1075 methionyl-tRNA formyltransferase	18.3	17.78	18.03	17.53	22.14	1.153
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1076	Tfu_1076 putative RNA-binding Sun protein					19.48	0.765
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1093	Tfu_1093 elongation factor P	17.28	16.62	17.72	18.58	22.8	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1120	Tfu_1120 isoleucyl-tRNA synthetase, class Ia	16.68	16.31	19.54	19.65	23.84	1.694
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1123	Tfu_1123 pseudouridine synthase, RluD					18.53	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1190	Tfu_1190 hypothetical protein						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1191	Tfu_1191 30S ribosomal protein S1	20.95	21.05	22.59	22.63	25.99	1.039
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1206	Tfu_1206 pseudouridine synthase, Rsu					18.38	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / phosphomannomutase	19.06	18.82	21.97	21.81	25.49	1.131
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1440	Tfu_1440 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal			11.04		19.52	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1572	Tfu_1572 hypothetical protein						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1642	Tfu_1642 RNA-binding S4					16.52	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1683	Tfu_1683 hypothetical protein						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1684	Tfu_1684 probable tRNA/rRNA methyltransferase					18.25	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1723	Tfu_1723 hypothetical protein	16.31	16.16			20.65	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1726	Tfu_1726 formylmethionine deformylase		16.72	17.51	16.93	21.31	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1806	Tfu_1806 hypothetical protein						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1810	Tfu_1810 tRNA (adenine-N(1)-)-methyltransferase	17.13	16.55	18.28	17.91	22.66	0.727
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1832	Tfu_1832 cysteinyl-tRNA synthetase	15.91	16.04	18.24	17.09	22.24	1.186
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1901	Tfu_1901 HRDC:3'-5' exonuclease	14.88		15.41	14.88	21.2	1.409
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1927	Tfu_1927 23S rRNA methyltransferase/RumA					17.67	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1936	Tfu_1936 valyl-tRNA synthetase	17.79	17.98	19.77	19.27	23.94	1.167
COG	J	Translation, ribosomal structure and biogenesis	Tfu_1961	Tfu_1961 Sua5/YciO/YrdC/YwlC					17.86	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2034	Tfu_2034 hemolysin A			14.28		19.26	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2043	Tfu_2043 tyrosyl-tRNA synthetase, class Ib	16.28	16.71	18.6	18.54	22.47	1.194
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2060	Tfu_2060 phenylalanyl-tRNA synthetase beta subunit	19.74	19.67	20.55	20.4	24.66	1.059
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2061	Tfu_2061 phenylalanyl-tRNA synthetase alpha subunit	16.56	17.28	19.09	18.91	22.49	0.719
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2063	Tfu_2063 putative rRNA methylase					14.77	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2064	Tfu_2064 50S ribosomal protein L20			15.65	15.5	19.28	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2065	Tfu_2065 ribosomal protein L35						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2066	Tfu_2066 initiation factor 3	18.42	17.25	19.25	18.52	22.85	1.339
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2070	Tfu_2070 alanyl-tRNA synthetase	18.51	18.11	19.5	19.52	23.9	1.221
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2086	Tfu_2086 aspartyl-tRNA synthetase	18.54	17.59	19.9	19.59	23.67	1.015

COG	J	Translation, ribosomal structure and biogenesis	Tfu_2108	Tfu_2108 threonyl-tRNA synthetase	18.4	18.24	19.7	19.43	23.68	1.178
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2128	Tfu_2128 hypothetical protein	20.85	20.91	19.78	19.34	23.97	1.009
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2143	Tfu_2143 putative guanyltransferase					17.31	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2156	Tfu_2156 leucyl-tRNA synthetase bacterial/mitochondrial, class Ia	20.17	20.38	21.64	21.31	25.2	1.161
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2181	Tfu_2181 Ribosomal protein L27	14.52		15.51	15.12	19.54	0.906
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2182	Tfu_2182 50S ribosomal protein L21	17.79	17.39	19.79	19.34	22.9	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2183	Tfu_2183 ribonuclease E and G	15.17	14.73	17.43	17.22	22.5	1.093
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2207	Tfu_2207 amidase					14.6	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2264	Tfu_2264 putative rRNA methylase					17.49	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2365	Tfu_2365 ribonuclease PH	18.55	18.11	18.5	18.13	22.43	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2376	Tfu_2376 tryptophanyl-tRNA synthetase, class Ib	15.16		16.88	16.16	20.45	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2417	Tfu_2417 Sua5/YciO/YrdC/YwlC				14.71	18.96	1.116
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2418	Tfu_2418 modification methylase HemK						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2419	Tfu_2419 peptide chain release factor 1	15.18	15.54	15.87	15.98	21.17	0.845
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2420	Tfu_2420 Ribosomal protein L31					17.35	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2426	Tfu_2426 similar to Arginyl-tRNA synthetase					16.36	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2433	Tfu_2433 formylmethionine deformylase						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2449	Tfu_2449 tRNA/rRNA methyltransferase					17.38	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2479	Tfu_2479 peptide chain release factor 2	15.85	16.74	19.05	19.08	22.95	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2492	Tfu_2492 sigma 54 modulation protein/ribosomal protein S30EA	15.31	14.72	16.81	17.57	21.64	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2600	Tfu_2600 hypothetical protein						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2613	Tfu_2613 30S ribosomal protein S9	16.28	16.43	18.85	18.6	21.99	1.059
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2614	Tfu_2614 50S ribosomal protein L13				14.95	20.12	1.466
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2616	Tfu_2616 tRNA pseudouridine synthase A			15.6	16.26	20.01	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2617	Tfu_2617 Ribosomal protein L17	14.15	13.66	16.98	16.52	21.77	1.229
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2619	Tfu_2619 30S ribosomal protein S11			14.35	14.19	19.17	1.403
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2620	Tfu_2620 putative ribosomal protein S13	17.69	17.39	19.98	19.49	23.4	1.368
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2622	Tfu_2622 translation initiation factor IF-1	16.62	16.17	18.43	18.04	19.84	0.915
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2624	Tfu_2624 peptidase M24A, methionine aminopeptidase, subfamily 1	15.62	14.46	17.87	17.48	22.13	1.234
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2627	Tfu_2627 50S ribosomal protein L15	17.62	17.41	19.68	20.07	23.57	1.242
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2628	Tfu_2628 Ribosomal protein L30, bacterial					16.5	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2629	Tfu_2629 30S ribosomal protein S5	17.94	18.12	20.32	20	23.82	1.26
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2630	Tfu_2630 Ribosomal protein L18	17.6	17.22	18.77	19.13	22.07	0.873
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2631	Tfu_2631 putative ribosomal protein L6	15.23		18.82	18.71	23.1	1.719
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2632	Tfu_2632 30S ribosomal protein S8			15.52	16.17	21.1	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2633	Tfu_2633 putative ribosomal protein S14						
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2634	Tfu_2634 50S ribosomal protein L5	17.41	16.86	20.33	19.9	24.12	0.923
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2635	Tfu_2635 50S ribosomal protein L24					19.57	1.272
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2636	Tfu_2636 Ribosomal protein L14, bacterial and organelle form	15.14	14.25	15.95	16.24	21.6	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2637	Tfu_2637 putative ribosomal protein S17	15.1		15.63	16.12	20.84	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2638	Tfu_2638 Ribosomal protein L29	17.98	17.84	19.81	19.63	23.41	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2639	Tfu_2639 Ribosomal protein L16	16.1	16.91	19.82	18.56	22.07	1.36
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2640	Tfu_2640 30S ribosomal protein S3	19.05	18.87	20.76	19.8	24.22	1.062
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2641	Tfu_2641 Ribosomal protein L22, bacterial and organelle form		17.55	18.98	18.79	22.53	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2642	Tfu_2642 Ribosomal protein S19, bacterial and organelle form					19.57	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2643	Tfu_2643 50S ribosomal protein L2	17.57	16.83	20.41	20.21	24.19	1.171
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2644	Tfu_2644 50S ribosomal protein L23			17.93	18.03	21.63	1.453
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2645	Tfu_2645 50S ribosomal protein L4	16.82	16.79	19.89	20.29	23.55	1.124
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2646	Tfu_2646 putative ribosomal protein L3	16.68	16.48	18.15	18.41	22.12	0.908
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2647	Tfu_2647 30S ribosomal protein S10	18.09	16.88	19.37	19.35	22.52	0.826
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2648	Tfu_2648 elongation factor Tu	24.67	24.31	25.26	25.17	28.09	0.927
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2649	Tfu_2649 translation elongation factor G:Small GTP-binding protein domain	20.66	20.45	22.29	21.99	25.33	1.172
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2650	Tfu_2650 Ribosomal protein S7, bacterial and organelle form	16.75	16.51	19.03	18.86	22.58	1.249
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2651	Tfu_2651 Ribosomal protein S12, bacterial and chloroplast form	16.08		16.9	16.88	20.29	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2655	Tfu_2655 Ribosomal protein L7/L12	21.46	20.23	22.23	22.22	24.59	0.514
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2656	Tfu_2656 50S ribosomal protein L10	18.93	18.9	20.97	20.1	23.88	1.042
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2657	Tfu_2657 Ribosomal protein L1, bacterial and chloroplast form	19.1	19.48	21.28	21.2	24.32	1.14
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2658	Tfu_2658 Ribosomal protein L11, bacterial			17.58	16.31	21.3	1.25
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2667	Tfu_2667 50S ribosomal protein L33						

COG	J	Translation, ribosomal structure and biogenesis	Tfu_2881	Tfu_2881 lysyl-tRNA synthetase, class-2	16.6	16.7	19.01	18.9	23.54	0.997
COG	J	Translation, ribosomal structure and biogenesis	Tfu_2922	Tfu_2922 D-tyrosyl-tRNA deacylase					20.07	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_3092	Tfu_3092 50S ribosomal protein L9	17.4	18.02	20.22	19.88	23.66	1.198
COG	J	Translation, ribosomal structure and biogenesis	Tfu_3093	Tfu_3093 30S ribosomal protein S18					20.17	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_3095	Tfu_3095 30S ribosomal protein S6	14.8	15.01	16.93	17.14	20.06	0.688
COG	J	Translation, ribosomal structure and biogenesis	Tfu_3102	Tfu_3102 metal-dependent phosphohydrolase		14.3	17.01	16.42	21.49	
COG	J	Translation, ribosomal structure and biogenesis	Tfu_3116	Tfu_3116 ribonuclease P protein	14.64	14.28	14.15	13.87	18.19	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_0073	Tfu_0073 similar to ATPase involved in chromosome partitioning	13.61	14.01			16.67	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_0129	Tfu_0129 putative septum site determining protein						
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_0427	Tfu_0427 hypothetical protein						
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_0429	Tfu_0429 hypothetical protein						
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_0476	Tfu_0476 similar to ATPase involved in chromosome partitioning	16.78	15.98	16.07	14.96	21.29	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_0508	Tfu_0508 ATP-binding protein involved in chromosome partitioning					18.22	1.361
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_0655	Tfu_0655 Chromosome segregation protein SMC					16.98	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_0754	Tfu_0754 putative ATP-binding protein						
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_0793	Tfu_0793 ATPase					19.18	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_1109	Tfu_1109 cell division protein FtsW						
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_1113	Tfu_1113 cell division protein FtsZ	16.59	16.14	16.85	15.24	21.4	0.787
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_1118	Tfu_1118 hypothetical protein	20.42	20.06	20.07	19.92	23.72	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_1202	Tfu_1202 putative partitioning or sporulation protein					18.28	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_1419	Tfu_1419 hypothetical protein	12.48	13.25	12.19	13.56	19.16	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_1792	Tfu_1792 calcium-binding EF-hand	15.41	16.91	17.31	16.86	19.29	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_2186	Tfu_2186 hypothetical protein						
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_2288	Tfu_2288 hypothetical protein						0.633
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_2434	Tfu_2434 hypothetical protein					15.41	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_2477	Tfu_2477 hypothetical protein			15.64	15.48	20.44	1.517
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_2478	Tfu_2478 ATPase	17.12	16.74	15.1	15.75	21.04	0.955
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_2601	Tfu_2601 hypothetical protein			14.66	15.56	21.44	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_2669	Tfu_2669 hypothetical protein	15.24	13.62			20.31	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_2897	Tfu_2897 helix-turn-helix, Fis-type					16.71	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_3029	Tfu_3029 hypothetical protein						
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_3030	Tfu_3030 putative integral membrane protein						
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_3063	Tfu_3063 putative FtsW/RodA/SpoVE-family cell cycle protein	16.95	15.34	14.96	15.86	20.33	
COG	D	Cell cycle control, cell division, chromosome partitioning	Tfu_3111	Tfu_3111 putative partitioning or sporulation protein					18.57	1.152
COG	C	Energy production and conversion	Tfu_0060	Tfu_0060 putative oxidoreductase, oxygen dependent, FAD-dependent protein					14.36	
COG	C	Energy production and conversion	Tfu_0072	Tfu_0072 putative quinone oxidoreductase	17.09	17.49	17.07	16.8	21.43	0.775
COG	C	Energy production and conversion	Tfu_0083	Tfu_0083 phosphoenolpyruvate carboxykinase (GTP)	18.4	18.56	20.72	20.61	24.19	1.846
COG	C	Energy production and conversion	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
COG	C	Energy production and conversion	Tfu_0134	Tfu_0134 inorganic H+ pyrophosphatase	23.51	23.41	21.68	21.58	25.23	0.963
COG	C	Energy production and conversion	Tfu_0180	Tfu_0180 pyruvate dehydrogenase (lipoamide)	20.47	20.54	21.95	22.05	25.45	0.974
COG	C	Energy production and conversion	Tfu_0181	Tfu_0181 putative branched-chain alpha keto acid dehydrogenase E1 beta subu	21.52	21.2	22.35	22.16	25.65	0.999
COG	C	Energy production and conversion	Tfu_0182	Tfu_0182 putative dihydrolipoamide acyltransferase component	22.33	22.24	22.85	22.66	25.78	1.092
COG	C	Energy production and conversion	Tfu_0195	Tfu_0195 hypothetical protein	17.41	17.35	16.91	15.86	21.46	1.273
COG	C	Energy production and conversion	Tfu_0203	Tfu_0203 similar to Coenzyme F420-dependent N5 N10-methylene tetrahydromethanopterin reductase and related flavin-depen						
COG	C	Energy production and conversion	Tfu_0245	Tfu_0245 glycerophosphoryl diester phosphodiesterase	13.34	13.18		14.83	20.82	
COG	C	Energy production and conversion	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
COG	C	Energy production and conversion	Tfu_0279	Tfu_0279 betaine-aldehyde dehydrogenase	21.7	21.51	19.8	20.02	23.9	0.958
COG	C	Energy production and conversion	Tfu_0340	Tfu_0340 trimethylamine-N-oxide reductase (cytochrome c)	16.72	15.79	15.16		21.33	
COG	C	Energy production and conversion	Tfu_0348	Tfu_0348 NADH dehydrogenase (quinone)			13.75			
COG	C	Energy production and conversion	Tfu_0350	Tfu_0350 NADH dehydrogenase (quinone)					16.01	
COG	C	Energy production and conversion	Tfu_0360	Tfu_0360 putative oxidoreductase					16.95	
COG	C	Energy production and conversion	Tfu_0399	Tfu_0399 putative fatty acid-CoA racemase	16.76	16.16	14.76	15.27	19.11	
COG	C	Energy production and conversion	Tfu_0423	Tfu_0423 flavohemoprotein						
COG	C	Energy production and conversion	Tfu_0432	Tfu_0432 NADH dehydrogenase					14.78	
COG	C	Energy production and conversion	Tfu_0433	Tfu_0433 delta-1-pyrroline-5-carboxylate dehydrogenase 1	20.87	20.52	20.5	20.22	24.05	1.051
COG	C	Energy production and conversion	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
COG	C	Energy production and conversion	Tfu_0491	Tfu_0491 ferredoxin	15.52	15.55	17.62	16.68	22.09	0.342
COG	C	Energy production and conversion	Tfu_0562	Tfu_0562 malate dehydrogenase (oxaloacetate decarboxylating)						
COG	C	Energy production and conversion	Tfu_0566	Tfu_0566 alpha-ketoglutarate decarboxylase	22.63	22.08	23.34	23.51	26.75	1.555

COG	C	Energy production and conversion	Tfu_0593	Tfu_0593 electron transfer flavoprotein, beta subunit	21.54	21.23	22.7	22.62	25.33	0.934
COG	C	Energy production and conversion	Tfu_0594	Tfu_0594 electron transfer flavoprotein, alpha subunit	21.73	21.25	22.61	22.91	25.95	1.089
COG	C	Energy production and conversion	Tfu_0615	Tfu_0615 3-isopropylmalate dehydrogenase	19.78	19.7	19.64	19.42	23.35	1.025
COG	C	Energy production and conversion	Tfu_0631	Tfu_0631 glycerol-3-phosphate dehydrogenase (NAD(P)+)	14.3	15.55	14.47		20.42	
COG	C	Energy production and conversion	Tfu_0635	Tfu_0635 hypothetical protein					19.62	
COG	C	Energy production and conversion	Tfu_0636	Tfu_0636 hypothetical protein					18.52	
COG	C	Energy production and conversion	Tfu_0637	Tfu_0637 cytochrome bd ubiquinol oxidase, subunit II			18.7	17.36	23.03	2.71
COG	C	Energy production and conversion	Tfu_0638	Tfu_0638 putative cytochrome oxidase subunit I			19.89	19.95	23.08	
COG	C	Energy production and conversion	Tfu_0653	Tfu_0653 acylphosphatase					17.12	
COG	C	Energy production and conversion	Tfu_0687	Tfu_0687 methylmalonate-semialdehyde dehydrogenase	18.43	17.24	18.03	18.14	22.37	1.017
COG	C	Energy production and conversion	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
COG	C	Energy production and conversion	Tfu_0765	Tfu_0765 putative cytochrome D ubiquinol oxidase subunit II						
COG	C	Energy production and conversion	Tfu_0766	Tfu_0766 highly similar to cytochrome D ubiquinol oxidase subunit I						
COG	C	Energy production and conversion	Tfu_0787	Tfu_0787 glycerol kinase	18.54	18.3	17.06	16.96	21.42	0.925
COG	C	Energy production and conversion	Tfu_0819	Tfu_0819 malate synthase	20.71	20.65	20.77	20.84	24.52	0.986
COG	C	Energy production and conversion	Tfu_0881	Tfu_0881 cytochrome-c oxidase			17.98	18.28	22.45	
COG	C	Energy production and conversion	Tfu_0950	Tfu_0950 NADH dehydrogenase	16.94	16.44	15.12	16.14	21.41	
COG	C	Energy production and conversion	Tfu_0980	Tfu_0980 putative oxidoreductase	15.99	15.61	16.18	15.12	20.6	0.848
COG	C	Energy production and conversion	Tfu_0993	Tfu_0993 dihydrolipoamide S-succinyltransferase	21.69	21.57	21.99	21.46	25.01	1.46
COG	C	Energy production and conversion	Tfu_0994	Tfu_0994 dihydrolipoamide dehydrogenase	23.87	23.67	23.96	23.71	27.03	1.154
COG	C	Energy production and conversion	Tfu_1004	Tfu_1004 K+ channel beta subunit	20.16	20.43	20.54	20.56	24.38	0.965
COG	C	Energy production and conversion	Tfu_1015	Tfu_1015 hypothetical protein	20.5	19.96	19.7	20.09	23.2	1.256
COG	C	Energy production and conversion	Tfu_1016	Tfu_1016 cytochrome-c oxidase					20.91	1.146
COG	C	Energy production and conversion	Tfu_1019	Tfu_1019 ubiquinol-cytochrome c reductase, cytochrome b subunit	20.02	19.57	20.62	20.81	24.55	1.089
COG	C	Energy production and conversion	Tfu_1020	Tfu_1020 ubiquinol-cytochrome c reductase iron-sulfur subunit	20.38	20.21	21.32	21.24	24.45	1.098
COG	C	Energy production and conversion	Tfu_1021	Tfu_1021 hypothetical protein	19.26	19.79	20.25	20.15	23.34	1.121
COG	C	Energy production and conversion	Tfu_1022	Tfu_1022 cytochrome c oxidase subunit III						
COG	C	Energy production and conversion	Tfu_1058	Tfu_1058 dihydroorotate dehydrogenase electron transfer subunit						
COG	C	Energy production and conversion	Tfu_1069	Tfu_1069 CaiB/BaiF family protein					17.39	0.688
COG	C	Energy production and conversion	Tfu_1216	Tfu_1216 hypothetical protein						
COG	C	Energy production and conversion	Tfu_1223	Tfu_1223 hypothetical protein					15.45	
COG	C	Energy production and conversion	Tfu_1226	Tfu_1226 hypothetical protein						
COG	C	Energy production and conversion	Tfu_1227	Tfu_1227 putative ferredoxin reductase						
COG	C	Energy production and conversion	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
COG	C	Energy production and conversion	Tfu_1275	Tfu_1275 hypothetical protein						
COG	C	Energy production and conversion	Tfu_1276	Tfu_1276 alcohol dehydrogenase	18.91	18.85	17.84	17.04	22.33	1.13
COG	C	Energy production and conversion	Tfu_1287	Tfu_1287 betaine-aldehyde dehydrogenase					18.53	
COG	C	Energy production and conversion	Tfu_1288	Tfu_1288 hypothetical protein					13.93	
COG	C	Energy production and conversion	Tfu_1301	Tfu_1301 similar to Coenzyme F420-dependent N5 N10-methylene tetrahydromethanopterin reductase and rela					18.53	
COG	C	Energy production and conversion	Tfu_1302	Tfu_1302 probable 6-carboxyhexanoate--COA ligase					15.64	
COG	C	Energy production and conversion	Tfu_1303	Tfu_1303 NADH:flavin oxidoreductase, Old Yellow enzyme family	15.79	15.27			19.14	
COG	C	Energy production and conversion	Tfu_1311	Tfu_1311 hypothetical protein	15.58	16.71	20.64	20.6	24.64	2.192
COG	C	Energy production and conversion	Tfu_1377	Tfu_1377 isocitrate lyase	17.24	15.99	17.23	17.21	21.54	
COG	C	Energy production and conversion	Tfu_1385	Tfu_1385 putative oxidoreductase	17.73	16.51	18.46	17.62	23.38	
COG	C	Energy production and conversion	Tfu_1439	Tfu_1439 hypothetical protein						
COG	C	Energy production and conversion	Tfu_1456	Tfu_1456 probable FMN oxidoreductase	20.48	20.07	21.61	21.43	25.22	0.815
COG	C	Energy production and conversion	Tfu_1471	Tfu_1471 betaine-aldehyde dehydrogenase					16.26	
COG	C	Energy production and conversion	Tfu_1473	Tfu_1473 putative pimeloyl-CoA synthetase					14.56	
COG	C	Energy production and conversion	Tfu_1479	Tfu_1479 putative ferredoxin						
COG	C	Energy production and conversion	Tfu_1480	Tfu_1480 subunit of CoA-transferase of family III						
COG	C	Energy production and conversion	Tfu_1481	Tfu_1481 putative subunit of succinyl-CoA:benzylsuccinate CoA-transferase						
COG	C	Energy production and conversion	Tfu_1488	Tfu_1488 NADH:flavin oxidoreductase, Old Yellow enzyme family						
COG	C	Energy production and conversion	Tfu_1497	Tfu_1497 alkanesulfonate monooxygenase						
COG	C	Energy production and conversion	Tfu_1500	Tfu_1500 alkanesulfonate monooxygenase						
COG	C	Energy production and conversion	Tfu_1502	Tfu_1502 alkanesulfonate monooxygenase						
COG	C	Energy production and conversion	Tfu_1565	Tfu_1565 hypothetical protein					18.32	
COG	C	Energy production and conversion	Tfu_1624	Tfu_1624 formate dehydrogenase accessory protein					15.08	
COG	C	Energy production and conversion	Tfu_1669	Tfu_1669 hypothetical protein						
COG	C	Energy production and conversion	Tfu_1674	Tfu_1674 putative oxidoreductase	18.87	19.09	19.5	19.48	23.56	1.164

COG	C	Energy production and conversion	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
COG	C	Energy production and conversion	Tfu_1693	Tfu_1693 putative monooxygenase						
COG	C	Energy production and conversion	Tfu_1695	Tfu_1695 cytochrome-c oxidase						
COG	C	Energy production and conversion	Tfu_1706	Tfu_1706 putative aldehyde dehydrogenase					17.58	
COG	C	Energy production and conversion	Tfu_1737	Tfu_1737 oxidoreductase alpha (molybdopterin) subunit			14.39	13.79	19.93	
COG	C	Energy production and conversion	Tfu_1757	Tfu_1757 putative glycerophosphoryl diester phosphodiesterase						
COG	C	Energy production and conversion	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
COG	C	Energy production and conversion	Tfu_1776	Tfu_1776 betaine-aldehyde dehydrogenase	16	15.03			18.4	
COG	C	Energy production and conversion	Tfu_1839	Tfu_1839 putative oxidoreductase					17.77	
COG	C	Energy production and conversion	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
COG	C	Energy production and conversion	Tfu_1926	Tfu_1926 hypothetical protein	19.98	19.2	19.99	19.94	23.09	0.884
COG	C	Energy production and conversion	Tfu_1930	Tfu_1930 putative monooxygenase					16.86	
COG	C	Energy production and conversion	Tfu_1946	Tfu_1946 FAD-linked oxidoreductase	20.44	20.72	18.89	18.06	22.64	0.891
COG	C	Energy production and conversion	Tfu_1982	Tfu_1982 SUF system FeS assembly protein					17.58	
COG	C	Energy production and conversion	Tfu_2023	Tfu_2023 hypothetical protein	14.71	14.54	17.28	17.48	20.61	
COG	C	Energy production and conversion	Tfu_2128	Tfu_2128 hypothetical protein	20.85	20.91	19.78	19.34	23.97	1.009
COG	C	Energy production and conversion	Tfu_2161	Tfu_2161 hypothetical protein	18.37	17.81	14.96	14.98	20.9	
COG	C	Energy production and conversion	Tfu_2185	Tfu_2185 Elongator protein 3/MiaB/NifB					15.37	
COG	C	Energy production and conversion	Tfu_2222	Tfu_2222 nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransfe	15.06		15.97	15.99	20.79	0.7
COG	C	Energy production and conversion	Tfu_2228	Tfu_2228 putative quinone oxidoreductase	18.91	19.37	18.34	18.58	21.72	0.952
COG	C	Energy production and conversion	Tfu_2268	Tfu_2268 hypothetical protein	18.93	18.42	18.68	18.56	22.72	
COG	C	Energy production and conversion	Tfu_2293	Tfu_2293 oxidoreductase	17.34	16.54	16.61	15.9	21.07	
COG	C	Energy production and conversion	Tfu_2348	Tfu_2348 putative ferredoxin reductase			13.92	13.25	19.42	
COG	C	Energy production and conversion	Tfu_2390	Tfu_2390 malate dehydrogenase (oxaloacetate decarboxylating)	15.54	15.17	14.98	15.9	20.7	0.661
COG	C	Energy production and conversion	Tfu_2406	Tfu_2406 H+-transporting two-sector ATPase, delta/epsilon subunit	17.61	17.4	18.54	18.5	21.47	
COG	C	Energy production and conversion	Tfu_2407	Tfu_2407 ATP synthase F1, beta subunit	21.37	21.44	23.04	22.88	26.22	1.194
COG	C	Energy production and conversion	Tfu_2408	Tfu_2408 H+-transporting two-sector ATPase, gamma subunit	20.11	19.39	21.19	20.62	23.67	
COG	C	Energy production and conversion	Tfu_2409	Tfu_2409 ATP synthase subunit A	21.64	21.69	23.06	22.63	26.34	1.138
COG	C	Energy production and conversion	Tfu_2410	Tfu_2410 H+-transporting two-sector ATPase, delta (OSCP) subunit	20.66	20.14	21.77	21.25	24.88	0.912
COG	C	Energy production and conversion	Tfu_2411	Tfu_2411 ATP synthase F0, subunit B	20.75	20.59	21	21.14	24.9	0.695
COG	C	Energy production and conversion	Tfu_2413	Tfu_2413 H+-transporting two-sector ATPase, A subunit						
COG	C	Energy production and conversion	Tfu_2451	Tfu_2451 succinate dehydrogenase	19.35	19.39	20.29	20.56	23.66	1.002
COG	C	Energy production and conversion	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
COG	C	Energy production and conversion	Tfu_2455	Tfu_2455 putative monooxygenase (putative secreted protein)	13.91				19.65	
COG	C	Energy production and conversion	Tfu_2461	Tfu_2461 putative oxidoreductase						
COG	C	Energy production and conversion	Tfu_2518	Tfu_2518 hypothetical protein			14.93		19.68	
COG	C	Energy production and conversion	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
COG	C	Energy production and conversion	Tfu_2533	Tfu_2533 putative glycerol 1-phosphate dehydrogenase					17.86	
COG	C	Energy production and conversion	Tfu_2540	Tfu_2540 glycerophosphoryl diester phosphodiesterase, putative					18.74	
COG	C	Energy production and conversion	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
COG	C	Energy production and conversion	Tfu_2559	Tfu_2559 dihydrolipoamide dehydrogenase	17.62	17.97	18.6	18.7	23.28	1.063
COG	C	Energy production and conversion	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
COG	C	Energy production and conversion	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
COG	C	Energy production and conversion	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
COG	C	Energy production and conversion	Tfu_2586	Tfu_2586 carbon monoxide dehydrogenase						
COG	C	Energy production and conversion	Tfu_2587	Tfu_2587 molybdopterin dehydrogenase						
COG	C	Energy production and conversion	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
COG	C	Energy production and conversion	Tfu_2593	Tfu_2593 glycerol-3-phosphate dehydrogenase	19.6	19.46	17.83	17.65	23.22	0.765
COG	C	Energy production and conversion	Tfu_2674	Tfu_2674 2-oxoglutarate ferredoxin oxidoreductase, alpha subunit	14.55		17.74	18.16	22.74	1.656
COG	C	Energy production and conversion	Tfu_2675	Tfu_2675 ferrodoxin oxidoreductase beta subunit			17.01	16.7	21.8	
COG	C	Energy production and conversion	Tfu_2682	Tfu_2682 NADH dehydrogenase subunit N	15.55	15.11	17.89	15.78	21.55	1.549
COG	C	Energy production and conversion	Tfu_2683	Tfu_2683 NADH dehydrogenase subunit M	15.96	15.61	18.67	18.21	22.04	1.217
COG	C	Energy production and conversion	Tfu_2684	Tfu_2684 NADH dehydrogenase subunit L	16.72	16.18	19.09	19.32	22.49	1.313
COG	C	Energy production and conversion	Tfu_2685	Tfu_2685 NADH dehydrogenase kappa subunit	15.96	16.12	17.42	17.06	21.01	1.226
COG	C	Energy production and conversion	Tfu_2686	Tfu_2686 NADH dehydrogenase subunit J	14.57		19.26	18.19	22.25	
COG	C	Energy production and conversion	Tfu_2687	Tfu_2687 NADH-quinone oxidoreductase, chain I	17.42	17.05	19.49	19.25	23.17	1.344
COG	C	Energy production and conversion	Tfu_2688	Tfu_2688 NADH dehydrogenase subunit H	16.85	15.81	18.1	18.62	22.74	1.366
COG	C	Energy production and conversion	Tfu_2689	Tfu_2689 NADH dehydrogenase gamma subunit	19.85	19.4	22.2	22.17	25.89	1.474
COG	C	Energy production and conversion	Tfu_2690	Tfu_2690 NADH-quinone oxidoreductase, F subunit	18.4	18.59	21.04	20.94	24.09	1.696

COG	C	Energy production and conversion	Tfu_2691	Tfu_2691 ATP synthase subunit E	18.11	17.48	19.19	19.38	23.19	
COG	C	Energy production and conversion	Tfu_2692	Tfu_2692 NADH dehydrogenase delta subunit	17.85	17.37	21.19	20.56	24.79	1.513
COG	C	Energy production and conversion	Tfu_2693	Tfu_2693 NADH dehydrogenase subunit C	17.89	18.01	20.34	20.17	23.82	1.361
COG	C	Energy production and conversion	Tfu_2694	Tfu_2694 NADH dehydrogenase beta subunit	17.52	17.43	19.51	19.02	23.25	1.847
COG	C	Energy production and conversion	Tfu_2695	Tfu_2695 NADH dehydrogenase alpha subunit	15.61	15.66	16.21	16.57	20.39	
COG	C	Energy production and conversion	Tfu_2696	Tfu_2696 geranylgeranyl reductase, plantal and prokaryotic	15.62	15.47	17.94	17.12	21.47	1.158
COG	C	Energy production and conversion	Tfu_2704	Tfu_2704 hypothetical protein					19.24	
COG	C	Energy production and conversion	Tfu_2801	Tfu_2801 glycerol dehydrogenase					18.62	
COG	C	Energy production and conversion	Tfu_2841	Tfu_2841 putative rifampin monooxygenase					17.42	
COG	C	Energy production and conversion	Tfu_2844	Tfu_2844 putative oxidoreductase	14.68	15.21			19.73	
COG	C	Energy production and conversion	Tfu_2902	Tfu_2902 inorganic diphosphatase	14.95		16.63	16.62	20.87	
COG	C	Energy production and conversion	Tfu_2949	Tfu_2949 succinate-semialdehyde dehydrogenase (NAD(P)+)	16.8	17.18	15.55	15.98	20.6	
COG	C	Energy production and conversion	Tfu_2971	Tfu_2971 acetate kinase					13.64	
COG	C	Energy production and conversion	Tfu_2980	Tfu_2980 (S)-2-hydroxy-acid oxidase					14.64	
COG	C	Energy production and conversion	Tfu_3023	Tfu_3023 similar to Flavodoxin						
COG	C	Energy production and conversion	Tfu_3031	Tfu_3031 similar to Coenzyme F420-dependent N5 N10-methylene tetrahydro	14.02				19.75	0.894
COG	C	Energy production and conversion	Tfu_3049	Tfu_3049 pyruvate dehydrogenase (lipoamide)	20.31	19.75	20.61	20.78	24.41	1.167
COG	C	Energy production and conversion	Tfu_3050	Tfu_3050 dehydrogenase complex, E1 component, beta subunit	20.68	20.22	21.86	21.38	24.75	1.231
COG	C	Energy production and conversion	Tfu_3051	Tfu_3051 pyruvate dehydrogenase complex, E2 component, dihydrolipoamide	21.68	21.7	22.67	22.41	25.66	1.062
COG	C	Energy production and conversion	Tfu_3088	Tfu_3088 putative lycopene cyclase						
COG	B	Chromatin structure and dynamics	Tfu_2707	Tfu_2707 putative acetoin utilization protein			16.17	15.33	21.16	1.239
COG	P	Inorganic ion transport and metabolism	Tfu_0111	Tfu_0111 putative ion-transporting ATPase					18.94	
COG	P	Inorganic ion transport and metabolism	Tfu_0112	Tfu_0112 putative ion-transporting ATPase					17.33	
COG	P	Inorganic ion transport and metabolism	Tfu_0139	Tfu_0139 ABC transporter, ATP-binding protein			14.9	15.05	20.84	
COG	P	Inorganic ion transport and metabolism	Tfu_0145	Tfu_0145 fur family transcriptional regulator						
COG	P	Inorganic ion transport and metabolism	Tfu_0318	Tfu_0318 cobalamin biosynthesis protein CobG, precorrin-3B synthase						
COG	P	Inorganic ion transport and metabolism	Tfu_0323	Tfu_0323 polyphosphate kinase	15.85	16.25	15.92	15.14	20.75	1.02
COG	P	Inorganic ion transport and metabolism	Tfu_0327	Tfu_0327 molybdate ABC transporter, inner membrane subunit						
COG	P	Inorganic ion transport and metabolism	Tfu_0328	Tfu_0328 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_0336	Tfu_0336 ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components					15.18	
COG	P	Inorganic ion transport and metabolism	Tfu_0337	Tfu_0337 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_0338	Tfu_0338 ABC-type Fe3+-siderophore transport system inner membrane subunit						
COG	P	Inorganic ion transport and metabolism	Tfu_0345	Tfu_0345 hypothetical protein					17.41	
COG	P	Inorganic ion transport and metabolism	Tfu_0346	Tfu_0346 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_0347	Tfu_0347 hypothetical protein					16.36	
COG	P	Inorganic ion transport and metabolism	Tfu_0348	Tfu_0348 NADH dehydrogenase (quinone)			13.75			
COG	P	Inorganic ion transport and metabolism	Tfu_0349	Tfu_0349 hypothetical protein					16.52	
COG	P	Inorganic ion transport and metabolism	Tfu_0350	Tfu_0350 NADH dehydrogenase (quinone)					16.01	
COG	P	Inorganic ion transport and metabolism	Tfu_0354	Tfu_0354 3-mercaptopyruvate sulfurtransferase					18.69	
COG	P	Inorganic ion transport and metabolism	Tfu_0418	Tfu_0418 3'-Phosphoadenosine 5'-phosphosulfate (PAPS) 3'-phosphatase					17.11	
COG	P	Inorganic ion transport and metabolism	Tfu_0420	Tfu_0420 Small GTP-binding protein domain:Sulfate adenylyltransferase, large subunit			14.13		18.76	0.81
COG	P	Inorganic ion transport and metabolism	Tfu_0425	Tfu_0425 adenylylsulfate kinase					17.66	
COG	P	Inorganic ion transport and metabolism	Tfu_0431	Tfu_0431 putative hydrolase					20.26	
COG	P	Inorganic ion transport and metabolism	Tfu_0520	Tfu_0520 molybdopterin biosynthesis protein MoeB	17.59	17.14	18.26	18.38	22.64	0.841
COG	P	Inorganic ion transport and metabolism	Tfu_0589	Tfu_0589 ABC-type cobalt transport system						1.778
COG	P	Inorganic ion transport and metabolism	Tfu_0656	Tfu_0656 hypothetical protein	23.25	22.38	22.91	22.99	26.12	0.903
COG	P	Inorganic ion transport and metabolism	Tfu_0657	Tfu_0657 hypothetical protein					15.45	
COG	P	Inorganic ion transport and metabolism	Tfu_0659	Tfu_0659 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_0799	Tfu_0799 hypothetical protein	20.2	19.98	19.74	19.89	22.61	0.883
COG	P	Inorganic ion transport and metabolism	Tfu_0817	Tfu_0817 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_0856	Tfu_0856 putative metal uptake regulation protein						
COG	P	Inorganic ion transport and metabolism	Tfu_0857	Tfu_0857 ABC zinc/manganese transport system permease protein						
COG	P	Inorganic ion transport and metabolism	Tfu_0858	Tfu_0858 ABC-type Mn/Zn transport systems ATPase component						
COG	P	Inorganic ion transport and metabolism	Tfu_0873	Tfu_0873 sulfate permease, SulP family						
COG	P	Inorganic ion transport and metabolism	Tfu_0886	Tfu_0886 catalase						
COG	P	Inorganic ion transport and metabolism	Tfu_0895	Tfu_0895 hypothetical protein					15.66	
COG	P	Inorganic ion transport and metabolism	Tfu_0911	Tfu_0911 ABC-type dipeptide/oligopeptide/nickel transport systems, permease components			15.01		17.95	
COG	P	Inorganic ion transport and metabolism	Tfu_0912	Tfu_0912 ABC-type dipeptide/oligopeptide/nickel transport systems, permease components				14.07	19.4	
COG	P	Inorganic ion transport and metabolism	Tfu_0913	Tfu_0913 oligopeptide/dipeptide ABC transporter, ATP-binding protein	17.06	17.13	17.75	18.6	22.63	

COG	P	Inorganic ion transport and metabolism	Tfu_0931	Tfu_0931 ABC-type metal ion transport system ATPase component	13.97	13.69	16.6	17.33	22.05	1.063
COG	P	Inorganic ion transport and metabolism	Tfu_0932	Tfu_0932 putative ABC transporter permease protein	14.82	14.67	15.81	15.77	18.33	
COG	P	Inorganic ion transport and metabolism	Tfu_0933	Tfu_0933 hypothetical protein	18.94	19.25	20.53	20.2	24	1.091
COG	P	Inorganic ion transport and metabolism	Tfu_0951	Tfu_0951 putative metal-binding protein						
COG	P	Inorganic ion transport and metabolism	Tfu_0957	Tfu_0957 superoxide dismutase	22.64	22.53	22.08	22.69	25.05	0.848
COG	P	Inorganic ion transport and metabolism	Tfu_0963	Tfu_0963 hypothetical protein					19.77	
COG	P	Inorganic ion transport and metabolism	Tfu_0987	Tfu_0987 small multidrug resistance protein, SMR family						
COG	P	Inorganic ion transport and metabolism	Tfu_1261	Tfu_1261 small multidrug resistance protein, SMR family						
COG	P	Inorganic ion transport and metabolism	Tfu_1304	Tfu_1304 similar to ABC-type nitrate/sulfonate/bicarbonate transport systems periplasmic components						
COG	P	Inorganic ion transport and metabolism	Tfu_1305	Tfu_1305 ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component						
COG	P	Inorganic ion transport and metabolism	Tfu_1306	Tfu_1306 ABC transporter, permease component						
COG	P	Inorganic ion transport and metabolism	Tfu_1307	Tfu_1307 similar to ABC-type Fe3+ transport system permease component						
COG	P	Inorganic ion transport and metabolism	Tfu_1309	Tfu_1309 hypothetical protein					17.12	
COG	P	Inorganic ion transport and metabolism	Tfu_1353	Tfu_1353 n-acetylgalactosamine-6-sulfate sulfatase					17.5	
COG	P	Inorganic ion transport and metabolism	Tfu_1375	Tfu_1375 putative integral membrane transporter						
COG	P	Inorganic ion transport and metabolism	Tfu_1391	Tfu_1391 arsenite-transporting ATPase						
COG	P	Inorganic ion transport and metabolism	Tfu_1428	Tfu_1428 Magnesium and cobalt transport protein CorA					17.83	
COG	P	Inorganic ion transport and metabolism	Tfu_1434	Tfu_1434 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1490	Tfu_1490 putative monooxygenase					16.06	
COG	P	Inorganic ion transport and metabolism	Tfu_1491	Tfu_1491 hypothetical protein	19	18.35	19.09	18.53	22.25	
COG	P	Inorganic ion transport and metabolism	Tfu_1492	Tfu_1492 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1493	Tfu_1493 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1494	Tfu_1494 ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components						
COG	P	Inorganic ion transport and metabolism	Tfu_1503	Tfu_1503 taurine ABC transporter, permease protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1504	Tfu_1504 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1505	Tfu_1505 ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component						
COG	P	Inorganic ion transport and metabolism	Tfu_1521	Tfu_1521 similar to Arsenate reductase and related proteins glutaredoxin family					17.85	
COG	P	Inorganic ion transport and metabolism	Tfu_1555	Tfu_1555 Arsenical-resistance protein ACR3						
COG	P	Inorganic ion transport and metabolism	Tfu_1566	Tfu_1566 putative oxidoreductase						
COG	P	Inorganic ion transport and metabolism	Tfu_1569	Tfu_1569 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1630	Tfu_1630 oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terr	15.55	15.84			18.2	
COG	P	Inorganic ion transport and metabolism	Tfu_1631	Tfu_1631 ABC transporter, permease protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1632	Tfu_1632 hypothetical protein	14.9				16.2	
COG	P	Inorganic ion transport and metabolism	Tfu_1636	Tfu_1636 hypothetical protein	16.98	17.02	17.32	16.79	21.14	0.529
COG	P	Inorganic ion transport and metabolism	Tfu_1649	Tfu_1649 catalase	20.13	19.98	21.56	21.24	24.73	0.727
COG	P	Inorganic ion transport and metabolism	Tfu_1661	Tfu_1661 putative ABC transporter membrane protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1662	Tfu_1662 ABC-type Mn/Zn transport systems ATPase component						
COG	P	Inorganic ion transport and metabolism	Tfu_1663	Tfu_1663 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1673	Tfu_1673 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1690	Tfu_1690 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1691	Tfu_1691 ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component						
COG	P	Inorganic ion transport and metabolism	Tfu_1692	Tfu_1692 putative ABC transporter membrane protein						
COG	P	Inorganic ion transport and metabolism	Tfu_1698	Tfu_1698 putative monooxygenase						
COG	P	Inorganic ion transport and metabolism	Tfu_1820	Tfu_1820 hypothetical protein	17.64	16.81			19.82	
COG	P	Inorganic ion transport and metabolism	Tfu_1822	Tfu_1822 oligopeptide transport integral membrane protein	16.87		16.15	15.61	21	
COG	P	Inorganic ion transport and metabolism	Tfu_1834	Tfu_1834 ATPase, E1-E2 type						
COG	P	Inorganic ion transport and metabolism	Tfu_1860	Tfu_1860 iron-chelator utilization protein	15.94	15.01	17.02	16.35	20.94	1.009
COG	P	Inorganic ion transport and metabolism	Tfu_1864	Tfu_1864 iron(III) dicitrate transport permease	13.1	12.99	16.58	16.44	21.12	0.92
COG	P	Inorganic ion transport and metabolism	Tfu_1888	Tfu_1888 putative nitrite/sulphite reductase	16.01	13.98	17.79	17.82	22.36	1.384
COG	P	Inorganic ion transport and metabolism	Tfu_1928	Tfu_1928 putative potassium transporter	15.27		15.71	15.35	20.93	1.026
COG	P	Inorganic ion transport and metabolism	Tfu_1929	Tfu_1929 putative potassium uptake protein	16.85	16.88			19.46	
COG	P	Inorganic ion transport and metabolism	Tfu_1967	Tfu_1967 hypothetical protein	14.15	15.73			18.03	
COG	P	Inorganic ion transport and metabolism	Tfu_1985	Tfu_1985 putative dioxygenase					17.16	
COG	P	Inorganic ion transport and metabolism	Tfu_2025	Tfu_2025 putative transporter membrane protein					17.38	
COG	P	Inorganic ion transport and metabolism	Tfu_2106	Tfu_2106 hypothetical protein					15.12	
COG	P	Inorganic ion transport and metabolism	Tfu_2132	Tfu_2132 carbonic anhydrase, putative					20.01	
COG	P	Inorganic ion transport and metabolism	Tfu_2199	Tfu_2199 divalent cation transporter	14.02		13.97		19.62	
COG	P	Inorganic ion transport and metabolism	Tfu_2291	Tfu_2291 oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal						
COG	P	Inorganic ion transport and metabolism	Tfu_2292	Tfu_2292 putative peptide ABC transporter permease protein						

COG	P	Inorganic ion transport and metabolism	Tfu_2300	Tfu_2300 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_2301	Tfu_2301 hypothetical protein	15.95	15.98	15.43	15.04	18.32	1.028
COG	P	Inorganic ion transport and metabolism	Tfu_2302	Tfu_2302 putative cation transporter						
COG	P	Inorganic ion transport and metabolism	Tfu_2303	Tfu_2303 putative cation transporter					17.86	
COG	P	Inorganic ion transport and metabolism	Tfu_2304	Tfu_2304 hypothetical protein					17.67	
COG	P	Inorganic ion transport and metabolism	Tfu_2312	Tfu_2312 putative cobalt transport system permease protein						1.095
COG	P	Inorganic ion transport and metabolism	Tfu_2313	Tfu_2313 ABC-type cobalt transport system ATPase component					19.2	0.595
COG	P	Inorganic ion transport and metabolism	Tfu_2345	Tfu_2345 heme oxygenase (decyclizing)						
COG	P	Inorganic ion transport and metabolism	Tfu_2384	Tfu_2384 ABC-type hemin transport system ATPase component						
COG	P	Inorganic ion transport and metabolism	Tfu_2385	Tfu_2385 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_2386	Tfu_2386 hypothetical protein					18.73	
COG	P	Inorganic ion transport and metabolism	Tfu_2504	Tfu_2504 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_2684	Tfu_2684 NADH dehydrogenase subunit L	16.72	16.18	19.09	19.32	22.49	1.313
COG	P	Inorganic ion transport and metabolism	Tfu_2719	Tfu_2719 thiosulfate sulfurtransferase	22.47	22.41	22.74	22.62	25.34	0.79
COG	P	Inorganic ion transport and metabolism	Tfu_2740	Tfu_2740 hypothetical protein	18.45	17.82	18.3	18.9	21.3	
COG	P	Inorganic ion transport and metabolism	Tfu_2741	Tfu_2741 phosphate ABC transporter, permease protein PstC					17.82	
COG	P	Inorganic ion transport and metabolism	Tfu_2742	Tfu_2742 Phosphate transport system permease protein 2					17.18	
COG	P	Inorganic ion transport and metabolism	Tfu_2743	Tfu_2743 Phosphate transport system permease protein 1	15.49	15.5	16.86	15.14	21.63	
COG	P	Inorganic ion transport and metabolism	Tfu_2744	Tfu_2744 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_2745	Tfu_2745 hypothetical protein			15.47		19.54	
COG	P	Inorganic ion transport and metabolism	Tfu_2810	Tfu_2810 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_2821	Tfu_2821 cation-transporting P-ATPase PacL						
COG	P	Inorganic ion transport and metabolism	Tfu_2848	Tfu_2848 ATPase, E1-E2 type:Copper-translocating P-type ATPase:Heavy metal translocating P-type ATPase					14.11	
COG	P	Inorganic ion transport and metabolism	Tfu_2908	Tfu_2908 PhoU	19.58	19.64	19.46	19.44	23.24	
COG	P	Inorganic ion transport and metabolism	Tfu_3007	Tfu_3007 similar to Uncharacterized protein involved in tolerance to divalent c	16.88	16.21			17.1	
COG	P	Inorganic ion transport and metabolism	Tfu_3040	Tfu_3040 ATPase, E1-E2 type			15.56	14.73	20.8	
COG	P	Inorganic ion transport and metabolism	Tfu_3058	Tfu_3058 rhodanese-like	15.72		16.83	17.05	20.94	
COG	P	Inorganic ion transport and metabolism	Tfu_3077	Tfu_3077 putative methylesterase						
COG	P	Inorganic ion transport and metabolism	Tfu_3078	Tfu_3078 hypothetical protein						
COG	P	Inorganic ion transport and metabolism	Tfu_3083	Tfu_3083 Rhodanese-like protein						
COG	P	Inorganic ion transport and metabolism	Tfu_3085	Tfu_3085 Rhodanese-like protein						
COG	I	Lipid transport and metabolism	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
COG	I	Lipid transport and metabolism	Tfu_0068	Tfu_0068 putative acyl-CoA dehydrogenase			22.01	21.61	24.8	
COG	I	Lipid transport and metabolism	Tfu_0081	Tfu_0081 3-hydroxybutyrate dehydrogenase	21.11	21.46	19.94	20.31	23.95	1.187
COG	I	Lipid transport and metabolism	Tfu_0154	Tfu_0154 similar to Phospholipid N-methyltransferase					18.64	
COG	I	Lipid transport and metabolism	Tfu_0155	Tfu_0155 esterase / lipase						
COG	I	Lipid transport and metabolism	Tfu_0210	Tfu_0210 putative acyl-CoA dehydrogenase	18.98	18.07	18.5	18.33	22.69	1.397
COG	I	Lipid transport and metabolism	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
COG	I	Lipid transport and metabolism	Tfu_0267	Tfu_0267 hypothetical protein					15.05	
COG	I	Lipid transport and metabolism	Tfu_0271	Tfu_0271 Fatty acid synthesis plsX protein		15.01			17.65	
COG	I	Lipid transport and metabolism	Tfu_0275	Tfu_0275 putative short chain dehydrogenase	19.38	19.27	18.64	18.26	23.3	
COG	I	Lipid transport and metabolism	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
COG	I	Lipid transport and metabolism	Tfu_0407	Tfu_0407 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase					17.64	
COG	I	Lipid transport and metabolism	Tfu_0413	Tfu_0413 stearoyl-CoA 9-desaturase						
COG	I	Lipid transport and metabolism	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
COG	I	Lipid transport and metabolism	Tfu_0456	Tfu_0456 di-trans-poly-cis-decaprenylcistransferase					16.85	
COG	I	Lipid transport and metabolism	Tfu_0471	Tfu_0471 4-hydroxy-3-methylbut-2-enyl diphosphate reductase					19.27	
COG	I	Lipid transport and metabolism	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
COG	I	Lipid transport and metabolism	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
COG	I	Lipid transport and metabolism	Tfu_0557	Tfu_0557 diacylglycerol kinase, catalytic region	17.83	17.28	18.34	17.87	22.19	1.054
COG	I	Lipid transport and metabolism	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
COG	I	Lipid transport and metabolism	Tfu_0630	Tfu_0630 phospholipid/glycerol acyltransferase	18.67	18.59	17.98	18.26	21.99	0.852
COG	I	Lipid transport and metabolism	Tfu_0680	Tfu_0680 phosphatidate cytidylyltransferase	15.69	15.29	15.87	15.37	19.59	
COG	I	Lipid transport and metabolism	Tfu_0747	Tfu_0747 1-deoxy-D-xylulose 5-phosphate reductoisomerase						
COG	I	Lipid transport and metabolism	Tfu_0749	Tfu_0749 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase					16.63	
COG	I	Lipid transport and metabolism	Tfu_0756	Tfu_0756 similar to Acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II						
COG	I	Lipid transport and metabolism	Tfu_0796	Tfu_0796 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase					15.36	
COG	I	Lipid transport and metabolism	Tfu_0853	Tfu_0853 di-trans-poly-cis-decaprenylcistransferase	16.33	16.31	16	16.58	20.43	0.931
COG	I	Lipid transport and metabolism	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	

COG	I	Lipid transport and metabolism	Tfu_0946	Tfu_0946 putative acyl-CoA dehydrogenase	20.62	20.44	21.21	21.21	24.67	0.91
COG	I	Lipid transport and metabolism	Tfu_0947	Tfu_0947 putative acetyl/propionyl CoA carboxylase alpha subunit: biotin carb	20.64	20.68	21.06	20.9	24.61	1.056
COG	I	Lipid transport and metabolism	Tfu_0948	Tfu_0948 propionyl-CoA carboxylase	20.47	20.23	20.41	20.19	24.8	
COG	I	Lipid transport and metabolism	Tfu_0958	Tfu_0958 hypothetical protein	16.01	16.15	16.31	16.35	19.61	
COG	I	Lipid transport and metabolism	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
COG	I	Lipid transport and metabolism	Tfu_1036	Tfu_1036 phospholipid/glycerol acyltransferase	18.2	17.54	17.83	17.5	21.56	
COG	I	Lipid transport and metabolism	Tfu_1068	Tfu_1068 glutaryl-CoA dehydrogenase	15.85	16.25	15.59	15.48	20.62	0.775
COG	I	Lipid transport and metabolism	Tfu_1215	Tfu_1215 methylmalonyl-CoA decarboxylase alpha chain						
COG	I	Lipid transport and metabolism	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
COG	I	Lipid transport and metabolism	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
COG	I	Lipid transport and metabolism	Tfu_1221	Tfu_1221 hypothetical protein						
COG	I	Lipid transport and metabolism	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
COG	I	Lipid transport and metabolism	Tfu_1224	Tfu_1224 putative 3-oxoacyl-(acyl-carrier protein) reductase						
COG	I	Lipid transport and metabolism	Tfu_1228	Tfu_1228 putative acyl-CoA carboxylase complex A subunit						
COG	I	Lipid transport and metabolism	Tfu_1229	Tfu_1229 putative 3-oxoacyl-ACP synthase III						
COG	I	Lipid transport and metabolism	Tfu_1234	Tfu_1234 putative hydrolase			13.82	13	20.38	
COG	I	Lipid transport and metabolism	Tfu_1242	Tfu_1242 short chain dehydrogenase					18.48	
COG	I	Lipid transport and metabolism	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
COG	I	Lipid transport and metabolism	Tfu_1265	Tfu_1265 2-hydroxy-3-oxopropionate reductase			15.84	13.26	19.37	
COG	I	Lipid transport and metabolism	Tfu_1278	Tfu_1278 thiolase						
COG	I	Lipid transport and metabolism	Tfu_1279	Tfu_1279 short chain dehydrogenase					16.87	
COG	I	Lipid transport and metabolism	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
COG	I	Lipid transport and metabolism	Tfu_1281	Tfu_1281 butyryl-CoA dehydrogenase						
COG	I	Lipid transport and metabolism	Tfu_1282	Tfu_1282 putative acyl-CoA dehydrogenase					18.17	
COG	I	Lipid transport and metabolism	Tfu_1283	Tfu_1283 probable short-chain type dehydrogenase/reductase						
COG	I	Lipid transport and metabolism	Tfu_1284	Tfu_1284 putative acyl-CoA dehydrogenase						
COG	I	Lipid transport and metabolism	Tfu_1286	Tfu_1286 possible dehydratase, MaoC family						
COG	I	Lipid transport and metabolism	Tfu_1298	Tfu_1298 2-deoxy-D-gluconate 3-dehydrogenase	15.48	14.84		13.51	17.6	
COG	I	Lipid transport and metabolism	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly related to diterpenoid m	16.49	15.45			20.78	
COG	I	Lipid transport and metabolism	Tfu_1312	Tfu_1312 hypothetical protein	17.51	15.88	15.76	16.08	20.86	
COG	I	Lipid transport and metabolism	Tfu_1347	Tfu_1347 putative lipase	17.63	17.41	16.91	16.15	21.47	1.189
COG	I	Lipid transport and metabolism	Tfu_1379	Tfu_1379 putative acyl-CoA dehydrogenase					16.7	
COG	I	Lipid transport and metabolism	Tfu_1393	Tfu_1393 putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase					15.45	
COG	I	Lipid transport and metabolism	Tfu_1408	Tfu_1408 putative ortho-succinylbenzoate-CoA synthetase						
COG	I	Lipid transport and metabolism	Tfu_1417	Tfu_1417 phospholipid/glycerol acyltransferase	13.91	13.6		12.45	17.58	
COG	I	Lipid transport and metabolism	Tfu_1466	Tfu_1466 short-chain alcohol dehydrogenase						
COG	I	Lipid transport and metabolism	Tfu_1468	Tfu_1468 similar to Acyl-CoA dehydrogenase						
COG	I	Lipid transport and metabolism	Tfu_1472	Tfu_1472 short-chain dehydrogenase/reductase (SDR) family protein						
COG	I	Lipid transport and metabolism	Tfu_1474	Tfu_1474 short chain dehydrogenase						
COG	I	Lipid transport and metabolism	Tfu_1483	Tfu_1483 hypothetical protein						
COG	I	Lipid transport and metabolism	Tfu_1484	Tfu_1484 hypothetical protein						
COG	I	Lipid transport and metabolism	Tfu_1487	Tfu_1487 hypothetical protein						
COG	I	Lipid transport and metabolism	Tfu_1495	Tfu_1495 hypothetical protein						
COG	I	Lipid transport and metabolism	Tfu_1496	Tfu_1496 FMNH2-dependent monooxygenase					15.36	
COG	I	Lipid transport and metabolism	Tfu_1512	Tfu_1512 putative acyl-CoA dehydrogenase	14.16	14.11		14.03	20.64	
COG	I	Lipid transport and metabolism	Tfu_1513	Tfu_1513 hypothetical protein						
COG	I	Lipid transport and metabolism	Tfu_1520	Tfu_1520 thiolase					15.67	
COG	I	Lipid transport and metabolism	Tfu_1530	Tfu_1530 similar to Acetyl/propionyl-CoA carboxylase alpha subunit	13.47		18.27	17.82	23.35	1.185
COG	I	Lipid transport and metabolism	Tfu_1544	Tfu_1544 putative enoyl-CoA hydratase/isomerase family protein	17.9	18.35	14.7	14.84	20.76	
COG	I	Lipid transport and metabolism	Tfu_1546	Tfu_1546 putative acyl-CoA synthetase					20.01	
COG	I	Lipid transport and metabolism	Tfu_1558	Tfu_1558 hypothetical protein	20.02	19.53	18.36	18.31	22.74	0.931
COG	I	Lipid transport and metabolism	Tfu_1647	Tfu_1647 acyl-CoA dehydrogenase	19.93	19.53	19.07	19.09	22.67	1.416
COG	I	Lipid transport and metabolism	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
COG	I	Lipid transport and metabolism	Tfu_1701	Tfu_1701 hypothetical protein						
COG	I	Lipid transport and metabolism	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
COG	I	Lipid transport and metabolism	Tfu_1766	Tfu_1766 Conserved hypothetical protein 147						
COG	I	Lipid transport and metabolism	Tfu_1777	Tfu_1777 putative acyl-CoA dehydrogenase	16.51	16.11	13.91		19.09	
COG	I	Lipid transport and metabolism	Tfu_1784	Tfu_1784 hypothetical protein	14.4				19.3	
COG	I	Lipid transport and metabolism	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	

COG	I	Lipid transport and metabolism	Tfu_1842	Tfu_1842 enoyl-(acyl carrier protein) reductase	20.49	19.93	21.16	21.07	24.76	1.053
COG	I	Lipid transport and metabolism	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
COG	I	Lipid transport and metabolism	Tfu_1873	Tfu_1873 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase					14.76	
COG	I	Lipid transport and metabolism	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
COG	I	Lipid transport and metabolism	Tfu_1894	Tfu_1894 phosphatidylserine decarboxylase	16.99	15.03	17.14	16.9	21.01	1.091
COG	I	Lipid transport and metabolism	Tfu_1895	Tfu_1895 putative phosphatidylserine synthase						
COG	I	Lipid transport and metabolism	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
COG	I	Lipid transport and metabolism	Tfu_1904	Tfu_1904 fatty acid oxidation complex alpha-subunit	20.01	20.04	19.24	18.76	23.49	1.256
COG	I	Lipid transport and metabolism	Tfu_1917	Tfu_1917 1-deoxy-D-xylulose-5-phosphate synthase					16.98	
COG	I	Lipid transport and metabolism	Tfu_1973	Tfu_1973 acyl-carrier-protein S-malonyltransferase	18.46	18.27	20.02	20.23	23.66	0.61
COG	I	Lipid transport and metabolism	Tfu_1974	Tfu_1974 3-oxoacyl-(acyl carrier protein) synthase	14.7	15.5	19.86	19.55	23.27	0.869
COG	I	Lipid transport and metabolism	Tfu_1975	Tfu_1975 acyl carrier protein	20.19	20.71	21.15	20.99	23.95	0.341
COG	I	Lipid transport and metabolism	Tfu_1976	Tfu_1976 putative 3-oxoacyl-ACP synthase II	18.39	18.02	19.63	19.4	22.79	0.718
COG	I	Lipid transport and metabolism	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
COG	I	Lipid transport and metabolism	Tfu_1999	Tfu_1999 acyl-CoA dehydrogenase						
COG	I	Lipid transport and metabolism	Tfu_2103	Tfu_2103 putative membrane transferase		14.75	15	14.79	18.49	
COG	I	Lipid transport and metabolism	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
COG	I	Lipid transport and metabolism	Tfu_2239	Tfu_2239 hypothetical protein	17.58	17.57	18.21	17.62	22.75	0.874
COG	I	Lipid transport and metabolism	Tfu_2245	Tfu_2245 acetoacetyl-CoA synthase	21.88	21.42	21.12	20.91	24.4	0.895
COG	I	Lipid transport and metabolism	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
COG	I	Lipid transport and metabolism	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
COG	I	Lipid transport and metabolism	Tfu_2309	Tfu_2309 putative acyl-CoA dehydrogenase	14.92	15.24	14.15		18.46	
COG	I	Lipid transport and metabolism	Tfu_2310	Tfu_2310 putative acyl-CoA dehydrogenase	11.82	14.18	10.94	10.95	18.06	
COG	I	Lipid transport and metabolism	Tfu_2359	Tfu_2359 hypothetical protein					18.4	
COG	I	Lipid transport and metabolism	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
COG	I	Lipid transport and metabolism	Tfu_2399	Tfu_2399 3-hydroxybutyryl-CoA dehydrogenase	19.01	18.42	18.82	18.43	22.92	1.184
COG	I	Lipid transport and metabolism	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
COG	I	Lipid transport and metabolism	Tfu_2439	Tfu_2439 hypothetical protein			17.33	17.12	20.66	
COG	I	Lipid transport and metabolism	Tfu_2458	Tfu_2458 putative acyltransferase						
COG	I	Lipid transport and metabolism	Tfu_2485	Tfu_2485 acyl-CoA dehydrogenase	14.3		15.52	15.96	21.16	
COG	I	Lipid transport and metabolism	Tfu_2532	Tfu_2532 putative transferase	15.65	15.38	16.18	15.86	19.86	1.349
COG	I	Lipid transport and metabolism	Tfu_2539	Tfu_2539 4-diphosphocytidyl-2C-methyl-D-erythritol synthase					18.51	
COG	I	Lipid transport and metabolism	Tfu_2555	Tfu_2555 propionyl-CoA carboxylase complex B subunit	18.59	18.29	18.47	17.99	22.37	0.744
COG	I	Lipid transport and metabolism	Tfu_2557	Tfu_2557 putative acyl-CoA carboxylase, alpha subunit	16.42	15.3	17.56	17.37	22.48	
COG	I	Lipid transport and metabolism	Tfu_2665	Tfu_2665 hypothetical protein			15.28	14.99	21.22	0.772
COG	I	Lipid transport and metabolism	Tfu_2666	Tfu_2666 hypothetical protein					20.08	
COG	I	Lipid transport and metabolism	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
COG	I	Lipid transport and metabolism	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
COG	I	Lipid transport and metabolism	Tfu_2808	Tfu_2808 putative acetyl-coenzyme A synthetase			16.12	15.88	21.7	
COG	I	Lipid transport and metabolism	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
COG	I	Lipid transport and metabolism	Tfu_2817	Tfu_2817 hypothetical protein					18.27	
COG	I	Lipid transport and metabolism	Tfu_2856	Tfu_2856 acetyl-coenzyme A synthetase	24.08	23.76	23.99	23.94	27	1.638
COG	I	Lipid transport and metabolism	Tfu_2906	Tfu_2906 MECDP-synthase	14.67		15.37		18.41	0.633
COG	I	Lipid transport and metabolism	Tfu_3047	Tfu_3047 phosphoesterase, PA-phosphatase related						
COG	I	Lipid transport and metabolism	Tfu_3076	Tfu_3076 putative phytoene synthase						
COG	I	Lipid transport and metabolism	Tfu_3099	Tfu_3099 myo-inositol-1-phosphate synthase	16.21	15.62	18.24	18.23	23.01	0.924
COG	V	Defense mechanisms	Tfu_0220	Tfu_0220 putative secreted esterase						
COG	V	Defense mechanisms	Tfu_0261	Tfu_0261 hypothetical protein	15.68	14.29		13.37	20.57	
COG	V	Defense mechanisms	Tfu_0291	Tfu_0291 ABC-type multidrug transport system ATPase component	18.3	18.34	12.27	14.38	19.26	0.945
COG	V	Defense mechanisms	Tfu_0461	Tfu_0461 ABC-type multidrug transport system ATPase component			14.83	15.65	20.1	
COG	V	Defense mechanisms	Tfu_0462	Tfu_0462 nodulation protein J					17.98	
COG	V	Defense mechanisms	Tfu_0698	Tfu_0698 hypothetical protein		15.16	16.07	16.01	21.38	0.625
COG	V	Defense mechanisms	Tfu_0812	Tfu_0812 ABC-type antimicrobial peptide transport system ATPase component					13.88	
COG	V	Defense mechanisms	Tfu_1142	Tfu_1142 hypothetical protein					15.86	
COG	V	Defense mechanisms	Tfu_1157	Tfu_1157 ABC-type multidrug transport system ATPase and permease components						
COG	V	Defense mechanisms	Tfu_1158	Tfu_1158 ABC-type multidrug transport system ATPase and permease components						
COG	V	Defense mechanisms	Tfu_1349	Tfu_1349 putative type I restriction system adenine methylase	16.01	16.48	15.79	15.41	21.5	1.053
COG	V	Defense mechanisms	Tfu_1436	Tfu_1436 ABC-type multidrug transport system ATPase component						
COG	V	Defense mechanisms	Tfu_1447	Tfu_1447 ABC-type multidrug transport system ATPase component	16.35	15.6	15.13	15.71	21.08	1.077

COG	V	Defense mechanisms	Tfu_1448	Tfu_1448 putative ABC transporter transmembrane protein				13.27	16.04	
COG	V	Defense mechanisms	Tfu_1697	Tfu_1697 ABC-type multidrug transport system ATPase and permease components						
COG	V	Defense mechanisms	Tfu_1838	Tfu_1838 undecaprenyl pyrophosphate phosphatase	17.56	17.35	17.39	17.14	20.29	0.764
COG	V	Defense mechanisms	Tfu_1847	Tfu_1847 ABC-type antimicrobial peptide transport system ATPase component						
COG	V	Defense mechanisms	Tfu_1989	Tfu_1989 ABC-type multidrug transport system ATPase componen		14.95	15.16	13.52	19.05	0.854
COG	V	Defense mechanisms	Tfu_1990	Tfu_1990 putative integral membrane transport protein						
COG	V	Defense mechanisms	Tfu_2197	Tfu_2197 ABC-type multidrug transport system ATPase and permease compon	13.74				19.25	
COG	V	Defense mechanisms	Tfu_2211	Tfu_2211 HNH nuclease						
COG	V	Defense mechanisms	Tfu_2296	Tfu_2296 hypothetical protein	16.6	16.49	16.15	16.92	21.65	0.89
COG	V	Defense mechanisms	Tfu_2311	Tfu_2311 hypothetical protein	14.21					
COG	V	Defense mechanisms	Tfu_2429	Tfu_2429 similar to Streptomycin 6-kinase		14.54			20.53	
COG	V	Defense mechanisms	Tfu_2865	Tfu_2865 hypothetical protein						
COG	V	Defense mechanisms	Tfu_3091	Tfu_3091 Multi antimicrobial extrusion protein MatE					16.17	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0120	Tfu_0120 putative serine protease						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0172	Tfu_0172 thioredoxin	15.85	16.52	17.35	17.78	21.04	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0196	Tfu_0196 molecular chaperone DnaK	22.33	22.35	22.87	22.74	26.1	0.904
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0197	Tfu_0197 similar to Molecular chaperone GrpE (heat shock protein)	19.7	19.79	19.71	19.46	22.91	0.598
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0198	Tfu_0198 Heat shock protein DnaJ	17.03	17.25	15.8	16.29	21.15	0.926
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0200	Tfu_0200 ATPase	20.26	19.85	19.67	19.84	24.19	0.868
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0221	Tfu_0221 similar to Subtilisin-like serine protease	15.91	15.38		14.86	19.47	1.177
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0228	Tfu_0228 chaperonin GroEL	21.86	21.8	23.6	23.54	26.74	0.839
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0353	Tfu_0353 trypsin-like serine protease typically periplasmic contain C-terminal PDZ domain						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0385	Tfu_0385 putative integral membrane protein	15.29	14.94	15.24	14.52	19.38	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0451	Tfu_0451 hypothetical protein	17.57	16.89	17.31	17.28	22.23	2.445
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0507	Tfu_0507 trypsin-like serine protease typically periplasmic contain C-terminal PDZ domain					16.4	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0529	Tfu_0529 Glutaredoxin-like protein GlrX					16.54	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0579	Tfu_0579 peptidase S49, protease IV:Peptidase S49, SppA	21.99	21.86	21.35	20.93	25.08	1.204
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0635	Tfu_0635 hypothetical protein					19.62	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0636	Tfu_0636 hypothetical protein					18.52	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0670	Tfu_0670 Mg chelatase-related protein						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0697	Tfu_0697 putative ATP/GTP binding protein	18.92	20.03	18.92	19.09	22.47	0.488
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0839	Tfu_0839 Heat shock protein DnaJ	16.06	14.77	15.48		20.29	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0924	Tfu_0924 putative ADP-ribosylglycohydrolase					15.77	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_0986	Tfu_0986 glutamate-ammonia-ligase adenylyltransferase					18.95	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1008	Tfu_1008 heat shock protein HtpX						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1014	Tfu_1014 putative aminotransferase						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1089	Tfu_1089 hypothetical protein						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1214	Tfu_1214 similar to Molecular chaperone (small heat shock protein)	18.69	18.41	21.43	21.1	24.6	1.429
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1437	Tfu_1437 band 7 protein	19.18	18.91	18.21	18.42	22.34	1.449
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1522	Tfu_1522 hypothetical protein						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1523	Tfu_1523 similar to Protein-disulfide isomerase						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1528	Tfu_1528 heat shock protein, class I						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1571	Tfu_1571 hypothetical protein					17.92	1.237
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1773	Tfu_1773 similar to FKBP-type peptidyl-prolyl cis-trans isomerase 1	18.39	18.19	17.36	17.39	22.49	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1789	Tfu_1789 putative 20S proteasome alpha-subunit	21.35	20.72	20.29	20.07	23.84	0.978
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1790	Tfu_1790 Proteasome endopeptidase complex	20.83	20.83	21.11	21.18	24.64	1.164
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1808	Tfu_1808 putative methyltransferase					14.61	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1809	Tfu_1809 vesicle-fusing ATPase	19.7	19.57	20.84	20.58	24.36	1.038
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1831	Tfu_1831 putative heat shock protein, hsp90-family						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1893	Tfu_1893 methionine sulfoxide reductase B	15.65	15.39		14.71	18.99	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1933	Tfu_1933 proteinase inhibitor I4, serpin	16.83	16.39	15.16	12.01	20.65	0.994
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1964	Tfu_1964 putative thiol-specific antioxidant protein					16.26	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1984	Tfu_1984 FeS assembly ATPase SufC	19.17	19.17	17.9	17.2	22.56	0.64
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1986	Tfu_1986 FeS assembly protein SufD	20.06	19.83	19.82	19.38	23.74	0.829
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1987	Tfu_1987 FeS assembly protein SufB	18.72	18.49	17.96	17.75	22.15	0.895
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_1995	Tfu_1995 putative integral membrane transport protein					18.49	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2144	Tfu_2144 hypothetical protein	14.84	14.67		15.54	20.28	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2147	Tfu_2147 band 7 protein	21.16	21.13	19.79	19.74	24.03	0.869

COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2148	Tfu_2148 band 7 protein	21.43	20.85	20.35	20.38	24.27	0.827
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2172	Tfu_2172 hypothetical protein	18.4	18.54	18.4	18.02	22.68	0.913
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2192	Tfu_2192 ATP-dependent protease ATP-binding subunit					15.67	1.556
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2193	Tfu_2193 ATP-dependent Clp protease proteolytic subunit	20.29	20.62	21.31	20.84	24.1	0.798
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2194	Tfu_2194 endopeptidase Clp	21.36	21.68	21.56	21.35	24.71	1.134
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2195	Tfu_2195 trigger factor	19.21	19.11	21.62	21.37	24.88	0.679
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2226	Tfu_2226 putative integral membrane protein		16.29			21.74	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2227	Tfu_2227 hypothetical protein	21.39	21.56	20.66	20.39	23.92	1.108
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2285	Tfu_2285 similar to FKBP-type peptidyl-prolyl cis-trans isomerase 1					18.88	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2360	Tfu_2360 bacterioferritin comigratory protein	17.08	16.37	18.22	18.06	22.15	1.027
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2392	Tfu_2392 putative thioredoxin	16.79	16.15	19.22	19.39	23.62	0.778
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2436	Tfu_2436 hypothetical protein						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2476	Tfu_2476 SsrA-binding protein	14.09				18.08	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2598	Tfu_2598 chaperonin GroEL	19.99	19.62	21.97	21.7	25.37	0.777
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2599	Tfu_2599 10 kD chaperone	21.51	21.07	21.74	21.3	24.36	0.372
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2602	Tfu_2602 peptidase M22, glycoprotease	14.17		16.74	16.68	20.36	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2604	Tfu_2604 hypothetical protein					18.8	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2673	Tfu_2673 putative peptidase						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2678	Tfu_2678 methionine sulfoxide reductase A					16.73	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2701	Tfu_2701 CcsB			14.54	13.15	18.64	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2702	Tfu_2702 putative integral membrane protein					16.49	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2703	Tfu_2703 hypothetical protein					15.06	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2704	Tfu_2704 hypothetical protein					19.24	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2711	Tfu_2711 DNA repair protein RadA						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2759	Tfu_2759 similar to Glutathione peroxidase		15.24			20.7	1.126
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2770	Tfu_2770 thioredoxin					17.56	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2820	Tfu_2820 hypothetical protein	17.27	18.07	15.39	15.23	20.65	
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2876	Tfu_2876 ATPase	20.28	20.39	21.5	21.1	25.26	1.046
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2895	Tfu_2895 hypothetical protein	18.74	18.46	19.98	19.65	23.82	1.538
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2917	Tfu_2917 integral membrane protein						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_2995	Tfu_2995 hypothetical protein	20.18	19.87	19.96	19.85	23.67	1.122
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_3003	Tfu_3003 putative O-methyltransferase						
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_3069	Tfu_3069 peptidylprolyl isomerase	14.49		16.71	16.23	20.71	0.843
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_3108	Tfu_3108 thioredoxin reductase	16.25	15.17	16.88	17.34	22.36	1.054
COG	O	Posttranslational modification, protein turnover, chaperones	Tfu_3109	Tfu_3109 thioredoxin	19.93	19.19	19.15	18.79	22.02	0.684

Appendix - E - Proteomics Data HOV: KEGG Pathway

CLASS	HOV	HOV-description	locus	locus-description	AV	AVR	CB	CBR	CB2D	iTRAQ
KEGG	M00113	Jasmonic acid biosynthesis	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
KEGG	M00113	Jasmonic acid biosynthesis	Tfu_1278	Tfu_1278 thiolase						
KEGG	M00113	Jasmonic acid biosynthesis	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
KEGG	M00113	Jasmonic acid biosynthesis	Tfu_2239	Tfu_2239 hypothetical protein	17.58	17.57	18.21	17.62	22.75	0.874
KEGG	M00543	Biphenyl degradation, biphenyl => 2-oxopent-4-enoate	Tfu_1273	Tfu_1273 putative oxidoreductase						
KEGG	M00543	Biphenyl degradation, biphenyl => 2-oxopent-4-enoate	Tfu_1985	Tfu_1985 putative dioxygenase					17.16	
KEGG	M00254	ABC-2 type transport system	Tfu_0291	Tfu_0291 ABC-type multidrug transport system ATPase co	18.3	18.34	12.27	14.38	19.26	0.945
KEGG	M00254	ABC-2 type transport system	Tfu_0462	Tfu_0462 nodulation protein J					17.98	
KEGG	M00254	ABC-2 type transport system	Tfu_1448	Tfu_1448 putative ABC transporter transmembrane protein				13.27	16.04	
KEGG	M00236	Putative polar amino acid transport system	Tfu_0303	Tfu_0303 hypothetical protein	14.25		14.59	14.35	18.3	
KEGG	M00236	Putative polar amino acid transport system	Tfu_0304	Tfu_0304 hypothetical protein						
KEGG	M00236	Putative polar amino acid transport system	Tfu_0305	Tfu_0305 amino acid ABC transporter, inner membrane subunit						
KEGG	M00236	Putative polar amino acid transport system	Tfu_0306	Tfu_0306 ABC-type polar amino acid transport system ATPase component					16.25	
KEGG	M00344	Formaldehyde assimilation, xylulose monophosphate pathway	Tfu_1716	Tfu_1716 glycerone kinase	16	15.49	13.71		18.65	
KEGG	M00344	Formaldehyde assimilation, xylulose monophosphate pathway	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
KEGG	M00127	Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P	Tfu_0643	Tfu_0643 thiamine monophosphate kinase					14.5	
KEGG	M00127	Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P	Tfu_1046	Tfu_1046 thiamine-phosphate pyrophosphorylase		14.35			19.31	
KEGG	M00127	Thiamine biosynthesis, AIR => thiamine-P/thiamine-2P	Tfu_2250	Tfu_2250 phosphomethylpyrimidine kinase	16.07	16.41	14.97		19.92	1.225
KEGG	M00208	Glycine betaine/proline transport system	Tfu_2928	Tfu_2928 hypothetical protein	20.69	21.33	20.08	19.7	23	0.829
KEGG	M00208	Glycine betaine/proline transport system	Tfu_2929	Tfu_2929 similar to ABC-type proline/glycine betaine transport system permease comp					18.2	
KEGG	M00208	Glycine betaine/proline transport system	Tfu_2930	Tfu_2930 glycine betaine/L-proline transport ATP-binding subunit			14.84		19.59	
KEGG	M00357	Methanogenesis, acetate => methane	Tfu_2971	Tfu_2971 acetate kinase					13.64	
KEGG	M00377	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	Tfu_1050	Tfu_1050 5,10-methylenetetrahydrofolate reductase						
KEGG	M00377	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
KEGG	M00377	Reductive acetyl-CoA pathway (Wood-Ljungdahl pathway)	Tfu_2971	Tfu_2971 acetate kinase					13.64	
KEGG	M00173	Reductive citric acid cycle (Arnon-Buchanan cycle)	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
KEGG	M00173	Reductive citric acid cycle (Arnon-Buchanan cycle)	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
KEGG	M00173	Reductive citric acid cycle (Arnon-Buchanan cycle)	Tfu_0863	Tfu_0863 pyruvate phosphate dikinase	17.84	17.11	21.38	21.45	25.04	1.455
KEGG	M00173	Reductive citric acid cycle (Arnon-Buchanan cycle)	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
KEGG	M00173	Reductive citric acid cycle (Arnon-Buchanan cycle)	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
KEGG	M00173	Reductive citric acid cycle (Arnon-Buchanan cycle)	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
KEGG	M00173	Reductive citric acid cycle (Arnon-Buchanan cycle)	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
KEGG	M00173	Reductive citric acid cycle (Arnon-Buchanan cycle)	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
KEGG	M00173	Reductive citric acid cycle (Arnon-Buchanan cycle)	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
KEGG	M00173	Reductive citric acid cycle (Arnon-Buchanan cycle)	Tfu_2674	Tfu_2674 2-oxoglutarate ferredoxin oxidoreductase, alpha	14.55		17.74	18.16	22.74	1.656
KEGG	M00006	Pentose phosphate pathway, oxidative phase, glucose 6P => ribu	Tfu_0003	Tfu_0003 6-phosphogluconate dehydrogenase	20.18	20.31	19.92	19.72	23.9	0.655
KEGG	M00006	Pentose phosphate pathway, oxidative phase, glucose 6P => ribu	Tfu_2005	Tfu_2005 glucose-6-phosphate 1-dehydrogenase	16.6	15.74	16.81	16.27	21.46	
KEGG	M00006	Pentose phosphate pathway, oxidative phase, glucose 6P => ribu	Tfu_2007	Tfu_2007 6-phosphogluconolactonase	18.7	19.13	18.21	17.98	22.37	0.913
KEGG	M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => ch	Tfu_0544	Tfu_0544 3-phosphoshikimate 1-carboxyvinyltransferase						
KEGG	M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => ch	Tfu_1039	Tfu_1039 phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 2						
KEGG	M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => ch	Tfu_1090	Tfu_1090 chorismate synthase	19.19	18.56	19.76	19.46	23.47	
KEGG	M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => ch	Tfu_1091	Tfu_1091 shikimate kinase					19.23	
KEGG	M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => ch	Tfu_1092	Tfu_1092 3-dehydroquinate synthase	18.86	18.36	19.22	18.34	23.14	1.077
KEGG	M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => ch	Tfu_1635	Tfu_1635 dehydroquinase, class II					16.28	
KEGG	M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => ch	Tfu_2067	Tfu_2067 shikimate 5-dehydrogenase					17.29	

KEGG	M00022	Shikimate pathway, phosphoenolpyruvate + erythrose-4P => ch	Tfu_2350	Tfu_2350 phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1			14.88	13.66	19.21	
KEGG	M00024	Phenylalanine biosynthesis, chorismate => phenylalanine	Tfu_1207	Tfu_1207 chorismate mutase of the AroH class						
KEGG	M00024	Phenylalanine biosynthesis, chorismate => phenylalanine	Tfu_3053	Tfu_3053 prephenate dehydratase					16.06	
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_0948	Tfu_0948 propionyl-CoA carboxylase	20.47	20.23	20.41	20.19	24.8	
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_0994	Tfu_0994 dihydrolipoamide dehydrogenase	23.87	23.67	23.96	23.71	27.03	1.154
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_1282	Tfu_1282 putative acyl-CoA dehydrogenase					18.17	
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_1284	Tfu_1284 putative acyl-CoA dehydrogenase						
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_1512	Tfu_1512 putative acyl-CoA dehydrogenase	14.16	14.11		14.03	20.64	
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_1647	Tfu_1647 acyl-CoA dehydrogenase	19.93	19.53	19.07	19.09	22.67	1.416
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_1999	Tfu_1999 acyl-CoA dehydrogenase						
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_2485	Tfu_2485 acyl-CoA dehydrogenase	14.3		15.52	15.96	21.16	
KEGG	M00036	Leucine degradation, leucine => acetoacetate + acetyl-CoA	Tfu_2559	Tfu_2559 dihydrolipoamide dehydrogenase	17.62	17.97	18.6	18.7	23.28	1.063
KEGG	M00167	Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
KEGG	M00167	Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
KEGG	M00167	Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
KEGG	M00167	Reductive pentose phosphate cycle, glyceraldehyde-3P => RuBP	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_0566	Tfu_0566 alpha-ketoglutarate decarboxylase	22.63	22.08	23.34	23.51	26.75	1.555
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_0993	Tfu_0993 dihydrolipoamide S-succinyltransferase	21.69	21.57	21.99	21.46	25.01	1.46
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_0994	Tfu_0994 dihydrolipoamide dehydrogenase	23.87	23.67	23.96	23.71	27.03	1.154
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_2451	Tfu_2451 succinate dehydrogenase	19.35	19.39	20.29	20.56	23.66	1.002
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_2453	Tfu_2453 succinate dehydrogenase, cytochrome b558 subunit					19.37	1.293
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_2559	Tfu_2559 dihydrolipoamide dehydrogenase	17.62	17.97	18.6	18.7	23.28	1.063
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
KEGG	M00009	Citrate cycle (TCA cycle, Krebs cycle)	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
KEGG	M00151	Cytochrome bc1 complex respiratory unit	Tfu_1019	Tfu_1019 ubiquinol-cytochrome c reductase, cytochrome b	20.02	19.57	20.62	20.81	24.55	1.089
KEGG	M00151	Cytochrome bc1 complex respiratory unit	Tfu_1020	Tfu_1020 ubiquinol-cytochrome c reductase iron-sulfur su	20.38	20.21	21.32	21.24	24.45	1.098
KEGG	M00151	Cytochrome bc1 complex respiratory unit	Tfu_1021	Tfu_1021 hypothetical protein	19.26	19.79	20.25	20.15	23.34	1.121
KEGG	M00350	Capsaicin biosynthesis, L-Phenylalanine => Capsaicin	Tfu_0966	Tfu_0966 caffeoyl-CoA O-methyltransferase		13.62			16.15	
KEGG	M00129	Ascorbate biosynthesis, animals, glucose-1P => ascorbate	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase, b	16.85	15	17.24	17.46	22.15	
KEGG	M00129	Ascorbate biosynthesis, animals, glucose-1P => ascorbate	Tfu_1946	Tfu_1946 FAD-linked oxidoreductase	20.44	20.72	18.89	18.06	22.64	0.891
KEGG	M00129	Ascorbate biosynthesis, animals, glucose-1P => ascorbate	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
KEGG	M00342	Bacterial proteasome	Tfu_1788	Tfu_1788 hypothetical protein	19.06	18.7	19.67	19.63	23.68	1.295
KEGG	M00342	Bacterial proteasome	Tfu_1789	Tfu_1789 putative 20S proteasome alpha-subunit	21.35	20.72	20.29	20.07	23.84	0.978
KEGG	M00342	Bacterial proteasome	Tfu_1790	Tfu_1790 Proteasome endopeptidase complex	20.83	20.83	21.11	21.18	24.64	1.164
KEGG	M00342	Bacterial proteasome	Tfu_1796	Tfu_1796 putative proteasome component	14.51	14.96	17.7	16.83	22.14	
KEGG	M00342	Bacterial proteasome	Tfu_1809	Tfu_1809 vesicle-fusing ATPase	19.7	19.57	20.84	20.58	24.36	1.038
KEGG	M00529	Denitrification, nitrate => nitrogen	Tfu_2794	Tfu_2794 hypothetical protein						
KEGG	M00179	Ribosome, archaea	Tfu_0676	Tfu_0676 30S ribosomal protein S2	19.71	20.16	22.1	21.87	25.09	1.094
KEGG	M00179	Ribosome, archaea	Tfu_0783	Tfu_0783 Ribosomal protein S15, bacterial chloroplast and	15.74		17.1	16.76	20.8	1.338
KEGG	M00179	Ribosome, archaea	Tfu_1013	Tfu_1013 30S ribosomal protein S4	17.09	15.75	19.47	19.58	23.57	1.141
KEGG	M00179	Ribosome, archaea	Tfu_2613	Tfu_2613 30S ribosomal protein S9	16.28	16.43	18.85	18.6	21.99	1.059
KEGG	M00179	Ribosome, archaea	Tfu_2614	Tfu_2614 50S ribosomal protein L13				14.95	20.12	1.466

KEGG	M00179	Ribosome, archaea	Tfu_2619	Tfu_2619 30S ribosomal protein S11			14.35	14.19	19.17	1.403
KEGG	M00179	Ribosome, archaea	Tfu_2620	Tfu_2620 putative ribosomal protein S13	17.69	17.39	19.98	19.49	23.4	1.368
KEGG	M00179	Ribosome, archaea	Tfu_2627	Tfu_2627 50S ribosomal protein L15	17.62	17.41	19.68	20.07	23.57	1.242
KEGG	M00179	Ribosome, archaea	Tfu_2628	Tfu_2628 Ribosomal protein L30, bacterial					16.5	
KEGG	M00179	Ribosome, archaea	Tfu_2629	Tfu_2629 30S ribosomal protein S5	17.94	18.12	20.32	20	23.82	1.26
KEGG	M00179	Ribosome, archaea	Tfu_2630	Tfu_2630 Ribosomal protein L18	17.6	17.22	18.77	19.13	22.07	0.873
KEGG	M00179	Ribosome, archaea	Tfu_2631	Tfu_2631 putative ribosomal protein L6	15.23		18.82	18.71	23.1	1.719
KEGG	M00179	Ribosome, archaea	Tfu_2632	Tfu_2632 30S ribosomal protein S8			15.52	16.17	21.1	
KEGG	M00179	Ribosome, archaea	Tfu_2633	Tfu_2633 putative ribosomal protein S14						
KEGG	M00179	Ribosome, archaea	Tfu_2634	Tfu_2634 50S ribosomal protein L5	17.41	16.86	20.33	19.9	24.12	0.923
KEGG	M00179	Ribosome, archaea	Tfu_2635	Tfu_2635 50S ribosomal protein L24					19.57	1.272
KEGG	M00179	Ribosome, archaea	Tfu_2636	Tfu_2636 Ribosomal protein L14, bacterial and organelle f	15.14	14.25	15.95	16.24	21.6	
KEGG	M00179	Ribosome, archaea	Tfu_2637	Tfu_2637 putative ribosomal protein S17	15.1		15.63	16.12	20.84	
KEGG	M00179	Ribosome, archaea	Tfu_2638	Tfu_2638 Ribosomal protein L29	17.98	17.84	19.81	19.63	23.41	
KEGG	M00179	Ribosome, archaea	Tfu_2640	Tfu_2640 30S ribosomal protein S3	19.05	18.87	20.76	19.8	24.22	1.062
KEGG	M00179	Ribosome, archaea	Tfu_2641	Tfu_2641 Ribosomal protein L22, bacterial and organelle form		17.55	18.98	18.79	22.53	
KEGG	M00179	Ribosome, archaea	Tfu_2642	Tfu_2642 Ribosomal protein S19, bacterial and organelle form					19.57	
KEGG	M00179	Ribosome, archaea	Tfu_2643	Tfu_2643 50S ribosomal protein L2	17.57	16.83	20.41	20.21	24.19	1.171
KEGG	M00179	Ribosome, archaea	Tfu_2644	Tfu_2644 50S ribosomal protein L23			17.93	18.03	21.63	1.453
KEGG	M00179	Ribosome, archaea	Tfu_2646	Tfu_2646 putative ribosomal protein L3	16.68	16.48	18.15	18.41	22.12	0.908
KEGG	M00179	Ribosome, archaea	Tfu_2647	Tfu_2647 30S ribosomal protein S10	18.09	16.88	19.37	19.35	22.52	0.826
KEGG	M00179	Ribosome, archaea	Tfu_2650	Tfu_2650 Ribosomal protein S7, bacterial and organelle for	16.75	16.51	19.03	18.86	22.58	1.249
KEGG	M00179	Ribosome, archaea	Tfu_2651	Tfu_2651 Ribosomal protein S12, bacterial and chloroplast	16.08		16.9	16.88	20.29	
KEGG	M00179	Ribosome, archaea	Tfu_2656	Tfu_2656 50S ribosomal protein L10	18.93	18.9	20.97	20.1	23.88	1.042
KEGG	M00179	Ribosome, archaea	Tfu_2657	Tfu_2657 Ribosomal protein L1, bacterial and chloroplast f	19.1	19.48	21.28	21.2	24.32	1.14
KEGG	M00179	Ribosome, archaea	Tfu_2658	Tfu_2658 Ribosomal protein L11, bacterial			17.58	16.31	21.3	1.25
KEGG	M00206	Cellobiose transport system	Tfu_0934	Tfu_0934 hypothetical protein	22.95	22.9	23.76	23.39	26.25	2.077
KEGG	M00206	Cellobiose transport system	Tfu_0935	Tfu_0935 multiple sugar transport system permease prote	16.27		17.74	17.07	21.52	0.973
KEGG	M00206	Cellobiose transport system	Tfu_0936	Tfu_0936 multiple sugar transport system permease prote	12.91	13.62	17.29	16.44	20.46	1.159
KEGG	M00124	Pyridoxal biosynthesis, erythrose-4P => pyridoxal-5P	Tfu_0246	Tfu_0246 phosphoserine aminotransferase	19.59	19.46	22.48	21.91	25.76	1.096
KEGG	M00124	Pyridoxal biosynthesis, erythrose-4P => pyridoxal-5P	Tfu_0248	Tfu_0248 pyridoxamine 5'-phosphate oxidase	15.34	14.98		14.89	18.71	
KEGG	M00097	beta-Carotene biosynthesis, GGAP => beta-carotene	Tfu_3076	Tfu_3076 putative phytoene synthase						
KEGG	M00097	beta-Carotene biosynthesis, GGAP => beta-carotene	Tfu_3088	Tfu_3088 putative lycopene cyclase						
KEGG	M00531	Assimilatory nitrate reduction, nitrate => ammonia	Tfu_1888	Tfu_1888 putative nitrite/sulphite reductase	16.01	13.98	17.79	17.82	22.36	1.384
KEGG	M00460	MprB-MprA (maintenance of persistent infection) 2-component	Tfu_0343	Tfu_0343 response regulator receiver	16.6	15.97	16.58	16.78	21.5	
KEGG	M00460	MprB-MprA (maintenance of persistent infection) 2-component	Tfu_0344	Tfu_0344 signal transduction histidine kinase					18.04	
KEGG	M00336	Twin-arginine translocation (Tat) system	Tfu_0381	Tfu_0381 sec-independent translocase						
KEGG	M00336	Twin-arginine translocation (Tat) system	Tfu_1768	Tfu_1768 sec-independent periplasmic protein translocase						
KEGG	M00336	Twin-arginine translocation (Tat) system	Tfu_1769	Tfu_1769 Twin-arginine translocation protein TatA/E		16.06		13.71	20.32	
KEGG	M00242	Zinc transport system	Tfu_0857	Tfu_0857 ABC zinc/manganese transport system permease protein						
KEGG	M00242	Zinc transport system	Tfu_0858	Tfu_0858 ABC-type Mn/Zn transport systems ATPase component						
KEGG	M00242	Zinc transport system	Tfu_2304	Tfu_2304 hypothetical protein					17.67	
KEGG	M00530	Dissimilatory nitrate reduction, nitrate => ammonia	Tfu_1888	Tfu_1888 putative nitrite/sulphite reductase	16.01	13.98	17.79	17.82	22.36	1.384
KEGG	M00540	Benzoate degradation, cyclohexanecarboxylic acid =>pimeloyl-C	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
KEGG	M00256	Cell division transport system	Tfu_2477	Tfu_2477 hypothetical protein			15.64	15.48	20.44	1.517
KEGG	M00256	Cell division transport system	Tfu_2478	Tfu_2478 ATPase	17.12	16.74	15.1	15.75	21.04	0.955
KEGG	M00015	Proline biosynthesis, glutamate => proline	Tfu_2175	Tfu_2175 gamma-glutamyl phosphate reductase GPR	16.65	16.53	17.82	17.26	21.71	
KEGG	M00015	Proline biosynthesis, glutamate => proline	Tfu_2179	Tfu_2179 gamma-glutamyl kinase					17.69	
KEGG	M00015	Proline biosynthesis, glutamate => proline	Tfu_2708	Tfu_2708 delta 1-pyrroline-5-carboxylate reductase	17.73	17.16	18.03	17.57	21.11	
KEGG	M00029	Urea cycle	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	

KEGG	M00029	Urea cycle	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
KEGG	M00029	Urea cycle	Tfu_2051	Tfu_2051 argininosuccinate lyase	15.68	16.51	18.68	18.9	22.79	
KEGG	M00029	Urea cycle	Tfu_2052	Tfu_2052 argininosuccinate synthase	13.3		18.49	17.16	22.53	
KEGG	M00201	alpha-Glucoside transport system	Tfu_2337	Tfu_2337 hypothetical protein	24.16	24.05	23.56	23.37	26.53	0.944
KEGG	M00201	alpha-Glucoside transport system	Tfu_2338	Tfu_2338 ABC-type glucosylglycerol transport system perr	19.81	19.69	17.52	14.17	21.74	
KEGG	M00201	alpha-Glucoside transport system	Tfu_2339	Tfu_2339 ABC-type glucosylglycerol transport system perr	19.46	18.37	17.61	16.97	21.61	
KEGG	M00394	RNA degradosome	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
KEGG	M00394	RNA degradosome	Tfu_0784	Tfu_0784 polyribonucleotide nucleotidyltransferase	20.08	19.88	21.21	21.25	24.81	1.127
KEGG	M00394	RNA degradosome	Tfu_2183	Tfu_2183 ribonuclease E and G	15.17	14.73	17.43	17.22	22.5	1.093
KEGG	M00258	Putative ABC transport system	Tfu_0812	Tfu_0812 ABC-type antimicrobial peptide transport system ATPase component					13.88	
KEGG	M00258	Putative ABC transport system	Tfu_1847	Tfu_1847 ABC-type antimicrobial peptide transport system ATPase component						
KEGG	M00258	Putative ABC transport system	Tfu_1848	Tfu_1848 hypothetical protein					13.81	
KEGG	M00365	C10-C20 isoprenoid biosynthesis, archaea	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
KEGG	M00188	NitT/TauT family transport system	Tfu_1304	Tfu_1304 similar to ABC-type nitrate/sulfonate/bicarbonate transport systems periplasmic componen						
KEGG	M00188	NitT/TauT family transport system	Tfu_1305	Tfu_1305 ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component						
KEGG	M00188	NitT/TauT family transport system	Tfu_1306	Tfu_1306 ABC transporter, permease component						
KEGG	M00188	NitT/TauT family transport system	Tfu_1503	Tfu_1503 taurine ABC transporter, permease protein						
KEGG	M00188	NitT/TauT family transport system	Tfu_1504	Tfu_1504 hypothetical protein						
KEGG	M00188	NitT/TauT family transport system	Tfu_1505	Tfu_1505 ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component						
KEGG	M00188	NitT/TauT family transport system	Tfu_1691	Tfu_1691 ABC-type nitrate/sulfonate/bicarbonate transport system ATPase component						
KEGG	M00188	NitT/TauT family transport system	Tfu_1692	Tfu_1692 putative ABC transporter membrane protein						
KEGG	M00095	C5 isoprenoid biosynthesis, mevalonate pathway	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
KEGG	M00095	C5 isoprenoid biosynthesis, mevalonate pathway	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
KEGG	M00095	C5 isoprenoid biosynthesis, mevalonate pathway	Tfu_1520	Tfu_1520 thiolase					15.67	
KEGG	M00095	C5 isoprenoid biosynthesis, mevalonate pathway	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
KEGG	M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1 r	18.57	18.71	20.61	20.33	23.82	0.982
KEGG	M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
KEGG	M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Tfu_0494	Tfu_0494 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-s	20.98	20.36	20.57	20.17	24.7	0.791
KEGG	M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Tfu_0495	Tfu_0495 succinyl-diaminopimelate desuccinylase	16.35	16.43	16.49	16.87	20.83	0.501
KEGG	M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Tfu_0568	Tfu_0568 hypothetical protein					18.2	
KEGG	M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Tfu_0786	Tfu_0786 dihydrodipicolinate reductase	18.87	17.45	19.64	18.4	23.22	0.825
KEGG	M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844
KEGG	M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Tfu_0816	Tfu_0816 diaminopimelate epimerase					18.06	
KEGG	M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
KEGG	M00016	Lysine biosynthesis, succinyl-DAP pathway, aspartate => lysine	Tfu_2425	Tfu_2425 diaminopimelate decarboxylase					18.01	
KEGG	M00374	Dicarboxylate-hydroxybutyrate cycle	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
KEGG	M00374	Dicarboxylate-hydroxybutyrate cycle	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
KEGG	M00374	Dicarboxylate-hydroxybutyrate cycle	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
KEGG	M00374	Dicarboxylate-hydroxybutyrate cycle	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
KEGG	M00374	Dicarboxylate-hydroxybutyrate cycle	Tfu_1520	Tfu_1520 thiolase					15.67	
KEGG	M00374	Dicarboxylate-hydroxybutyrate cycle	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
KEGG	M00374	Dicarboxylate-hydroxybutyrate cycle	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
KEGG	M00374	Dicarboxylate-hydroxybutyrate cycle	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
KEGG	M00374	Dicarboxylate-hydroxybutyrate cycle	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
KEGG	M00374	Dicarboxylate-hydroxybutyrate cycle	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
KEGG	M00082	Fatty acid biosynthesis, initiation	Tfu_1229	Tfu_1229 putative 3-oxoacyl-ACP synthase III						
KEGG	M00082	Fatty acid biosynthesis, initiation	Tfu_1973	Tfu_1973 acyl-carrier-protein S-malonyltransferase	18.46	18.27	20.02	20.23	23.66	0.61
KEGG	M00082	Fatty acid biosynthesis, initiation	Tfu_1974	Tfu_1974 3-oxoacyl-(acyl carrier protein) synthase	14.7	15.5	19.86	19.55	23.27	0.869
KEGG	M00082	Fatty acid biosynthesis, initiation	Tfu_1976	Tfu_1976 putative 3-oxoacyl-ACP synthase II	18.39	18.02	19.63	19.4	22.79	0.718
KEGG	M00045	Histidine degradation, histidine => N-formiminoglutamate => gl	Tfu_0821	Tfu_0821 imidazolonepropionase					17.2	

KEGG	M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	Tfu_0180	Tfu_0180 pyruvate dehydrogenase (lipoamide)	20.47	20.54	21.95	22.05	25.45	0.974
KEGG	M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	Tfu_0182	Tfu_0182 putative dihydrolipoamide acyltransferase comp	22.33	22.24	22.85	22.66	25.78	1.092
KEGG	M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	Tfu_0994	Tfu_0994 dihydrolipoamide dehydrogenase	23.87	23.67	23.96	23.71	27.03	1.154
KEGG	M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	Tfu_2559	Tfu_2559 dihydrolipoamide dehydrogenase	17.62	17.97	18.6	18.7	23.28	1.063
KEGG	M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	Tfu_3049	Tfu_3049 pyruvate dehydrogenase (lipoamide)	20.31	19.75	20.61	20.78	24.41	1.167
KEGG	M00307	Pyruvate oxidation, pyruvate => acetyl-CoA	Tfu_3051	Tfu_3051 pyruvate dehydrogenase complex, E2 componen	21.68	21.7	22.67	22.41	25.66	1.062
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_0174	Tfu_0174 ATP phosphoribosyltransferase	19.33	18.84	19.91	18.99	23.24	1.037
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_0175	Tfu_0175 phosphoribosyl-ATP pyrophosphatase	17.66	17.21	14.18	15.95	21.68	0.868
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_0542	Tfu_0542 histidinol-phosphate phosphatase, putative, inos	18.79	18.37	16.97	17.19	21.21	
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_1150	Tfu_1150 histidinol dehydrogenase	19.66	19.37	19.47	19.89	23.27	0.966
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_1151	Tfu_1151 histidinol-phosphate aminotransferase					19.66	1.354
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_1152	Tfu_1152 imidazoleglycerol-phosphate dehydratase					17.24	
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_1155	Tfu_1155 1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methyliden			15.7	16.67	21.72	
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_1156	Tfu_1156 histidine biosynthesis protein HisF	14.6	14.45	14.77	14.57	20.69	
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_1159	Tfu_1159 phosphoribosyl-AMP cyclohydrolase					16.88	
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_2223	Tfu_2223 putative aminotransferase					16.25	
KEGG	M00026	Histidine biosynthesis, PRPP => histidine	Tfu_3018	Tfu_3018 putative aminotransferase					19.29	1.473
KEGG	M00429	Competence-related DNA transformation transporter	Tfu_0825	Tfu_0825 ComEC/Rec2-related protein						
KEGG	M00429	Competence-related DNA transformation transporter	Tfu_0826	Tfu_0826 helix-hairpin-helix DNA-binding, class 1						
KEGG	M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
KEGG	M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
KEGG	M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	Tfu_2625	Tfu_2625 adenylate kinase, subfamily	19.36	20.27	22.16	21.48	24.95	0.736
KEGG	M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	Tfu_3012	Tfu_3012 adenylosuccinate synthetase	15.75	15.57	18.76	18.61	22.25	0.954
KEGG	M00049	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	Tfu_3014	Tfu_3014 adenylosuccinate lyase	18.68	18.68	20.17	19.69	23.57	0.954
KEGG	M00233	Glutamate transport system	Tfu_0807	Tfu_0807 amino acid ABC transporter, permease protein, 3	18.54	17.53	15.99	15.66	20.16	0.846
KEGG	M00233	Glutamate transport system	Tfu_0808	Tfu_0808 amino acid ABC transporter, permease protein, 3	20.17	18.67	18.21	18.6	21.97	1.222
KEGG	M00233	Glutamate transport system	Tfu_0809	Tfu_0809 hypothetical protein	23.78	23.37	21.95	21.85	24.44	0.831
KEGG	M00233	Glutamate transport system	Tfu_0810	Tfu_0810 ABC-type polar amino acid transport system ATP	20.65	20.47	19.17	19	22.36	1.163
KEGG	M00268	PTS system, arbutin-like II component	Tfu_2489	Tfu_2489 putative phosphoenolpyruvate-dependent sugar phosphotransferase					16.36	
KEGG	M00141	C1-unit interconversion, eukaryotes	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
KEGG	M00126	Tetrahydrofolate biosynthesis, GTP => THF	Tfu_1314	Tfu_1314 dihydropteroate synthase	16.71	16.84	17.22	16.91	22.57	1.071
KEGG	M00126	Tetrahydrofolate biosynthesis, GTP => THF	Tfu_1673	Tfu_1673 hypothetical protein						
KEGG	M00126	Tetrahydrofolate biosynthesis, GTP => THF	Tfu_2190	Tfu_2190 folylpolyglutamate synthetase					19.35	
KEGG	M00126	Tetrahydrofolate biosynthesis, GTP => THF	Tfu_2890	Tfu_2890 7, 8-Dihydro-6-hydroxymethylpterin-pyrophosphokinase, HPPK					15.52	
KEGG	M00126	Tetrahydrofolate biosynthesis, GTP => THF	Tfu_2891	Tfu_2891 dihydroneopterin aldolase family:Dihydroneopte	14.95	14.62	16	15.74	20.08	
KEGG	M00126	Tetrahydrofolate biosynthesis, GTP => THF	Tfu_2893	Tfu_2893 dihydropteroate synthase	18.01	17.46	18.35	17.82	21.56	1.133
KEGG	M00126	Tetrahydrofolate biosynthesis, GTP => THF	Tfu_2894	Tfu_2894 GTP cyclohydrolase I		15.85	17.62	17.38	21.27	0.628
KEGG	M00155	Cytochrome c oxidase, prokaryotes	Tfu_0881	Tfu_0881 cytochrome-c oxidase			17.98	18.28	22.45	
KEGG	M00155	Cytochrome c oxidase, prokaryotes	Tfu_1015	Tfu_1015 hypothetical protein	20.5	19.96	19.7	20.09	23.2	1.256
KEGG	M00155	Cytochrome c oxidase, prokaryotes	Tfu_1016	Tfu_1016 cytochrome-c oxidase					20.91	1.146
KEGG	M00155	Cytochrome c oxidase, prokaryotes	Tfu_1022	Tfu_1022 cytochrome c oxidase subunit III						
KEGG	M00155	Cytochrome c oxidase, prokaryotes	Tfu_1695	Tfu_1695 cytochrome-c oxidase						
KEGG	M00010	Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutar	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
KEGG	M00010	Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutar	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
KEGG	M00010	Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutar	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
KEGG	M00221	Putative simple sugar transport system	Tfu_1920	Tfu_1920 putative ABC transporter transmembrane transp	15.44	16.24	17	17.75	21.57	1.079
KEGG	M00221	Putative simple sugar transport system	Tfu_1921	Tfu_1921 ABC-type sugar transport system ATPase compo	16.87	16.94	19.92	20.01	23.32	0.871
KEGG	M00221	Putative simple sugar transport system	Tfu_1922	Tfu_1922 hypothetical protein	23.01	22.64	23.83	23.66	26.57	0.607
KEGG	M00491	Putative arabinogalactan oligomer transport system	Tfu_1763	Tfu_1763 ABC-type sugar transport systems ATPase compo	22.15	21.91	22.51	21.98	25.88	1.102

KEGG	M00133	Polyamine biosynthesis, arginine => agmatine => putrescine =>	Tfu_0058	Tfu_0058 putative agmatinase	15.19	15.1			18.15	1.47
KEGG	M00133	Polyamine biosynthesis, arginine => agmatine => putrescine =>	Tfu_2234	Tfu_2234 spermidine synthase						
KEGG	M00172	C4-dicarboxylic acid cycle, NADP+ -malic enzyme type	Tfu_0863	Tfu_0863 pyruvate phosphate dikinase	17.84	17.11	21.38	21.45	25.04	1.455
KEGG	M00172	C4-dicarboxylic acid cycle, NADP+ -malic enzyme type	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
KEGG	M00272	PTS system, arbutin-, cellobiose-, and salicin-specific II compone	Tfu_2489	Tfu_2489 putative phosphoenolpyruvate-dependent sugar phosphotransferase					16.36	
KEGG	M00012	Glyoxylate cycle	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
KEGG	M00012	Glyoxylate cycle	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
KEGG	M00012	Glyoxylate cycle	Tfu_0819	Tfu_0819 malate synthase	20.71	20.65	20.77	20.84	24.52	0.986
KEGG	M00012	Glyoxylate cycle	Tfu_1377	Tfu_1377 isocitrate lyase	17.24	15.99	17.23	17.21	21.54	
KEGG	M00012	Glyoxylate cycle	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
KEGG	M00052	Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/	Tfu_1199	Tfu_1199 CTP synthetase	15.21	15.76	18.58	17.89	22.8	1.201
KEGG	M00052	Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/	Tfu_1209	Tfu_1209 cytidylate kinase	15.69	15.43		14.19	19.62	
KEGG	M00052	Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
KEGG	M00248	Putative antibiotic transport system	Tfu_1436	Tfu_1436 ABC-type multidrug transport system ATPase component						
KEGG	M00248	Putative antibiotic transport system	Tfu_1447	Tfu_1447 ABC-type multidrug transport system ATPase co	16.35	15.6	15.13	15.71	21.08	1.077
KEGG	M00248	Putative antibiotic transport system	Tfu_1989	Tfu_1989 ABC-type multidrug transport system ATPase componer	14.95	15.16	13.52		19.05	0.854
KEGG	M00248	Putative antibiotic transport system	Tfu_1990	Tfu_1990 putative integral membrane transport protein						
KEGG	M00190	Iron(III) transport system	Tfu_1307	Tfu_1307 similar to ABC-type Fe3+ transport system permease component						
KEGG	M00190	Iron(III) transport system	Tfu_1308	Tfu_1308 ABC-type spermidine/putrescine transport systems ATPase components						
KEGG	M00190	Iron(III) transport system	Tfu_1309	Tfu_1309 hypothetical protein					17.12	
KEGG	M00536	Ornithine biosynthesis, glutamate => ornithine, without N-acety	Tfu_2175	Tfu_2175 gamma-glutamyl phosphate reductase GPR	16.65	16.53	17.82	17.26	21.71	
KEGG	M00536	Ornithine biosynthesis, glutamate => ornithine, without N-acety	Tfu_2179	Tfu_2179 gamma-glutamyl kinase					17.69	
KEGG	M00536	Ornithine biosynthesis, glutamate => ornithine, without N-acety	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
KEGG	M00240	Iron complex transport system	Tfu_0139	Tfu_0139 ABC transporter, ATP-binding protein			14.9	15.05	20.84	
KEGG	M00240	Iron complex transport system	Tfu_0336	Tfu_0336 ABC-type cobalamin/Fe3+-siderophores transport systems ATPase componer					15.18	
KEGG	M00240	Iron complex transport system	Tfu_0337	Tfu_0337 hypothetical protein						
KEGG	M00240	Iron complex transport system	Tfu_0338	Tfu_0338 ABC-type Fe3+-siderophore transport system inner membrane subunit						
KEGG	M00240	Iron complex transport system	Tfu_0656	Tfu_0656 hypothetical protein	23.25	22.38	22.91	22.99	26.12	0.903
KEGG	M00240	Iron complex transport system	Tfu_0657	Tfu_0657 hypothetical protein					15.45	
KEGG	M00240	Iron complex transport system	Tfu_1491	Tfu_1491 hypothetical protein	19	18.35	19.09	18.53	22.25	
KEGG	M00240	Iron complex transport system	Tfu_1492	Tfu_1492 hypothetical protein						
KEGG	M00240	Iron complex transport system	Tfu_1493	Tfu_1493 hypothetical protein						
KEGG	M00240	Iron complex transport system	Tfu_1494	Tfu_1494 ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components						
KEGG	M00240	Iron complex transport system	Tfu_1864	Tfu_1864 iron(III) dicitrate transport permease	13.1	12.99	16.58	16.44	21.12	0.92
KEGG	M00240	Iron complex transport system	Tfu_2384	Tfu_2384 ABC-type hemin transport system ATPase component						
KEGG	M00240	Iron complex transport system	Tfu_2385	Tfu_2385 hypothetical protein						
KEGG	M00240	Iron complex transport system	Tfu_2386	Tfu_2386 hypothetical protein					18.73	
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_0031	Tfu_0031 seryl-tRNA synthetase	19.71	19.5	20.47	20.38	23.8	0.939
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_0212	Tfu_0212 cysteinyl-tRNA synthetase	16.41	14.49	18.9	18.08	23.01	1.169
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_0269	Tfu_0269 arginyl-tRNA synthetase, class Ic	17.72	17.49	20.13	19.85	24.16	1.223
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_0389	Tfu_0389 methionyl-tRNA synthetase	18.09	18	20.33	20.35	23.82	1.106
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_0623	Tfu_0623 glutamyl-tRNA synthetase bacterial/mitochondr	18.5	17.36	18.79	19.22	23.34	0.908
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_0759	Tfu_0759 histidine--tRNA ligase	16.98	16.75	18.26	18.29	22.52	0.925
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_0772	Tfu_0772 prolyl-tRNA synthetase	19.32	19.13	19.74	19.37	23.57	1.007
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_0861	Tfu_0861 glycyl-tRNA synthetase	18.27	17.66	19.58	19.58	23.56	1.154
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_1120	Tfu_1120 isoleucyl-tRNA synthetase, class Ia	16.68	16.31	19.54	19.65	23.84	1.694
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_1832	Tfu_1832 cysteinyl-tRNA synthetase	15.91	16.04	18.24	17.09	22.24	1.186
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_1936	Tfu_1936 valyl-tRNA synthetase	17.79	17.98	19.77	19.27	23.94	1.167
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_2043	Tfu_2043 tyrosyl-tRNA synthetase, class Ib	16.28	16.71	18.6	18.54	22.47	1.194
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_2060	Tfu_2060 phenylalanyl-tRNA synthetase beta subunit	19.74	19.67	20.55	20.4	24.66	1.059

KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_2061	Tfu_2061 phenylalanyl-tRNA synthetase alpha subunit	16.56	17.28	19.09	18.91	22.49	0.719
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_2070	Tfu_2070 alanyl-tRNA synthetase	18.51	18.11	19.5	19.52	23.9	1.221
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_2086	Tfu_2086 aspartyl-tRNA synthetase	18.54	17.59	19.9	19.59	23.67	1.015
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_2108	Tfu_2108 threonyl-tRNA synthetase	18.4	18.24	19.7	19.43	23.68	1.178
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_2156	Tfu_2156 leucyl-tRNA synthetase bacterial/mitochondrial,	20.17	20.38	21.64	21.31	25.2	1.161
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_2376	Tfu_2376 tryptophanyl-tRNA synthetase, class Ib	15.16		16.88	16.16	20.45	
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_2426	Tfu_2426 similar to Arginyl-tRNA synthetase					16.36	
KEGG	M00360	Aminoacyl-tRNA biosynthesis, prokaryotes	Tfu_2881	Tfu_2881 lysyl-tRNA synthetase, class-2	16.6	16.7	19.01	18.9	23.54	0.997
KEGG	M00005	PRPP biosynthesis, ribose 5P => PRPP	Tfu_0415	Tfu_0415 ribose-phosphate pyrophosphokinase	18.35	17.7	20.22	20.21	23.7	1.099
KEGG	M00193	Putative spermidine/putrescine transport system	Tfu_1434	Tfu_1434 hypothetical protein						
KEGG	M00007	Pentose phosphate pathway, non-oxidative phase, fructose 6P =	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
KEGG	M00007	Pentose phosphate pathway, non-oxidative phase, fructose 6P =	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
KEGG	M00007	Pentose phosphate pathway, non-oxidative phase, fructose 6P =	Tfu_2003	Tfu_2003 transaldolase	20.04	20.08	21.54	21.1	24.47	1.211
KEGG	M00007	Pentose phosphate pathway, non-oxidative phase, fructose 6P =	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
KEGG	M00479	DesK-DesR (membrane lipid fluidity regulation) two-component	Tfu_0288	Tfu_0288 regulatory protein, LuxR:Response regulator receiver						
KEGG	M00479	DesK-DesR (membrane lipid fluidity regulation) two-component	Tfu_0289	Tfu_0289 hypothetical protein						
KEGG	M00246	Nickel transport system	Tfu_0588	Tfu_0588 ATPase						2.621
KEGG	M00246	Nickel transport system	Tfu_0589	Tfu_0589 ABC-type cobalt transport system						1.778
KEGG	M00246	Nickel transport system	Tfu_2312	Tfu_2312 putative cobalt transport system permease protein						1.095
KEGG	M00246	Nickel transport system	Tfu_2313	Tfu_2313 ABC-type cobalt transport system ATPase component					19.2	0.595
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_0623	Tfu_0623 glutamyl-tRNA synthetase bacterial/mitochondr	18.5	17.36	18.79	19.22	23.34	0.908
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_0739	Tfu_0739 coproporphyrinogen III oxidase						
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_0835	Tfu_0835 putative oxygen-independent coproporphyrinogen III oxidase						
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_1897	Tfu_1897 protoporphyrinogen oxidase			14.61		20.74	1.244
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_1899	Tfu_1899 uroporphyrinogen decarboxylase HemE		14.37	15.41	15.99	20.69	0.856
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_1945	Tfu_1945 ferrochelatase		13.87	18.69	18.79	22.82	1.023
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_2221	Tfu_2221 uroporphyrin-III C-methyltransferase, C-termina	17.11	16.52	17.24	16.23	21.37	0.99
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_2726	Tfu_2726 glutamate-1-semialdehyde aminotransferase	17.89	17.41	18.76	18.54	22.7	
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_2730	Tfu_2730 porphobilinogen synthase					18.56	
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_2731	Tfu_2731 putative uroporphyrin-III C-methyltransferase/u	19.75	19.58	19.91	19.51	24.15	1.231
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_2732	Tfu_2732 porphobilinogen deaminase	13.44				19.8	
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_2733	Tfu_2733 glutamyl-tRNA reductase						
KEGG	M00121	Heme biosynthesis, glutamate => protoheme/siroheme	Tfu_3023	Tfu_3023 similar to Flavodoxin						
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2682	Tfu_2682 NADH dehydrogenase subunit N	15.55	15.11	17.89	15.78	21.55	1.549
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2683	Tfu_2683 NADH dehydrogenase subunit M	15.96	15.61	18.67	18.21	22.04	1.217
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2684	Tfu_2684 NADH dehydrogenase subunit L	16.72	16.18	19.09	19.32	22.49	1.313
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2685	Tfu_2685 NADH dehydrogenase kappa subunit	15.96	16.12	17.42	17.06	21.01	1.226
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2686	Tfu_2686 NADH dehydrogenase subunit J	14.57		19.26	18.19	22.25	
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2687	Tfu_2687 NADH-quinone oxidoreductase, chain I	17.42	17.05	19.49	19.25	23.17	1.344
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2688	Tfu_2688 NADH dehydrogenase subunit H	16.85	15.81	18.1	18.62	22.74	1.366
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2689	Tfu_2689 NADH dehydrogenase gamma subunit	19.85	19.4	22.2	22.17	25.89	1.474
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2690	Tfu_2690 NADH-quinone oxidoreductase, F subunit	18.4	18.59	21.04	20.94	24.09	1.696
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2691	Tfu_2691 ATP synthase subunit E	18.11	17.48	19.19	19.38	23.19	
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2692	Tfu_2692 NADH dehydrogenase delta subunit	17.85	17.37	21.19	20.56	24.79	1.513
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2693	Tfu_2693 NADH dehydrogenase subunit C	17.89	18.01	20.34	20.17	23.82	1.361
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2694	Tfu_2694 NADH dehydrogenase beta subunit	17.52	17.43	19.51	19.02	23.25	1.847
KEGG	M00144	NADH:quinone oxidoreductase, prokaryotes	Tfu_2695	Tfu_2695 NADH dehydrogenase alpha subunit	15.61	15.66	16.21	16.57	20.39	
KEGG	M00153	Cytochrome d ubiquinol oxidase	Tfu_0637	Tfu_0637 cytochrome bd ubiquinol oxidase, subunit II			18.7	17.36	23.03	2.71
KEGG	M00153	Cytochrome d ubiquinol oxidase	Tfu_0638	Tfu_0638 putative cytochrome oxidase subunit I			19.89	19.95	23.08	
KEGG	M00153	Cytochrome d ubiquinol oxidase	Tfu_0766	Tfu_0766 highly similar to cytochrome D ubiquinol oxidase subunit I						

KEGG	M00378	F420 biosynthesis	Tfu_0629	Tfu_0629 hypothetical protein						
KEGG	M00378	F420 biosynthesis	Tfu_2517	Tfu_2517 LPPG:Fo 2-phospho-L-lactate transferase			14.64	15.51	20.71	
KEGG	M00378	F420 biosynthesis	Tfu_2518	Tfu_2518 hypothetical protein			14.93		19.68	
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_0613	Tfu_0613 ketol-acid reductoisomerase	19.9	19.77	19.96	19.71	23.42	0.799
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_0615	Tfu_0615 3-isopropylmalate dehydrogenase	19.78	19.7	19.64	19.42	23.35	1.025
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_0617	Tfu_0617 2-isopropylmalate synthase	16.51	16.22	15.8	13.84	20.9	
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_0626	Tfu_0626 isopropylmalate isomerase large subunit			15.08	14.46	19.36	
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_0627	Tfu_0627 isopropylmalate isomerase small subunit	13.33				18.83	
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_0850	Tfu_0850 2-isopropylmalate synthase	16.67	16.9	16.57	16.17	21.98	
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
KEGG	M00019	Leucine biosynthesis, pyruvate => 2-oxoisovalerate => leucine	Tfu_2209	Tfu_2209 dihydroxy-acid dehydratase	14.66	14.56	15.67	16.08	21.64	
KEGG	M00169	CAM (Crassulacean acid metabolism), light	Tfu_0863	Tfu_0863 pyruvate phosphate dikinase	17.84	17.11	21.38	21.45	25.04	1.455
KEGG	M00086	beta-Oxidation, acyl-CoA synthesis	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
KEGG	M00086	beta-Oxidation, acyl-CoA synthesis	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
KEGG	M00086	beta-Oxidation, acyl-CoA synthesis	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
KEGG	M00086	beta-Oxidation, acyl-CoA synthesis	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
KEGG	M00034	Methionine salvage pathway	Tfu_1065	Tfu_1065 S-adenosylmethionine synthetase	15.28	15.32	15.74	16.4	20.99	0.962
KEGG	M00034	Methionine salvage pathway	Tfu_2234	Tfu_2234 spermidine synthase						
KEGG	M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	Tfu_1062	Tfu_1062 guanylate kinase			14.95	15.22	19.61	
KEGG	M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
KEGG	M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
KEGG	M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	Tfu_2440	Tfu_2440 inositol-5-monophosphate dehydrogenase	19.82	19.85	19.51	19.28	23.25	1.113
KEGG	M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	Tfu_2589	Tfu_2589 bifunctional GMP synthase/glutamine amidotran	14.94		18.4	18.53	23.34	1.278
KEGG	M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	Tfu_2595	Tfu_2595 inositol-5-monophosphate dehydrogenase	18.6	18.73	20.9	20.27	24.94	0.944
KEGG	M00050	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	Tfu_2596	Tfu_2596 IMP dehydrogenase	17.6	17.76	20.1	19.82	24.11	1.035
KEGG	M00362	Nucleotide sugar biosynthesis, prokaryotes	Tfu_0169	Tfu_0169 nucleoside-diphosphate-sugar epimerase (UDP-g	14.49	16.6	18.84	18.16	22.51	0.845
KEGG	M00362	Nucleotide sugar biosynthesis, prokaryotes	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase, b	16.85	15	17.24	17.46	22.15	
KEGG	M00362	Nucleotide sugar biosynthesis, prokaryotes	Tfu_0414	Tfu_0414 UDP-N-acetylglucosamine pyrophosphorylase	19.4	19.37	19.9	19.97	23.72	1.114
KEGG	M00362	Nucleotide sugar biosynthesis, prokaryotes	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / phc	19.06	18.82	21.97	21.81	25.49	1.131
KEGG	M00362	Nucleotide sugar biosynthesis, prokaryotes	Tfu_1622	Tfu_1622 UDP-glucose 4-epimerase						
KEGG	M00362	Nucleotide sugar biosynthesis, prokaryotes	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
KEGG	M00362	Nucleotide sugar biosynthesis, prokaryotes	Tfu_2591	Tfu_2591 UDP-glucose 4-epimerase					14.83	
KEGG	M00362	Nucleotide sugar biosynthesis, prokaryotes	Tfu_2723	Tfu_2723 putative epimerase						
KEGG	M00135	GABA biosynthesis, eukaryotes, putrescine => GABA	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
KEGG	M00135	GABA biosynthesis, eukaryotes, putrescine => GABA	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
KEGG	M00135	GABA biosynthesis, eukaryotes, putrescine => GABA	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
KEGG	M00183	RNA polymerase, bacteria	Tfu_1063	Tfu_1063 DNA-directed RNA polymerase omega subunit						
KEGG	M00183	RNA polymerase, bacteria	Tfu_2618	Tfu_2618 DNA-directed RNA polymerase alpha subunit	20.3	20.33	21.62	21.41	24.58	1.11
KEGG	M00183	RNA polymerase, bacteria	Tfu_2653	Tfu_2653 DNA-directed RNA polymerase beta' subunit	20.69	20.49	21.52	21.3	25.54	1.261
KEGG	M00183	RNA polymerase, bacteria	Tfu_2654	Tfu_2654 DNA-directed RNA polymerase beta subunit	20.88	20.63	21.68	21.31	25.36	1.169
KEGG	M00239	Peptides/nickel transport system	Tfu_0817	Tfu_0817 hypothetical protein						
KEGG	M00239	Peptides/nickel transport system	Tfu_0818	Tfu_0818 hypothetical protein	17.3	17.04	15.39	15.33	20.85	
KEGG	M00239	Peptides/nickel transport system	Tfu_0910	Tfu_0910 hypothetical protein	23.09	23.21	22.87	22.38	25.97	1.94
KEGG	M00239	Peptides/nickel transport system	Tfu_0911	Tfu_0911 ABC-type dipeptide/oligopeptide/nickel transport systems, per			15.01		17.95	
KEGG	M00239	Peptides/nickel transport system	Tfu_0912	Tfu_0912 ABC-type dipeptide/oligopeptide/nickel transport systems, permease				14.07	19.4	
KEGG	M00239	Peptides/nickel transport system	Tfu_0913	Tfu_0913 oligopeptide/dipeptide ABC transporter, ATP-bir	17.06	17.13	17.75	18.6	22.63	

KEGG	M00239	Peptides/nickel transport system	Tfu_0914	Tfu_0914 ABC-type oligopeptide transport system ATPase	16.1	16.25	18.3	17.89	22.26	2.047
KEGG	M00239	Peptides/nickel transport system	Tfu_1630	Tfu_1630 oligopeptide/dipeptide ABC transporter, ATP-bi	15.55	15.84			18.2	
KEGG	M00239	Peptides/nickel transport system	Tfu_1631	Tfu_1631 ABC transporter, permease protein						
KEGG	M00239	Peptides/nickel transport system	Tfu_1632	Tfu_1632 hypothetical protein	14.9				16.2	
KEGG	M00239	Peptides/nickel transport system	Tfu_1633	Tfu_1633 hypothetical protein	21.04	20.99	19.85	19.66	23.61	0.589
KEGG	M00239	Peptides/nickel transport system	Tfu_1819	Tfu_1819 ATPase components of various ABC-type transpo	20.66	20.33	19.05	19.09	23.49	2.058
KEGG	M00239	Peptides/nickel transport system	Tfu_1820	Tfu_1820 hypothetical protein	17.64	16.81			19.82	
KEGG	M00239	Peptides/nickel transport system	Tfu_1821	Tfu_1821 hypothetical protein	24.51	24.26	23.96	23.7	26.74	1.154
KEGG	M00239	Peptides/nickel transport system	Tfu_1822	Tfu_1822 oligopeptide transport integral membrane prote	16.87		16.15	15.61	21	
KEGG	M00239	Peptides/nickel transport system	Tfu_2291	Tfu_2291 oligopeptide/dipeptide ABC transporter, ATP-binding protein, C-terminal						
KEGG	M00239	Peptides/nickel transport system	Tfu_2292	Tfu_2292 putative peptide ABC transporter permease protein						
KEGG	M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
KEGG	M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
KEGG	M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
KEGG	M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	Tfu_0566	Tfu_0566 alpha-ketoglutarate decarboxylase	22.63	22.08	23.34	23.51	26.75	1.555
KEGG	M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
KEGG	M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	Tfu_0993	Tfu_0993 dihydrolipoamide S-succinyltransferase	21.69	21.57	21.99	21.46	25.01	1.46
KEGG	M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	Tfu_1068	Tfu_1068 glutaryl-CoA dehydrogenase	15.85	16.25	15.59	15.48	20.62	0.775
KEGG	M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
KEGG	M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
KEGG	M00032	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
KEGG	M00311	2-oxoglutarate:ferredoxin oxidoreductase	Tfu_2674	Tfu_2674 2-oxoglutarate ferredoxin oxidoreductase, alpha	14.55		17.74	18.16	22.74	1.656
KEGG	M00311	2-oxoglutarate:ferredoxin oxidoreductase	Tfu_2675	Tfu_2675 ferrodoxin oxidoreductase beta subunit			17.01	16.7	21.8	
KEGG	M00170	C4-dicarboxylic acid cycle, phosphoenolpyruvate carboxykinase	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
KEGG	M00270	PTS system, trehalose-specific II component	Tfu_2489	Tfu_2489 putative phosphoenolpyruvate-dependent sugar phosphotransferase					16.36	
KEGG	M00002	Glycolysis, core module involving three-carbon compounds	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
KEGG	M00002	Glycolysis, core module involving three-carbon compounds	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
KEGG	M00002	Glycolysis, core module involving three-carbon compounds	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
KEGG	M00002	Glycolysis, core module involving three-carbon compounds	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
KEGG	M00002	Glycolysis, core module involving three-carbon compounds	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
KEGG	M00002	Glycolysis, core module involving three-carbon compounds	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
KEGG	M00002	Glycolysis, core module involving three-carbon compounds	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, typ	23.03	22.77	25.37	25.33	28.17	1.113
KEGG	M00002	Glycolysis, core module involving three-carbon compounds	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
KEGG	M00002	Glycolysis, core module involving three-carbon compounds	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
KEGG	M00347	Methanogenesis, formate => methane	Tfu_1737	Tfu_1737 oxidoreductase alpha (molybdopterin) subunit			14.39	13.79	19.93	
KEGG	M00545	Trans-cinnamate degradation, trans-cinnamate => 2-oxopent-4-	Tfu_1273	Tfu_1273 putative oxidoreductase						
KEGG	M00545	Trans-cinnamate degradation, trans-cinnamate => 2-oxopent-4-	Tfu_1985	Tfu_1985 putative dioxygenase					17.16	
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_0031	Tfu_0031 seryl-tRNA synthetase	19.71	19.5	20.47	20.38	23.8	0.939
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_0212	Tfu_0212 cysteinyl-tRNA synthetase	16.41	14.49	18.9	18.08	23.01	1.169
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_0269	Tfu_0269 arginyl-tRNA synthetase, class Ic	17.72	17.49	20.13	19.85	24.16	1.223
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_0389	Tfu_0389 methionyl-tRNA synthetase	18.09	18	20.33	20.35	23.82	1.106
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_0623	Tfu_0623 glutamyl-tRNA synthetase bacterial/mitochondr	18.5	17.36	18.79	19.22	23.34	0.908
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_0759	Tfu_0759 histidine--tRNA ligase	16.98	16.75	18.26	18.29	22.52	0.925
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_0772	Tfu_0772 prolyl-tRNA synthetase	19.32	19.13	19.74	19.37	23.57	1.007
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_0861	Tfu_0861 glycyl-tRNA synthetase	18.27	17.66	19.58	19.58	23.56	1.154
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_1120	Tfu_1120 isoleucyl-tRNA synthetase, class Ia	16.68	16.31	19.54	19.65	23.84	1.694
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_1832	Tfu_1832 cysteinyl-tRNA synthetase	15.91	16.04	18.24	17.09	22.24	1.186
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_1936	Tfu_1936 valyl-tRNA synthetase	17.79	17.98	19.77	19.27	23.94	1.167
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_2043	Tfu_2043 tyrosyl-tRNA synthetase, class Ib	16.28	16.71	18.6	18.54	22.47	1.194
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_2060	Tfu_2060 phenylalanyl-tRNA synthetase beta subunit	19.74	19.67	20.55	20.4	24.66	1.059

KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_2061	Tfu_2061 phenylalanyl-tRNA synthetase alpha subunit	16.56	17.28	19.09	18.91	22.49	0.719
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_2070	Tfu_2070 alanyl-tRNA synthetase	18.51	18.11	19.5	19.52	23.9	1.221
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_2086	Tfu_2086 aspartyl-tRNA synthetase	18.54	17.59	19.9	19.59	23.67	1.015
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_2108	Tfu_2108 threonyl-tRNA synthetase	18.4	18.24	19.7	19.43	23.68	1.178
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_2156	Tfu_2156 leucyl-tRNA synthetase bacterial/mitochondrial,	20.17	20.38	21.64	21.31	25.2	1.161
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_2376	Tfu_2376 tryptophanyl-tRNA synthetase, class Ib	15.16		16.88	16.16	20.45	
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_2426	Tfu_2426 similar to Arginyl-tRNA synthetase					16.36	
KEGG	M00359	Aminoacyl-tRNA biosynthesis, eukaryotes	Tfu_2881	Tfu_2881 lysyl-tRNA synthetase, class-2	16.6	16.7	19.01	18.9	23.54	0.997
KEGG	M00008	Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P +	Tfu_0188	Tfu_0188 2-dehydro-3-deoxyphosphogluconate aldolase /	14.36				15.14	
KEGG	M00008	Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P +	Tfu_2005	Tfu_2005 glucose-6-phosphate 1-dehydrogenase	16.6	15.74	16.81	16.27	21.46	
KEGG	M00008	Entner-Doudoroff pathway, glucose-6P => glyceraldehyde-3P +	Tfu_2007	Tfu_2007 6-phosphogluconolactonase	18.7	19.13	18.21	17.98	22.37	0.913
KEGG	M00364	C10-C20 isoprenoid biosynthesis, bacteria	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
KEGG	M00091	Phosphatidylcholine (PC) biosynthesis, PE => PC	Tfu_0735	Tfu_0735 ubiquinone/menaquinone biosynthesis methyltransferase						
KEGG	M00087	beta-Oxidation	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
KEGG	M00087	beta-Oxidation	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
KEGG	M00087	beta-Oxidation	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
KEGG	M00087	beta-Oxidation	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
KEGG	M00087	beta-Oxidation	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
KEGG	M00087	beta-Oxidation	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
KEGG	M00087	beta-Oxidation	Tfu_1278	Tfu_1278 thiolase						
KEGG	M00087	beta-Oxidation	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
KEGG	M00087	beta-Oxidation	Tfu_1282	Tfu_1282 putative acyl-CoA dehydrogenase					18.17	
KEGG	M00087	beta-Oxidation	Tfu_1284	Tfu_1284 putative acyl-CoA dehydrogenase						
KEGG	M00087	beta-Oxidation	Tfu_1512	Tfu_1512 putative acyl-CoA dehydrogenase	14.16	14.11		14.03	20.64	
KEGG	M00087	beta-Oxidation	Tfu_1647	Tfu_1647 acyl-CoA dehydrogenase	19.93	19.53	19.07	19.09	22.67	1.416
KEGG	M00087	beta-Oxidation	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
KEGG	M00087	beta-Oxidation	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
KEGG	M00087	beta-Oxidation	Tfu_1999	Tfu_1999 acyl-CoA dehydrogenase						
KEGG	M00087	beta-Oxidation	Tfu_2239	Tfu_2239 hypothetical protein	17.58	17.57	18.21	17.62	22.75	0.874
KEGG	M00087	beta-Oxidation	Tfu_2485	Tfu_2485 acyl-CoA dehydrogenase	14.3		15.52	15.96	21.16	
KEGG	M00021	Cysteine biosynthesis, serine => cysteine	Tfu_2368	Tfu_2368 cysteine synthase K/M		14.5	14.44		19.69	
KEGG	M00116	Menaquinone biosynthesis, chorismate => menaquinone	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
KEGG	M00116	Menaquinone biosynthesis, chorismate => menaquinone	Tfu_0960	Tfu_0960 n-acylamino acid racemase : O-succinylbenzoate-CoA synthase					19.49	
KEGG	M00116	Menaquinone biosynthesis, chorismate => menaquinone	Tfu_1408	Tfu_1408 putative ortho-succinylbenzoate-CoA synthetase						
KEGG	M00116	Menaquinone biosynthesis, chorismate => menaquinone	Tfu_1409	Tfu_1409 naphthoate synthase	16.03	15.45	18.71	18.23	22.53	
KEGG	M00116	Menaquinone biosynthesis, chorismate => menaquinone	Tfu_1410	Tfu_1410 O-succinylbenzoate synthase					15.48	
KEGG	M00116	Menaquinone biosynthesis, chorismate => menaquinone	Tfu_1411	Tfu_1411 Menaquinone biosynthesis protein					16.81	
KEGG	M00116	Menaquinone biosynthesis, chorismate => menaquinone	Tfu_1413	Tfu_1413 isochorismate synthase						
KEGG	M00116	Menaquinone biosynthesis, chorismate => menaquinone	Tfu_1872	Tfu_1872 isochorismate synthase					17.85	
KEGG	M00116	Menaquinone biosynthesis, chorismate => menaquinone	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
KEGG	M00245	Cobalt transport system	Tfu_0588	Tfu_0588 ATPase						2.621
KEGG	M00245	Cobalt transport system	Tfu_0589	Tfu_0589 ABC-type cobalt transport system						1.778
KEGG	M00245	Cobalt transport system	Tfu_2312	Tfu_2312 putative cobalt transport system permease protein						1.095
KEGG	M00245	Cobalt transport system	Tfu_2313	Tfu_2313 ABC-type cobalt transport system ATPase component					19.2	0.595
KEGG	M00194	Maltose/maltodextrin transport system	Tfu_0830	Tfu_0830 hypothetical protein					15.17	
KEGG	M00194	Maltose/maltodextrin transport system	Tfu_0831	Tfu_0831 multiple sugar transport system permease protein					15.83	
KEGG	M00194	Maltose/maltodextrin transport system	Tfu_0832	Tfu_0832 hypothetical protein	18.27	18.49	16.35	16.47	22.2	
KEGG	M00194	Maltose/maltodextrin transport system	Tfu_1763	Tfu_1763 ABC-type sugar transport systems ATPase comp	22.15	21.91	22.51	21.98	25.88	1.102
KEGG	M00237	Branched-chain amino acid transport system	Tfu_0074	Tfu_0074 hypothetical protein	22.9	22.75	20.91	20.91	24.27	0.895
KEGG	M00237	Branched-chain amino acid transport system	Tfu_0075	Tfu_0075 ABC-type branched-chain amino acid transport s	18.61	18.36	16.71	15.78	20.43	

KEGG	M00237	Branched-chain amino acid transport system	Tfu_0076	Tfu_0076 ABC-type branched-chain amino acid transport s	20.12	19.67	17.26	16.94	22.02	
KEGG	M00237	Branched-chain amino acid transport system	Tfu_0077	Tfu_0077 branched-chain amino acid ABC transporter permease protein						
KEGG	M00237	Branched-chain amino acid transport system	Tfu_0078	Tfu_0078 branched-chain amino acid ABC transporter perı	19.29	19.14	15.68	16.2	20.45	0.777
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1182	Tfu_1182 hypothetical protein	18.55	17.76	17.76	17.69	21.61	1.107
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1183	Tfu_1183 branched-chain amino acid transport system per	15.85	13.37		13.2	19.42	
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1184	Tfu_1184 branched-chain amino acid transport system ATI	19.81	19.69	19.88	20.05	23.28	0.869
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1185	Tfu_1185 ABC-type branched-chain amino acid transport s	20.76	20.17	19.92	19.93	23.52	0.915
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1186	Tfu_1186 hypothetical protein	23.7	23.37	23.34	22.75	25.45	0.832
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1290	Tfu_1290 hypothetical protein					17	
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1291	Tfu_1291 probable amino-acid transmembrane lipoprotein ABC transporter						
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1292	Tfu_1292 similar to ABC-type branched-chain amino acid transport system permease component						
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1293	Tfu_1293 ABC-type branched-chain amino acid transport systems ATPase component						
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1294	Tfu_1294 ABC-type branched-chain amino acid transport systems ATPase component						
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1780	Tfu_1780 ABC transporter permease protein						
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1781	Tfu_1781 possible ABC transporter, permease protein						
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1782	Tfu_1782 ABC-type branched-chain amino acid transport systems ATPase component						
KEGG	M00237	Branched-chain amino acid transport system	Tfu_1783	Tfu_1783 ABC-type branched-chain amino acid transport systems ATPase component						
KEGG	M00207	Putative multiple sugar transport system	Tfu_0753	Tfu_0753 hypothetical protein						
KEGG	M00207	Putative multiple sugar transport system	Tfu_1610	Tfu_1610 putative transport system integral membrane protein						
KEGG	M00207	Putative multiple sugar transport system	Tfu_1611	Tfu_1611 putative transport system integral membrane protein						
KEGG	M00207	Putative multiple sugar transport system	Tfu_1617	Tfu_1617 putative binding-protein-dependent transport protein						
KEGG	M00207	Putative multiple sugar transport system	Tfu_1618	Tfu_1618 hypothetical protein					15.44	
KEGG	M00207	Putative multiple sugar transport system	Tfu_1619	Tfu_1619 hypothetical protein	22.73	22.95	21.17	20.85	24.52	1.352
KEGG	M00207	Putative multiple sugar transport system	Tfu_1702	Tfu_1702 hypothetical protein	20.15	19.13	18.05	17.45	22.1	
KEGG	M00207	Putative multiple sugar transport system	Tfu_1703	Tfu_1703 putative transport system permease ABC transporter protein						
KEGG	M00207	Putative multiple sugar transport system	Tfu_1704	Tfu_1704 putative transport system permease ABC transporter protein						
KEGG	M00266	PTS system, maltose and glucose-specific II component	Tfu_2489	Tfu_2489 putative phosphoenolpyruvate-dependent sugar phosphotransferase					16.36	
KEGG	M00222	Phosphate transport system	Tfu_1636	Tfu_1636 hypothetical protein	16.98	17.02	17.32	16.79	21.14	0.529
KEGG	M00222	Phosphate transport system	Tfu_2740	Tfu_2740 hypothetical protein	18.45	17.82	18.3	18.9	21.3	
KEGG	M00222	Phosphate transport system	Tfu_2741	Tfu_2741 phosphate ABC transporter, permease protein PstC					17.82	
KEGG	M00222	Phosphate transport system	Tfu_2742	Tfu_2742 Phosphate transport system permease protein 2					17.18	
KEGG	M00222	Phosphate transport system	Tfu_2743	Tfu_2743 Phosphate transport system permease protein 1	15.49	15.5	16.86	15.14	21.63	
KEGG	M00338	Cysteine biosynthesis, homocysteine + serine => cysteine	Tfu_0438	Tfu_0438 cystathionine beta-synthase	13		14.49	12.98	20.18	
KEGG	M00376	3-Hydroxypropionate bicycle	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
KEGG	M00376	3-Hydroxypropionate bicycle	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
KEGG	M00376	3-Hydroxypropionate bicycle	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
KEGG	M00376	3-Hydroxypropionate bicycle	Tfu_2555	Tfu_2555 propionyl-CoA carboxylase complex B subunit	18.59	18.29	18.47	17.99	22.37	0.744
KEGG	M00376	3-Hydroxypropionate bicycle	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
KEGG	M00376	3-Hydroxypropionate bicycle	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
KEGG	M00376	3-Hydroxypropionate bicycle	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
KEGG	M00119	Pantothenate biosynthesis, valine/L-aspartate => pantothenate	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
KEGG	M00119	Pantothenate biosynthesis, valine/L-aspartate => pantothenate	Tfu_0981	Tfu_0981 3-methyl-2-oxobutanoate hydroxymethyltransfe	18.23	17.36	19.12	19.31	23.68	0.787
KEGG	M00119	Pantothenate biosynthesis, valine/L-aspartate => pantothenate	Tfu_1862	Tfu_1862 aspartate 1-decarboxylase precursor			14.98		19.99	
KEGG	M00119	Pantothenate biosynthesis, valine/L-aspartate => pantothenate	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
KEGG	M00119	Pantothenate biosynthesis, valine/L-aspartate => pantothenate	Tfu_2884	Tfu_2884 pantoate-beta-alanine ligase	18.94	18.13	19.39	18.92	22.68	1.137
KEGG	M00418	Toluene degradation, anaerobic, toluene => benzoyl-CoA	Tfu_1480	Tfu_1480 subunit of CoA-transferase of family III						
KEGG	M00345	Formaldehyde assimilation, ribulose monophosphate pathway	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
KEGG	M00174	Methane oxidation, methylotroph, methane => CO2	Tfu_1649	Tfu_1649 catalase	20.13	19.98	21.56	21.24	24.73	0.727
KEGG	M00174	Methane oxidation, methylotroph, methane => CO2	Tfu_1737	Tfu_1737 oxidoreductase alpha (molybdopterin) subunit			14.39	13.79	19.93	
KEGG	M00174	Methane oxidation, methylotroph, methane => CO2	Tfu_3025	Tfu_3025 putative alcohol dehydrogenase	18.7	19.04	16.64	17.19	21.72	

KEGG	M00154	Cytochrome c oxidase	Tfu_1995	Tfu_1995 putative integral membrane transport protein					18.49	
KEGG	M00526	Lysine biosynthesis, DAP dehydrogenase pathway, aspartate =>	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1 r	18.57	18.71	20.61	20.33	23.82	0.982
KEGG	M00526	Lysine biosynthesis, DAP dehydrogenase pathway, aspartate =>	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
KEGG	M00526	Lysine biosynthesis, DAP dehydrogenase pathway, aspartate =>	Tfu_0786	Tfu_0786 dihydrodipicolinate reductase	18.87	17.45	19.64	18.4	23.22	0.825
KEGG	M00526	Lysine biosynthesis, DAP dehydrogenase pathway, aspartate =>	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844
KEGG	M00526	Lysine biosynthesis, DAP dehydrogenase pathway, aspartate =>	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
KEGG	M00526	Lysine biosynthesis, DAP dehydrogenase pathway, aspartate =>	Tfu_2425	Tfu_2425 diaminopimelate decarboxylase					18.01	
KEGG	M00093	Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE	Tfu_0680	Tfu_0680 phosphatidate cytidylyltransferase	15.69	15.29	15.87	15.37	19.59	
KEGG	M00093	Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE	Tfu_1894	Tfu_1894 phosphatidylserine decarboxylase	16.99	15.03	17.14	16.9	21.01	1.091
KEGG	M00093	Phosphatidylethanolamine (PE) biosynthesis, PA => PS => PE	Tfu_1895	Tfu_1895 putative phosphatidylserine synthase						
KEGG	M00028	Ornithine biosynthesis, glutamate => ornithine	Tfu_2054	Tfu_2054 acetylornithine and succinylornithine aminotran	16.33	18.16	18.68	18.83	22.2	1.056
KEGG	M00028	Ornithine biosynthesis, glutamate => ornithine	Tfu_2055	Tfu_2055 acetylglutamate kinase		13.89	16.85	16.6	21.88	1.485
KEGG	M00028	Ornithine biosynthesis, glutamate => ornithine	Tfu_2056	Tfu_2056 bifunctional ornithine acetyltransferase/N-acety	17.05	16.43	18.49	17.65	22.7	
KEGG	M00028	Ornithine biosynthesis, glutamate => ornithine	Tfu_2057	Tfu_2057 N-acetyl-gamma-glutamyl-phosphate reductase					20.33	
KEGG	M00028	Ornithine biosynthesis, glutamate => ornithine	Tfu_2879	Tfu_2879 hypothetical protein	13.85	13.58			19.82	
KEGG	M00432	Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate	Tfu_0615	Tfu_0615 3-isopropylmalate dehydrogenase	19.78	19.7	19.64	19.42	23.35	1.025
KEGG	M00432	Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate	Tfu_0617	Tfu_0617 2-isopropylmalate synthase	16.51	16.22	15.8	13.84	20.9	
KEGG	M00432	Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate	Tfu_0626	Tfu_0626 isopropylmalate isomerase large subunit			15.08	14.46	19.36	
KEGG	M00432	Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate	Tfu_0627	Tfu_0627 isopropylmalate isomerase small subunit	13.33				18.83	
KEGG	M00432	Leucine biosynthesis, 2-oxoisovalerate => 2-oxoisocaproate	Tfu_0850	Tfu_0850 2-isopropylmalate synthase	16.67	16.9	16.57	16.17	21.98	
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_0687	Tfu_0687 methylmalonate-semialdehyde dehydrogenase	18.43	17.24	18.03	18.14	22.37	1.017
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_1282	Tfu_1282 putative acyl-CoA dehydrogenase					18.17	
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_1284	Tfu_1284 putative acyl-CoA dehydrogenase						
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_1512	Tfu_1512 putative acyl-CoA dehydrogenase	14.16	14.11		14.03	20.64	
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_1647	Tfu_1647 acyl-CoA dehydrogenase	19.93	19.53	19.07	19.09	22.67	1.416
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_1999	Tfu_1999 acyl-CoA dehydrogenase						
KEGG	M00013	Malonate semialdehyde pathway, propanoyl-CoA => Acetyl-CoA	Tfu_2485	Tfu_2485 acyl-CoA dehydrogenase	14.3		15.52	15.96	21.16	
KEGG	M00168	CAM (Crassulacean acid metabolism), dark	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
KEGG	M00168	CAM (Crassulacean acid metabolism), dark	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
KEGG	M00197	Putative fructooligosaccharide transport system	Tfu_1763	Tfu_1763 ABC-type sugar transport systems ATPase compo	22.15	21.91	22.51	21.98	25.88	1.102
KEGG	M00089	Triacylglycerol biosynthesis	Tfu_0271	Tfu_0271 Fatty acid synthesis plsX protein		15.01			17.65	
KEGG	M00089	Triacylglycerol biosynthesis	Tfu_1036	Tfu_1036 phospholipid/glycerol acyltransferase	18.2	17.54	17.83	17.5	21.56	
KEGG	M00089	Triacylglycerol biosynthesis	Tfu_1417	Tfu_1417 phospholipid/glycerol acyltransferase	13.91	13.6		12.45	17.58	
KEGG	M00189	Putative molybdate transport system	Tfu_0326	Tfu_0326 ABC-type spermidine/putrescine transport systems ATPase components						
KEGG	M00189	Putative molybdate transport system	Tfu_0327	Tfu_0327 molybdate ABC transporter, inner membrane subunit						
KEGG	M00189	Putative molybdate transport system	Tfu_0328	Tfu_0328 hypothetical protein						
KEGG	M00020	Serine biosynthesis, glycerate-3P => serine	Tfu_0136	Tfu_0136 phosphoserine phosphatase SerB:HAD-superfamily hydrolase subfamily IB, P					16.25	
KEGG	M00020	Serine biosynthesis, glycerate-3P => serine	Tfu_0246	Tfu_0246 phosphoserine aminotransferase	19.59	19.46	22.48	21.91	25.76	1.096
KEGG	M00020	Serine biosynthesis, glycerate-3P => serine	Tfu_0614	Tfu_0614 D-3-phosphoglycerate dehydrogenase	20.25	20.04	22.34	22.29	25.26	1.066
KEGG	M00020	Serine biosynthesis, glycerate-3P => serine	Tfu_2259	Tfu_2259 similar to Phosphoglycerate dehydrogenase and related dehydrogenase						
KEGG	M00114	Ascorbate biosynthesis, plants, glucose-6P => ascorbate	Tfu_0016	Tfu_0016 mannose-6-phosphate isomerase, type I						
KEGG	M00114	Ascorbate biosynthesis, plants, glucose-6P => ascorbate	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / phc	19.06	18.82	21.97	21.81	25.49	1.131
KEGG	M00114	Ascorbate biosynthesis, plants, glucose-6P => ascorbate	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989

KEGG	M00114	Ascorbate biosynthesis, plants, glucose-6P => ascorbate	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
KEGG	M00114	Ascorbate biosynthesis, plants, glucose-6P => ascorbate	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
KEGG	M00343	Archaeal proteasome	Tfu_1789	Tfu_1789 putative 20S proteasome alpha-subunit	21.35	20.72	20.29	20.07	23.84	0.978
KEGG	M00343	Archaeal proteasome	Tfu_1790	Tfu_1790 Proteasome endopeptidase complex	20.83	20.83	21.11	21.18	24.64	1.164
KEGG	M00196	Multiple sugar transport system	Tfu_1763	Tfu_1763 ABC-type sugar transport systems ATPase compo	22.15	21.91	22.51	21.98	25.88	1.102
KEGG	M00140	C1-unit interconversion, prokaryotes	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
KEGG	M00140	C1-unit interconversion, prokaryotes	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
KEGG	M00243	Manganese/iron transport system	Tfu_1661	Tfu_1661 putative ABC transporter membrane protein						
KEGG	M00243	Manganese/iron transport system	Tfu_1662	Tfu_1662 ABC-type Mn/Zn transport systems ATPase component						
KEGG	M00243	Manganese/iron transport system	Tfu_1663	Tfu_1663 hypothetical protein						
KEGG	M00250	Lipopolysaccharide transport system	Tfu_2537	Tfu_2537 ABC-type polysaccharide/polyol phosphate trans	18.53	18.3	17.74	17.74	21.66	1.185
KEGG	M00250	Lipopolysaccharide transport system	Tfu_2538	Tfu_2538 lipopolysaccharide exporter	17.08	16.98	17	16.55	20.46	0.958
KEGG	M00165	Reductive pentose phosphate cycle (Calvin cycle)	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
KEGG	M00165	Reductive pentose phosphate cycle (Calvin cycle)	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
KEGG	M00165	Reductive pentose phosphate cycle (Calvin cycle)	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
KEGG	M00165	Reductive pentose phosphate cycle (Calvin cycle)	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
KEGG	M00165	Reductive pentose phosphate cycle (Calvin cycle)	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
KEGG	M00461	MtrB-MtrA (osmotic stress response) two-component regulatory	Tfu_2495	Tfu_2495 ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histidine kina					17.64	
KEGG	M00461	MtrB-MtrA (osmotic stress response) two-component regulatory	Tfu_2496	Tfu_2496 response regulator receiver	18.2	17.46	19.26	18.65	23.51	0.942
KEGG	M00157	F-type ATPase, bacteria	Tfu_2406	Tfu_2406 H+-transporting two-sector ATPase, delta/epsilo	17.61	17.4	18.54	18.5	21.47	
KEGG	M00157	F-type ATPase, bacteria	Tfu_2407	Tfu_2407 ATP synthase F1, beta subunit	21.37	21.44	23.04	22.88	26.22	1.194
KEGG	M00157	F-type ATPase, bacteria	Tfu_2408	Tfu_2408 H+-transporting two-sector ATPase, gamma subu	20.11	19.39	21.19	20.62	23.67	
KEGG	M00157	F-type ATPase, bacteria	Tfu_2409	Tfu_2409 ATP synthase subunit A	21.64	21.69	23.06	22.63	26.34	1.138
KEGG	M00157	F-type ATPase, bacteria	Tfu_2410	Tfu_2410 H+-transporting two-sector ATPase, delta (OSCP	20.66	20.14	21.77	21.25	24.88	0.912
KEGG	M00157	F-type ATPase, bacteria	Tfu_2411	Tfu_2411 ATP synthase F0, subunit B	20.75	20.59	21	21.14	24.9	0.695
KEGG	M00157	F-type ATPase, bacteria	Tfu_2412	Tfu_2412 ATP synthase F0, C subunit						
KEGG	M00157	F-type ATPase, bacteria	Tfu_2413	Tfu_2413 H+-transporting two-sector ATPase, A subunit						
KEGG	M00014	Glucuronate pathway (uronate pathway)	Tfu_1575	Tfu_1575 putative sugar kinase protein						
KEGG	M00014	Glucuronate pathway (uronate pathway)	Tfu_1604	Tfu_1604 xylulokinase	16.69	16.85	17.01	17.12	22.06	
KEGG	M00014	Glucuronate pathway (uronate pathway)	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
KEGG	M00299	Spermidine/putrescine transport system	Tfu_0280	Tfu_0280 spermidine/putrescine ABC transporter ATP-bin	16.15	16.84	16.09	16.49	21.27	
KEGG	M00299	Spermidine/putrescine transport system	Tfu_0281	Tfu_0281 hypothetical protein	18.47	18.78	17.46	17.13	21.33	1.121
KEGG	M00299	Spermidine/putrescine transport system	Tfu_0282	Tfu_0282 polyamine ABC-transporter, inner membrane subunit					17.78	
KEGG	M00299	Spermidine/putrescine transport system	Tfu_0283	Tfu_0283 polyamine ABC-transporter, inner membrane subunit						
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_0002	Tfu_0002 DNA polymerase III subunit beta			14.09		20.64	
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_0047	Tfu_0047 DNA polymerase III subunit alpha					14.78	
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_0051	Tfu_0051 DNA polymerase III subunits gamma and tau					16.27	
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_0086	Tfu_0086 DNA polymerase III subunit beta	14.58			14.38	19.46	
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_0183	Tfu_0183 DNA polymerase III subunit epsilon					16.34	
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_0714	Tfu_0714 exonuclease	20.07	19.91	16.25	15.46	21.16	1.005
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_0823	Tfu_0823 DNA polymerase III, delta subunit					18.6	
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_0902	Tfu_0902 DNA polymerase III, epsilon subunit						
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_1027	Tfu_1027 hypothetical protein						
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_2347	Tfu_2347 exonuclease					16.03	
KEGG	M00260	DNA polymerase III complex, bacteria	Tfu_2782	Tfu_2782 DNA polymerase III delta prime subunit					15.08	
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_0566	Tfu_0566 alpha-ketoglutarate decarboxylase	22.63	22.08	23.34	23.51	26.75	1.555
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_0993	Tfu_0993 dihydrolipoamide S-succinyltransferase	21.69	21.57	21.99	21.46	25.01	1.46
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_0994	Tfu_0994 dihydrolipoamide dehydrogenase	23.87	23.67	23.96	23.71	27.03	1.154

KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_2451	Tfu_2451 succinate dehydrogenase	19.35	19.39	20.29	20.56	23.66	1.002
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_2453	Tfu_2453 succinate dehydrogenase, cytochrome b558 subunit					19.37	1.293
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_2559	Tfu_2559 dihydrolipoamide dehydrogenase	17.62	17.97	18.6	18.7	23.28	1.063
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_2674	Tfu_2674 2-oxoglutarate ferredoxin oxidoreductase, alpha	14.55		17.74	18.16	22.74	1.656
KEGG	M00011	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloa	Tfu_2675	Tfu_2675 ferrodoxin oxidoreductase beta subunit			17.01	16.7	21.8	
KEGG	M00178	Ribosome, bacteria	Tfu_0416	Tfu_0416 Ribosomal protein L25	15.18	16.55	19.26	18.89	22.21	0.898
KEGG	M00178	Ribosome, bacteria	Tfu_0645	Tfu_0645 50S ribosomal protein L28					19.58	
KEGG	M00178	Ribosome, bacteria	Tfu_0650	Tfu_0650 50S ribosomal protein L32					19.03	
KEGG	M00178	Ribosome, bacteria	Tfu_0662	Tfu_0662 Ribosomal protein S16	18.39	18.66	20.07	19.55	23.34	1.197
KEGG	M00178	Ribosome, bacteria	Tfu_0666	Tfu_0666 Ribosomal protein L19	18.01	16.27	19.85	18.82	23.06	1.347
KEGG	M00178	Ribosome, bacteria	Tfu_0676	Tfu_0676 30S ribosomal protein S2	19.71	20.16	22.1	21.87	25.09	1.094
KEGG	M00178	Ribosome, bacteria	Tfu_0783	Tfu_0783 Ribosomal protein S15, bacterial chloroplast and	15.74		17.1	16.76	20.8	1.338
KEGG	M00178	Ribosome, bacteria	Tfu_0827	Tfu_0827 Ribosomal protein S20p	15.94	15.42	17.36	17.25	21.3	0.872
KEGG	M00178	Ribosome, bacteria	Tfu_1013	Tfu_1013 30S ribosomal protein S4	17.09	15.75	19.47	19.58	23.57	1.141
KEGG	M00178	Ribosome, bacteria	Tfu_1191	Tfu_1191 30S ribosomal protein S1	20.95	21.05	22.59	22.63	25.99	1.039
KEGG	M00178	Ribosome, bacteria	Tfu_2064	Tfu_2064 50S ribosomal protein L20			15.65	15.5	19.28	
KEGG	M00178	Ribosome, bacteria	Tfu_2065	Tfu_2065 ribosomal protein L35						
KEGG	M00178	Ribosome, bacteria	Tfu_2181	Tfu_2181 Ribosomal protein L27	14.52		15.51	15.12	19.54	0.906
KEGG	M00178	Ribosome, bacteria	Tfu_2182	Tfu_2182 50S ribosomal protein L21	17.79	17.39	19.79	19.34	22.9	
KEGG	M00178	Ribosome, bacteria	Tfu_2420	Tfu_2420 Ribosomal protein L31					17.35	
KEGG	M00178	Ribosome, bacteria	Tfu_2613	Tfu_2613 30S ribosomal protein S9	16.28	16.43	18.85	18.6	21.99	1.059
KEGG	M00178	Ribosome, bacteria	Tfu_2614	Tfu_2614 50S ribosomal protein L13				14.95	20.12	1.466
KEGG	M00178	Ribosome, bacteria	Tfu_2617	Tfu_2617 Ribosomal protein L17	14.15	13.66	16.98	16.52	21.77	1.229
KEGG	M00178	Ribosome, bacteria	Tfu_2619	Tfu_2619 30S ribosomal protein S11			14.35	14.19	19.17	1.403
KEGG	M00178	Ribosome, bacteria	Tfu_2620	Tfu_2620 putative ribosomal protein S13	17.69	17.39	19.98	19.49	23.4	1.368
KEGG	M00178	Ribosome, bacteria	Tfu_2621	Tfu_2621 Ribosomal protein L36						
KEGG	M00178	Ribosome, bacteria	Tfu_2627	Tfu_2627 50S ribosomal protein L15	17.62	17.41	19.68	20.07	23.57	1.242
KEGG	M00178	Ribosome, bacteria	Tfu_2628	Tfu_2628 Ribosomal protein L30, bacterial					16.5	
KEGG	M00178	Ribosome, bacteria	Tfu_2629	Tfu_2629 30S ribosomal protein S5	17.94	18.12	20.32	20	23.82	1.26
KEGG	M00178	Ribosome, bacteria	Tfu_2630	Tfu_2630 Ribosomal protein L18	17.6	17.22	18.77	19.13	22.07	0.873
KEGG	M00178	Ribosome, bacteria	Tfu_2631	Tfu_2631 putative ribosomal protein L6	15.23		18.82	18.71	23.1	1.719
KEGG	M00178	Ribosome, bacteria	Tfu_2632	Tfu_2632 30S ribosomal protein S8			15.52	16.17	21.1	
KEGG	M00178	Ribosome, bacteria	Tfu_2633	Tfu_2633 putative ribosomal protein S14						
KEGG	M00178	Ribosome, bacteria	Tfu_2634	Tfu_2634 50S ribosomal protein L5	17.41	16.86	20.33	19.9	24.12	0.923
KEGG	M00178	Ribosome, bacteria	Tfu_2635	Tfu_2635 50S ribosomal protein L24					19.57	1.272
KEGG	M00178	Ribosome, bacteria	Tfu_2636	Tfu_2636 Ribosomal protein L14, bacterial and organelle f	15.14	14.25	15.95	16.24	21.6	
KEGG	M00178	Ribosome, bacteria	Tfu_2637	Tfu_2637 putative ribosomal protein S17	15.1		15.63	16.12	20.84	
KEGG	M00178	Ribosome, bacteria	Tfu_2638	Tfu_2638 Ribosomal protein L29	17.98	17.84	19.81	19.63	23.41	
KEGG	M00178	Ribosome, bacteria	Tfu_2639	Tfu_2639 Ribosomal protein L16	16.1	16.91	19.82	18.56	22.07	1.36
KEGG	M00178	Ribosome, bacteria	Tfu_2640	Tfu_2640 30S ribosomal protein S3	19.05	18.87	20.76	19.8	24.22	1.062
KEGG	M00178	Ribosome, bacteria	Tfu_2641	Tfu_2641 Ribosomal protein L22, bacterial and organelle form		17.55	18.98	18.79	22.53	
KEGG	M00178	Ribosome, bacteria	Tfu_2642	Tfu_2642 Ribosomal protein S19, bacterial and organelle form					19.57	
KEGG	M00178	Ribosome, bacteria	Tfu_2643	Tfu_2643 50S ribosomal protein L2	17.57	16.83	20.41	20.21	24.19	1.171
KEGG	M00178	Ribosome, bacteria	Tfu_2644	Tfu_2644 50S ribosomal protein L23			17.93	18.03	21.63	1.453
KEGG	M00178	Ribosome, bacteria	Tfu_2645	Tfu_2645 50S ribosomal protein L4	16.82	16.79	19.89	20.29	23.55	1.124
KEGG	M00178	Ribosome, bacteria	Tfu_2646	Tfu_2646 putative ribosomal protein L3	16.68	16.48	18.15	18.41	22.12	0.908
KEGG	M00178	Ribosome, bacteria	Tfu_2647	Tfu_2647 30S ribosomal protein S10	18.09	16.88	19.37	19.35	22.52	0.826

KEGG	M00178	Ribosome, bacteria	Tfu_2650	Tfu_2650 Ribosomal protein S7, bacterial and organelle for	16.75	16.51	19.03	18.86	22.58	1.249
KEGG	M00178	Ribosome, bacteria	Tfu_2651	Tfu_2651 Ribosomal protein S12, bacterial and chloroplast	16.08		16.9	16.88	20.29	
KEGG	M00178	Ribosome, bacteria	Tfu_2655	Tfu_2655 Ribosomal protein L7/L12	21.46	20.23	22.23	22.22	24.59	0.514
KEGG	M00178	Ribosome, bacteria	Tfu_2656	Tfu_2656 50S ribosomal protein L10	18.93	18.9	20.97	20.1	23.88	1.042
KEGG	M00178	Ribosome, bacteria	Tfu_2657	Tfu_2657 Ribosomal protein L1, bacterial and chloroplast f	19.1	19.48	21.28	21.2	24.32	1.14
KEGG	M00178	Ribosome, bacteria	Tfu_2658	Tfu_2658 Ribosomal protein L11, bacterial			17.58	16.31	21.3	1.25
KEGG	M00178	Ribosome, bacteria	Tfu_2667	Tfu_2667 50S ribosomal protein L33						
KEGG	M00178	Ribosome, bacteria	Tfu_3092	Tfu_3092 50S ribosomal protein L9	17.4	18.02	20.22	19.88	23.66	1.198
KEGG	M00178	Ribosome, bacteria	Tfu_3093	Tfu_3093 30S ribosomal protein S18					20.17	
KEGG	M00178	Ribosome, bacteria	Tfu_3095	Tfu_3095 30S ribosomal protein S6	14.8	15.01	16.93	17.14	20.06	0.688
KEGG	M00178	Ribosome, bacteria	Tfu_3117	Tfu_3117 50S ribosomal protein L34						
KEGG	M00131	Inositol phosphate metabolism, Ins(1,3,4,5)P4 => Ins(1,3,4)P3 =	Tfu_1212	Tfu_1212 archaeal fructose-1 6-bisphosphatase and relate	14.95	15.73	15.51	15.72	20.15	0.894
KEGG	M00131	Inositol phosphate metabolism, Ins(1,3,4,5)P4 => Ins(1,3,4)P3 =	Tfu_1943	Tfu_1943 inositol-1(or 4)-monophosphatase	16.16	15.99			19.17	0.652
KEGG	M00083	Fatty acid biosynthesis, elongation	Tfu_1229	Tfu_1229 putative 3-oxoacyl-ACP synthase III						
KEGG	M00083	Fatty acid biosynthesis, elongation	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
KEGG	M00083	Fatty acid biosynthesis, elongation	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
KEGG	M00083	Fatty acid biosynthesis, elongation	Tfu_1842	Tfu_1842 enoyl-(acyl carrier protein) reductase	20.49	19.93	21.16	21.07	24.76	1.053
KEGG	M00083	Fatty acid biosynthesis, elongation	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
KEGG	M00083	Fatty acid biosynthesis, elongation	Tfu_1974	Tfu_1974 3-oxoacyl-(acyl carrier protein) synthase	14.7	15.5	19.86	19.55	23.27	0.869
KEGG	M00083	Fatty acid biosynthesis, elongation	Tfu_1976	Tfu_1976 putative 3-oxoacyl-ACP synthase II	18.39	18.02	19.63	19.4	22.79	0.718
KEGG	M00083	Fatty acid biosynthesis, elongation	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
KEGG	M00117	Ubiquinone biosynthesis, prokaryotes, chorismate => ubiquinon	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
KEGG	M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Tfu_0003	Tfu_0003 6-phosphogluconate dehydrogenase	20.18	20.31	19.92	19.72	23.9	0.655
KEGG	M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
KEGG	M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
KEGG	M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Tfu_2003	Tfu_2003 transaldolase	20.04	20.08	21.54	21.1	24.47	1.211
KEGG	M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
KEGG	M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Tfu_2005	Tfu_2005 glucose-6-phosphate 1-dehydrogenase	16.6	15.74	16.81	16.27	21.46	
KEGG	M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Tfu_2007	Tfu_2007 6-phosphogluconolactonase	18.7	19.13	18.21	17.98	22.37	0.913
KEGG	M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
KEGG	M00004	Pentose phosphate pathway (Pentose phosphate cycle)	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, typ	23.03	22.77	25.37	25.33	28.17	1.113
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
KEGG	M00001	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
KEGG	M00027	GABA (gamma-Aminobutyrate) shunt	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
KEGG	M00027	GABA (gamma-Aminobutyrate) shunt	Tfu_2949	Tfu_2949 succinate-semialdehyde dehydrogenase (NAD(P	16.8	17.18	15.55	15.98	20.6	
KEGG	M00166	Reductive pentose phosphate cycle, RuBP + CO2 => glyceraldehy	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
KEGG	M00527	Lysine biosynthesis, DAP aminotransferase pathway, aspartate =	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1 r	18.57	18.71	20.61	20.33	23.82	0.982
KEGG	M00527	Lysine biosynthesis, DAP aminotransferase pathway, aspartate =	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
KEGG	M00527	Lysine biosynthesis, DAP aminotransferase pathway, aspartate =	Tfu_0786	Tfu_0786 dihydrodipicolinate reductase	18.87	17.45	19.64	18.4	23.22	0.825
KEGG	M00527	Lysine biosynthesis, DAP aminotransferase pathway, aspartate =	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844

KEGG	M00527	Lysine biosynthesis, DAP aminotransferase pathway, aspartate =	Tfu_0816	Tfu_0816 diaminopimelate epimerase					18.06	
KEGG	M00527	Lysine biosynthesis, DAP aminotransferase pathway, aspartate =	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
KEGG	M00527	Lysine biosynthesis, DAP aminotransferase pathway, aspartate =	Tfu_2425	Tfu_2425 diaminopimelate decarboxylase					18.01	
KEGG	M00176	Sulfur reduction, sulfate => H2S	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
KEGG	M00176	Sulfur reduction, sulfate => H2S	Tfu_0420	Tfu_0420 Small GTP-binding protein domain:Sulfate adenylyltransferase,			14.13		18.76	0.81
KEGG	M00176	Sulfur reduction, sulfate => H2S	Tfu_0425	Tfu_0425 adenylylsulfate kinase					17.66	
KEGG	M00176	Sulfur reduction, sulfate => H2S	Tfu_1888	Tfu_1888 putative nitrite/sulphite reductase	16.01	13.98	17.79	17.82	22.36	1.384
KEGG	M00176	Sulfur reduction, sulfate => H2S	Tfu_1889	Tfu_1889 phosphoadenosine phosphosulfate reductase						
KEGG	M00164	ATP synthase	Tfu_2406	Tfu_2406 H+-transporting two-sector ATPase, delta/epsilo	17.61	17.4	18.54	18.5	21.47	
KEGG	M00164	ATP synthase	Tfu_2407	Tfu_2407 ATP synthase F1, beta subunit	21.37	21.44	23.04	22.88	26.22	1.194
KEGG	M00164	ATP synthase	Tfu_2408	Tfu_2408 H+-transporting two-sector ATPase, gamma subu	20.11	19.39	21.19	20.62	23.67	
KEGG	M00164	ATP synthase	Tfu_2409	Tfu_2409 ATP synthase subunit A	21.64	21.69	23.06	22.63	26.34	1.138
KEGG	M00164	ATP synthase	Tfu_2410	Tfu_2410 H+-transporting two-sector ATPase, delta (OSCP	20.66	20.14	21.77	21.25	24.88	0.912
KEGG	M00164	ATP synthase	Tfu_2411	Tfu_2411 ATP synthase F0, subunit B	20.75	20.59	21	21.14	24.9	0.695
KEGG	M00164	ATP synthase	Tfu_2412	Tfu_2412 ATP synthase F0, C subunit						
KEGG	M00164	ATP synthase	Tfu_2413	Tfu_2413 H+-transporting two-sector ATPase, A subunit						
KEGG	M00053	Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP	Tfu_1935	Tfu_1935 deoxyUTP pyrophosphatase subfamily 1					16.91	
KEGG	M00053	Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP	Tfu_2149	Tfu_2149 ribonucleotide-diphosphate reductase alpha sub	14.41		17.19	15.02	21.83	0.68
KEGG	M00053	Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
KEGG	M00053	Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP	Tfu_2783	Tfu_2783 thymidylate kinase	19.41	19.13	18.67	18.47	22.51	0.962
KEGG	M00053	Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP	Tfu_2932	Tfu_2932 deoxycytidine triphosphate deaminase					19.21	
KEGG	M00053	Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP	Tfu_3001	Tfu_3001 ribonucleoside-diphosphate reductase	13.73	13.7	18.55	18.52	22.84	1.196
KEGG	M00053	Pyrimidine deoxyribonuleotide biosynthesis, CDP/CTP => dCDP	Tfu_3002	Tfu_3002 ribonucleoside-diphosphate reductase			18.75	18.62	22.88	0.758
KEGG	M00308	Semi-phosphorylative Entner-Doudoroff pathway, gluconate =>	Tfu_0188	Tfu_0188 2-dehydro-3-deoxyphosphogluconate aldolase /	14.36				15.14	
KEGG	M00308	Semi-phosphorylative Entner-Doudoroff pathway, gluconate =>	Tfu_0189	Tfu_0189 putative PfkB-family carbohydrate kinase						
KEGG	M00373	Ethylmalonyl pathway	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
KEGG	M00373	Ethylmalonyl pathway	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
KEGG	M00373	Ethylmalonyl pathway	Tfu_1520	Tfu_1520 thiolase					15.67	
KEGG	M00373	Ethylmalonyl pathway	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
KEGG	M00373	Ethylmalonyl pathway	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
KEGG	M00373	Ethylmalonyl pathway	Tfu_2555	Tfu_2555 propionyl-CoA carboxylase complex B subunit	18.59	18.29	18.47	17.99	22.37	0.744
KEGG	M00373	Ethylmalonyl pathway	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
KEGG	M00373	Ethylmalonyl pathway	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
KEGG	M00375	Hydroxypropionate-hydroxybutylate cycle	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
KEGG	M00375	Hydroxypropionate-hydroxybutylate cycle	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
KEGG	M00375	Hydroxypropionate-hydroxybutylate cycle	Tfu_1520	Tfu_1520 thiolase					15.67	
KEGG	M00375	Hydroxypropionate-hydroxybutylate cycle	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
KEGG	M00375	Hydroxypropionate-hydroxybutylate cycle	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
KEGG	M00375	Hydroxypropionate-hydroxybutylate cycle	Tfu_2555	Tfu_2555 propionyl-CoA carboxylase complex B subunit	18.59	18.29	18.47	17.99	22.37	0.744
KEGG	M00375	Hydroxypropionate-hydroxybutylate cycle	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
KEGG	M00375	Hydroxypropionate-hydroxybutylate cycle	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
KEGG	M00375	Hydroxypropionate-hydroxybutylate cycle	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
KEGG	M00335	Sec (secretion) system	Tfu_0185	Tfu_0185 hypothetical protein						
KEGG	M00335	Sec (secretion) system	Tfu_0387	Tfu_0387 SecD/SecF/SecDF export membrane protein	19.33	19.06	19.71	19.81	23.88	1.494
KEGG	M00335	Sec (secretion) system	Tfu_0658	Tfu_0658 cell division transporter substrate-binding prote	17.49	17.82	18.43	17.13	21.68	1.002
KEGG	M00335	Sec (secretion) system	Tfu_0661	Tfu_0661 Signal recognition particle protein	17.98	18.05	17.79	18.57	22.6	0.989
KEGG	M00335	Sec (secretion) system	Tfu_0761	Tfu_0761 translocase	17.24	16.09	18.23	18.27	23.03	
KEGG	M00335	Sec (secretion) system	Tfu_2014	Tfu_2014 protein-export membrane protein			15.76		17.98	
KEGG	M00335	Sec (secretion) system	Tfu_2092	Tfu_2092 YajC	18.01	17.71	17.08		19.96	
KEGG	M00335	Sec (secretion) system	Tfu_2490	Tfu_2490 translocase	20.43	20.09	21.04	20.76	24.79	

KEGG	M00335	Sec (secretion) system	Tfu_2626	Tfu_2626 preprotein translocase SecY	15.35	15.15	18.03	17.57	21.22	0.946
KEGG	M00335	Sec (secretion) system	Tfu_2660	Tfu_2660 SecE subunit of protein translocation complex	16.2	15.85			16.67	
KEGG	M00335	Sec (secretion) system	Tfu_3114	Tfu_3114 hypothetical protein		14.35	14.79		19.03	
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_0156	Tfu_0156 phosphoribosylformylglycinamidine synthase I			15.57	15.14	21.14	0.902
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_0158	Tfu_0158 phosphoribosylformylglycinamidine synthase su	13.89	15.06	17.93	18.1	22.88	0.924
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_0178	Tfu_0178 phosphoribosylformylglycinamidine synthase					17.74	
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_2546	Tfu_2546 1-(5-Phosphoribosyl)-5-amino-4-imidazole- carb	17.46	17.22	17.98	17.21	21.62	
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_2547	Tfu_2547 phosphoribosylaminoimidazole carboxylase, ATPase subunit					18.27	
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_2572	Tfu_2572 bifunctional phosphoribosylaminoimidazolecarb	19.86	19.04	20.76	20.79	24.53	0.912
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_2573	Tfu_2573 phosphoribosylglycinamide formyltransferase	14.49	14.7	17.07	16.78	21.38	
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_2747	Tfu_2747 amidophosphoribosyltransferase						
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_2748	Tfu_2748 phosphoribosylaminoimidazole synthetase	14.77		17.56	17.33	20.81	0.689
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_3013	Tfu_3013 phosphoribosylglycinamide synthetase			17.63	17.26	21.77	
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_3014	Tfu_3014 adenylosuccinate lyase	18.68	18.68	20.17	19.69	23.57	0.954
KEGG	M00048	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	Tfu_3015	Tfu_3015 phosphoribosylaminoimidazole-succinocarboxa	17.2	16.06	17.97	17.67	21.89	0.805
KEGG	M00532	Photorespiration	Tfu_1010	Tfu_1010 glycerate kinase			14.48		20.4	
KEGG	M00532	Photorespiration	Tfu_1649	Tfu_1649 catalase	20.13	19.98	21.56	21.24	24.73	0.727
KEGG	M00532	Photorespiration	Tfu_2352	Tfu_2352 Glycine cleavage H-protein		14.52			17.57	0.666
KEGG	M00532	Photorespiration	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
KEGG	M00532	Photorespiration	Tfu_2980	Tfu_2980 (S)-2-hydroxy-acid oxidase					14.64	
KEGG	M00098	Acylglycerol degradation	Tfu_0155	Tfu_0155 esterase / lipase						
KEGG	M00098	Acylglycerol degradation	Tfu_0882	Tfu_0882 hypothetical protein						
KEGG	M00098	Acylglycerol degradation	Tfu_0883	Tfu_0883 hypothetical protein						
KEGG	M00238	D-Methionine transport system	Tfu_0931	Tfu_0931 ABC-type metal ion transport system ATPase cor	13.97	13.69	16.6	17.33	22.05	1.063
KEGG	M00238	D-Methionine transport system	Tfu_0932	Tfu_0932 putative ABC transporter permease protein	14.82	14.67	15.81	15.77	18.33	
KEGG	M00238	D-Methionine transport system	Tfu_0933	Tfu_0933 hypothetical protein	18.94	19.25	20.53	20.2	24	1.091
KEGG	M00252	Lipooligosaccharide transport system	Tfu_0461	Tfu_0461 ABC-type multidrug transport system ATPase component			14.83	15.65	20.1	
KEGG	M00038	Tryptophan metabolism, tryptophan => kynurenine => 2-amino	Tfu_0921	Tfu_0921 putative tryptophan 2,3-dioxygenase	13.54	14.16			17.35	
KEGG	M00038	Tryptophan metabolism, tryptophan => kynurenine => 2-amino	Tfu_0922	Tfu_0922 kynureninase	16.91	15.34	13.9	14.63	19.53	1.172
KEGG	M00038	Tryptophan metabolism, tryptophan => kynurenine => 2-amino	Tfu_1418	Tfu_1418 hypothetical protein	18.89	18.42	20.57	20.44	23.75	0.572
KEGG	M00038	Tryptophan metabolism, tryptophan => kynurenine => 2-amino	Tfu_1722	Tfu_1722 hypothetical protein					14.24	
KEGG	M00104	Bile acid biosynthesis, cholesterol => cholate	Tfu_0399	Tfu_0399 putative fatty acid-CoA racemase	16.76	16.16	14.76	15.27	19.11	
KEGG	M00035	Methionine degradation	Tfu_0438	Tfu_0438 cystathionine beta-synthase	13		14.49	12.98	20.18	
KEGG	M00035	Methionine degradation	Tfu_1065	Tfu_1065 S-adenosylmethionine synthetase	15.28	15.32	15.74	16.4	20.99	0.962
KEGG	M00035	Methionine degradation	Tfu_2505	Tfu_2505 S-adenosyl-L-homocysteine hydrolase	18.66	19.01	19.8	19.23	23.56	1.126
KEGG	M00346	Formaldehyde assimilation, serine pathway	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
KEGG	M00346	Formaldehyde assimilation, serine pathway	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
KEGG	M00346	Formaldehyde assimilation, serine pathway	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
KEGG	M00346	Formaldehyde assimilation, serine pathway	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
KEGG	M00368	Ethylene biosynthesis, methionine => ethylene	Tfu_1065	Tfu_1065 S-adenosylmethionine synthetase	15.28	15.32	15.74	16.4	20.99	0.962
KEGG	M00115	NAD biosynthesis, aspartate => NAD	Tfu_0575	Tfu_0575 quinolinate synthetase						
KEGG	M00115	NAD biosynthesis, aspartate => NAD	Tfu_0983	Tfu_0983 NAD+ synthase	16.91	16.85	17.72	17.22	22.21	0.82
KEGG	M00115	NAD biosynthesis, aspartate => NAD	Tfu_2171	Tfu_2171 nicotinic acid mononucleotide adenyltransferase					18.95	
KEGG	M00115	NAD biosynthesis, aspartate => NAD	Tfu_2883	Tfu_2883 L-aspartate oxidase			15.62	16.95	20.84	
KEGG	M00171	C4-dicarboxylic acid cycle, NAD+ -malic enzyme type	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
KEGG	M00171	C4-dicarboxylic acid cycle, NAD+ -malic enzyme type	Tfu_0863	Tfu_0863 pyruvate phosphate dikinase	17.84	17.11	21.38	21.45	25.04	1.455
KEGG	M00171	C4-dicarboxylic acid cycle, NAD+ -malic enzyme type	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
KEGG	M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UM	Tfu_0927	Tfu_0927 dihydroorotate dehydrogenase	17.12	17.21	17.52	17.43	21.74	
KEGG	M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UM	Tfu_0962	Tfu_0962 allantoinase						
KEGG	M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UM	Tfu_1054	Tfu_1054 aspartate carbamoyltransferase catalytic subunit					19.72	1.183

KEGG	M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UM	Tfu_1055	Tfu_1055 dihydroorotase	13.79		18.6	18.17	22.62	
KEGG	M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UM	Tfu_1056	Tfu_1056 carbamoyl-phosphate synthase, small subunit		15.52	17.25	17.26	22.56	0.884
KEGG	M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UM	Tfu_1057	Tfu_1057 carbamoyl-phosphate synthase, large subunit, gl	16.53	16.24	19.8	19.69	24.13	0.99
KEGG	M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UM	Tfu_1059	Tfu_1059 dihydroorotate dehydrogenase 1						
KEGG	M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UM	Tfu_1060	Tfu_1060 orotidine 5'-phosphate decarboxylase	17.31	17.43	16.58	16.96	22.37	0.988
KEGG	M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UM	Tfu_2378	Tfu_2378 hypothetical protein					16.58	
KEGG	M00051	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UM	Tfu_3008	Tfu_3008 orotate phosphoribosyltransferase	17.41	17.4	17.96	17.05	22.2	0.852
KEGG	M00134	Polyamine biosynthesis, arginine => ornithine => putrescine	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
KEGG	M00265	PTS system, glucose-specific II component	Tfu_2489	Tfu_2489 putative phosphoenolpyruvate-dependent sugar phosphotransferase					16.36	
KEGG	M00033	Ectoine biosynthesis, aspartate => ectoine	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1 r	18.57	18.71	20.61	20.33	23.82	0.982
KEGG	M00033	Ectoine biosynthesis, aspartate => ectoine	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
KEGG	M00033	Ectoine biosynthesis, aspartate => ectoine	Tfu_0300	Tfu_0300 putative acetyltransferase						
KEGG	M00033	Ectoine biosynthesis, aspartate => ectoine	Tfu_0301	Tfu_0301 diaminobutyrate--2-oxoglutarate aminotransferase						
KEGG	M00033	Ectoine biosynthesis, aspartate => ectoine	Tfu_0302	Tfu_0302 putative condensing enzyme					17.04	
KEGG	M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Tfu_0083	Tfu_0083 phosphoenolpyruvate carboxykinase (GTP)	18.4	18.56	20.72	20.61	24.19	1.846
KEGG	M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
KEGG	M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
KEGG	M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
KEGG	M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
KEGG	M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, typ	23.03	22.77	25.37	25.33	28.17	1.113
KEGG	M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
KEGG	M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
KEGG	M00003	Gluconeogenesis, oxaloacetate => fructose-6P	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
KEGG	M00060	Lipopolysaccharide biosynthesis, KDO2-lipid A	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
KEGG	M00023	Tryptophan biosynthesis, chorismate => tryptophan	Tfu_1024	Tfu_1024 anthranilate phosphoribosyltransferase						
KEGG	M00023	Tryptophan biosynthesis, chorismate => tryptophan	Tfu_1155	Tfu_1155 1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methyliden			15.7	16.67	21.72	
KEGG	M00023	Tryptophan biosynthesis, chorismate => tryptophan	Tfu_1164	Tfu_1164 indole-3-glycerol-phosphate synthase					20.46	1.072
KEGG	M00023	Tryptophan biosynthesis, chorismate => tryptophan	Tfu_1165	Tfu_1165 tryptophan synthase, beta chain					18.55	
KEGG	M00023	Tryptophan biosynthesis, chorismate => tryptophan	Tfu_1166	Tfu_1166 tryptophan synthase subunit alpha					18.24	
KEGG	M00023	Tryptophan biosynthesis, chorismate => tryptophan	Tfu_1386	Tfu_1386 glutamine amidotransferase of anthranilate synt	14.29	15.3	14.48	14.83	21.47	1.207
KEGG	M00361	Nucleotide sugar biosynthesis, eukaryotes	Tfu_0169	Tfu_0169 nucleoside-diphosphate-sugar epimerase (UDP-g	14.49	16.6	18.84	18.16	22.51	0.845
KEGG	M00361	Nucleotide sugar biosynthesis, eukaryotes	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase, b	16.85	15	17.24	17.46	22.15	
KEGG	M00361	Nucleotide sugar biosynthesis, eukaryotes	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / phc	19.06	18.82	21.97	21.81	25.49	1.131
KEGG	M00361	Nucleotide sugar biosynthesis, eukaryotes	Tfu_1622	Tfu_1622 UDP-glucose 4-epimerase						
KEGG	M00361	Nucleotide sugar biosynthesis, eukaryotes	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
KEGG	M00361	Nucleotide sugar biosynthesis, eukaryotes	Tfu_2591	Tfu_2591 UDP-glucose 4-epimerase					14.83	
KEGG	M00361	Nucleotide sugar biosynthesis, eukaryotes	Tfu_2723	Tfu_2723 putative epimerase						
KEGG	M00435	Taurine transport system	Tfu_1504	Tfu_1504 hypothetical protein						
KEGG	M00025	Tyrosine biosynthesis, chorismate => tyrosine	Tfu_1207	Tfu_1207 chorismate mutase of the AroH class						
KEGG	M00025	Tyrosine biosynthesis, chorismate => tyrosine	Tfu_1208	Tfu_1208 prephenate dehydrogenase						
KEGG	M00017	Methionine biosynthesis, apartate => homoserine => methionine	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1 r	18.57	18.71	20.61	20.33	23.82	0.982
KEGG	M00017	Methionine biosynthesis, apartate => homoserine => methionine	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
KEGG	M00017	Methionine biosynthesis, apartate => homoserine => methionine	Tfu_0440	Tfu_0440 cystathionine gamma-synthase					17.4	
KEGG	M00017	Methionine biosynthesis, apartate => homoserine => methionine	Tfu_0632	Tfu_0632 cystathionine gamma-synthase					15.55	0.471
KEGG	M00017	Methionine biosynthesis, apartate => homoserine => methionine	Tfu_1825	Tfu_1825 5-methyltetrahydrofolate--homocysteine methyltransferase					15.39	
KEGG	M00017	Methionine biosynthesis, apartate => homoserine => methionine	Tfu_2424	Tfu_2424 homoserine dehydrogenase					18.67	1.062
KEGG	M00125	Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD	Tfu_0782	Tfu_0782 Cytidyltransferase-related		13.35	14.92	14.18	20.03	
KEGG	M00125	Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD	Tfu_0876	Tfu_0876 5-amino-6-(5-phosphoribosylamino)uracil reductase					18.52	
KEGG	M00125	Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD	Tfu_0877	Tfu_0877 hypothetical protein					17.13	
KEGG	M00125	Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD	Tfu_1078	Tfu_1078 Lumazine-binding protein		13.92	16.4	17.05	20.31	

KEGG	M00125	Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD	Tfu_1080	Tfu_1080 bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein						
KEGG	M00125	Riboflavin biosynthesis, GTP => riboflavin/FMN/FAD	Tfu_1081	Tfu_1081 6,7-dimethyl-8-ribityllumazine synthase	15.97	15.69	16.33	16.62	21.62	
KEGG	M00149	Succinate dehydrogenase, prokaryotes	Tfu_2451	Tfu_2451 succinate dehydrogenase	19.35	19.39	20.29	20.56	23.66	1.002
KEGG	M00149	Succinate dehydrogenase, prokaryotes	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
KEGG	M00149	Succinate dehydrogenase, prokaryotes	Tfu_2453	Tfu_2453 succinate dehydrogenase, cytochrome b558 subunit					19.37	1.293
KEGG	M00525	Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1 r	18.57	18.71	20.61	20.33	23.82	0.982
KEGG	M00525	Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
KEGG	M00525	Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine	Tfu_0786	Tfu_0786 dihydrodipicolinate reductase	18.87	17.45	19.64	18.4	23.22	0.825
KEGG	M00525	Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844
KEGG	M00525	Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine	Tfu_0816	Tfu_0816 diaminopimelate epimerase					18.06	
KEGG	M00525	Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
KEGG	M00525	Lysine biosynthesis, acetyl-DAP pathway, aspartate => lysine	Tfu_2425	Tfu_2425 diaminopimelate decarboxylase					18.01	
KEGG	M00096	C5 isoprenoid biosynthesis, non-mevalonate pathway	Tfu_0407	Tfu_0407 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase					17.64	
KEGG	M00096	C5 isoprenoid biosynthesis, non-mevalonate pathway	Tfu_0471	Tfu_0471 4-hydroxy-3-methylbut-2-enyl diphosphate reductase					19.27	
KEGG	M00096	C5 isoprenoid biosynthesis, non-mevalonate pathway	Tfu_0747	Tfu_0747 1-deoxy-D-xylulose 5-phosphate reductoisomerase						
KEGG	M00096	C5 isoprenoid biosynthesis, non-mevalonate pathway	Tfu_0749	Tfu_0749 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase					16.63	
KEGG	M00096	C5 isoprenoid biosynthesis, non-mevalonate pathway	Tfu_1917	Tfu_1917 1-deoxy-D-xylulose-5-phosphate synthase					16.98	
KEGG	M00096	C5 isoprenoid biosynthesis, non-mevalonate pathway	Tfu_2906	Tfu_2906 MECDP-synthase	14.67		15.37		18.41	0.633
KEGG	M00120	Coenzyme A biosynthesis, pantothenate => CoA	Tfu_0648	Tfu_0648 coenzyme A biosynthesis protein:Cytidyltransfer	18.01	16.72	17.97	17.55	22.5	1.132
KEGG	M00120	Coenzyme A biosynthesis, pantothenate => CoA	Tfu_1064	Tfu_1064 phosphopantothenoylcysteine synthase/decarbo	18.49	18.47	18.49	18.95	22.74	1.103
KEGG	M00120	Coenzyme A biosynthesis, pantothenate => CoA	Tfu_1192	Tfu_1192 dephospho-CoA kinase	17.51	17.36	16.73	16.92	20.12	
KEGG	M00120	Coenzyme A biosynthesis, pantothenate => CoA	Tfu_2610	Tfu_2610 pantothenate kinase			14.28		19	
KEGG	M00120	Coenzyme A biosynthesis, pantothenate => CoA	Tfu_2882	Tfu_2882 Bvg accessory factor	15.79	15.26	16.09	15.65	20.23	
KEGG	M00303	PTS system, N-acetylmuramic acid-specific II component	Tfu_2489	Tfu_2489 putative phosphoenolpyruvate-dependent sugar phosphotransferase					16.36	
KEGG	M00535	Isoleucine biosynthesis, pyruvate => 2-oxobutanoate	Tfu_0615	Tfu_0615 3-isopropylmalate dehydrogenase	19.78	19.7	19.64	19.42	23.35	1.025
KEGG	M00535	Isoleucine biosynthesis, pyruvate => 2-oxobutanoate	Tfu_0626	Tfu_0626 isopropylmalate isomerase large subunit			15.08	14.46	19.36	
KEGG	M00535	Isoleucine biosynthesis, pyruvate => 2-oxobutanoate	Tfu_0627	Tfu_0627 isopropylmalate isomerase small subunit	13.33				18.83	
KEGG	M00443	SenX3-RegX3 (phosphate starvation response) two-component	Tfu_2909	Tfu_2909 ATP-binding region, ATPase-like:Histidine kinase A, N-terminal					18.74	
KEGG	M00443	SenX3-RegX3 (phosphate starvation response) two-component	Tfu_2910	Tfu_2910 response regulator receiver	16.38	16.03	17	17.51	21.88	1.079
KEGG	M00018	Threonine biosynthesis, apartate => homoserine => threonine	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1 r	18.57	18.71	20.61	20.33	23.82	0.982
KEGG	M00018	Threonine biosynthesis, apartate => homoserine => threonine	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
KEGG	M00018	Threonine biosynthesis, apartate => homoserine => threonine	Tfu_0226	Tfu_0226 threonine synthase	15.9	15.94	18.57	18.65	22.91	1.385
KEGG	M00018	Threonine biosynthesis, apartate => homoserine => threonine	Tfu_2422	Tfu_2422 homoserine kinase					19.33	0.823
KEGG	M00018	Threonine biosynthesis, apartate => homoserine => threonine	Tfu_2423	Tfu_2423 threonine synthase	13.86				17.31	
KEGG	M00018	Threonine biosynthesis, apartate => homoserine => threonine	Tfu_2424	Tfu_2424 homoserine dehydrogenase					18.67	1.062
KEGG	M00088	Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydrox	Tfu_0081	Tfu_0081 3-hydroxybutyrate dehydrogenase	21.11	21.46	19.94	20.31	23.95	1.187
KEGG	M00088	Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydrox	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
KEGG	M00088	Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydrox	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
KEGG	M00088	Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydrox	Tfu_1520	Tfu_1520 thiolase					15.67	
KEGG	M00088	Ketone body biosynthesis, acetyl-CoA => acetoacetate/3-hydrox	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
KEGG	M00122	Cobalamin biosynthesis, cobinamide => cobalamin	Tfu_0309	Tfu_0309 cobyric acid synthase					19.41	
KEGG	M00122	Cobalamin biosynthesis, cobinamide => cobalamin	Tfu_0312	Tfu_0312 cob(I)yrinic acid a,c-diamide adenosyltransferase					16.96	
KEGG	M00122	Cobalamin biosynthesis, cobinamide => cobalamin	Tfu_0996	Tfu_0996 putative cobalamin (5'-phosphate) synthase : adenosylcobinamide-GDP ribazoletransferase						
KEGG	M00122	Cobalamin biosynthesis, cobinamide => cobalamin	Tfu_0997	Tfu_0997 adenosylcobinamide kinase / adenosylcobinamide-phos	15.35		15.47	20.21		
KEGG	M00122	Cobalamin biosynthesis, cobinamide => cobalamin	Tfu_2222	Tfu_2222 nicotinate-nucleotide-dimethylbenzimidazole ph	15.06		15.97	15.99	20.79	0.7
KEGG	M00122	Cobalamin biosynthesis, cobinamide => cobalamin	Tfu_2224	Tfu_2224 cobalamin biosynthesis protein						

Appendix - E - Proteomics Data HOV: EC Associations

CLASS	HOV	HOV-description	locus	locus-description	AV	AVR	CB	CBR	CB2D	iTRAQ
EC	1.-	Oxidoreductases.	Tfu_0314	Tfu_0314 SAM (and some other nucleotide) binding motif						
EC	1.1.1.-	Oxidoreductases. Acting on the CH-OH group of donors.	Tfu_1221	Tfu_1221 hypothetical protein						
EC	1.1.1.-	Oxidoreductases. Acting on the CH-OH group of donors.	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
EC	1.1.1.1	Alcohol dehydrogenase.	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
EC	1.1.1.1	Alcohol dehydrogenase.	Tfu_1489	Tfu_1489 oxidoreductase						
EC	1.1.1.1	Alcohol dehydrogenase.	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
EC	1.1.1.1	Alcohol dehydrogenase.	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
EC	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase.	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
EC	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase.	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
EC	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase.	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
EC	1.1.1.100	3-oxoacyl-[acyl-carrier-protein] reductase.	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
EC	1.1.1.125	2-deoxy-D-gluconate 3-dehydrogenase.	Tfu_1298	Tfu_1298 2-deoxy-D-gluconate 3-dehydrogenase	15.48	14.84		13.51	17.6	
EC	1.1.1.157	3-hydroxybutyryl-CoA dehydrogenase.	Tfu_2399	Tfu_2399 3-hydroxybutyryl-CoA dehydrogenase	19.01	18.42	18.82	18.43	22.92	1.184
EC	1.1.1.158	UDP-N-acetylmuramate dehydrogenase.	Tfu_2664	Tfu_2664 UDP-N-acetylenolpyruvoylglucosamine reductase	13.88				20.85	
EC	1.1.1.193	5-amino-6-(5-phosphoribosylamino)uracil reductase.	Tfu_0876	Tfu_0876 5-amino-6-(5-phosphoribosylamino)uracil reductase					18.52	
EC	1.1.1.193	5-amino-6-(5-phosphoribosylamino)uracil reductase.	Tfu_0877	Tfu_0877 hypothetical protein					17.13	
EC	1.1.1.205	IMP dehydrogenase.	Tfu_2440	Tfu_2440 inositol-5-monophosphate dehydrogenase	19.82	19.85	19.51	19.28	23.25	1.113
EC	1.1.1.205	IMP dehydrogenase.	Tfu_2595	Tfu_2595 inositol-5-monophosphate dehydrogenase	18.6	18.73	20.9	20.27	24.94	0.944
EC	1.1.1.205	IMP dehydrogenase.	Tfu_2596	Tfu_2596 IMP dehydrogenase	17.6	17.76	20.1	19.82	24.11	1.035
EC	1.1.1.22	UDP-glucose 6-dehydrogenase.	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
EC	1.1.1.23	Histidinol dehydrogenase.	Tfu_1150	Tfu_1150 histidinol dehydrogenase	19.66	19.37	19.47	19.89	23.27	0.966
EC	1.1.1.25	Shikimate dehydrogenase.	Tfu_2067	Tfu_2067 shikimate 5-dehydrogenase					17.29	
EC	1.1.1.261	sn-glycerol-1-phosphate dehydrogenase.	Tfu_2533	Tfu_2533 putative glycerol 1-phosphate dehydrogenase					17.86	
EC	1.1.1.267	1-deoxy-D-xylulose-5-phosphate reductoisomerase.	Tfu_0747	Tfu_0747 1-deoxy-D-xylulose 5-phosphate reductoisomerase						
EC	1.1.1.274	2,5-didehydrogluconate reductase.	Tfu_1687	Tfu_1687 2,5-didehydrogluconate reductase	19.87	19.39	15.9	16.75	21.51	0.632
EC	1.1.1.284	S-(hydroxymethyl)glutathione dehydrogenase.	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
EC	1.1.1.284	S-(hydroxymethyl)glutathione dehydrogenase.	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
EC	1.1.1.3	Homoserine dehydrogenase.	Tfu_2424	Tfu_2424 homoserine dehydrogenase					18.67	1.062
EC	1.1.1.30	3-hydroxybutyrate dehydrogenase.	Tfu_0081	Tfu_0081 3-hydroxybutyrate dehydrogenase	21.11	21.46	19.94	20.31	23.95	1.187
EC	1.1.1.37	Malate dehydrogenase.	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
EC	1.1.1.38	Malate dehydrogenase (oxaloacetate-decarboxylating).	Tfu_0562	Tfu_0562 malate dehydrogenase (oxaloacetate decarboxylating)						
EC	1.1.1.38	Malate dehydrogenase (oxaloacetate-decarboxylating).	Tfu_2390	Tfu_2390 malate dehydrogenase (oxaloacetate decarboxylating)	15.54	15.17	14.98	15.9	20.7	0.661
EC	1.1.1.42	Isocitrate dehydrogenase (NADP(+)).	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
EC	1.1.1.44	Phosphogluconate dehydrogenase (decarboxylating).	Tfu_0003	Tfu_0003 6-phosphogluconate dehydrogenase	20.18	20.31	19.92	19.72	23.9	0.655
EC	1.1.1.49	Glucose-6-phosphate dehydrogenase.	Tfu_2005	Tfu_2005 glucose-6-phosphate 1-dehydrogenase	16.6	15.74	16.81	16.27	21.46	
EC	1.1.1.6	Glycerol dehydrogenase.	Tfu_2801	Tfu_2801 glycerol dehydrogenase					18.62	
EC	1.1.1.60	2-hydroxy-3-oxopropionate reductase.	Tfu_1265	Tfu_1265 2-hydroxy-3-oxopropionate reductase			15.84	13.26	19.37	
EC	1.1.1.85	3-isopropylmalate dehydrogenase.	Tfu_0615	Tfu_0615 3-isopropylmalate dehydrogenase	19.78	19.7	19.64	19.42	23.35	1.025
EC	1.1.1.86	Ketol-acid reductoisomerase.	Tfu_0613	Tfu_0613 ketol-acid reductoisomerase	19.9	19.77	19.96	19.71	23.42	0.799
EC	1.1.1.94	Glycerol-3-phosphate dehydrogenase (NAD(P)(+)).	Tfu_0631	Tfu_0631 glycerol-3-phosphate dehydrogenase (NAD(P)+)	14.3	15.55	14.47		20.42	
EC	1.1.1.95	Phosphoglycerate dehydrogenase.	Tfu_0614	Tfu_0614 D-3-phosphoglycerate dehydrogenase	20.25	20.04	22.34	22.29	25.26	1.066
EC	1.1.1.95	Phosphoglycerate dehydrogenase.	Tfu_2259	Tfu_2259 similar to Phosphoglycerate dehydrogenase and related dehydrogenase						
EC	1.1.3.15	(S)-2-hydroxy-acid oxidase.	Tfu_2980	Tfu_2980 (S)-2-hydroxy-acid oxidase					14.64	
EC	1.1.3.6	Cholesterol oxidase.	Tfu_2332	Tfu_2332 putative cholesterol oxidase					14.87	
EC	1.1.3.8	L-gulonolactone oxidase.	Tfu_1946	Tfu_1946 FAD-linked oxidoreductase	20.44	20.72	18.89	18.06	22.64	0.891
EC	1.1.5.3	Glycerol-3-phosphate dehydrogenase.	Tfu_2593	Tfu_2593 glycerol-3-phosphate dehydrogenase	19.6	19.46	17.83	17.65	23.22	0.765

EC	1.10.3.-	Oxidoreductases. Acting on diphenols and related substa	Tfu_0637	Tfu_0637 cytochrome bd ubiquinol oxidase, subunit II			18.7	17.36	23.03	2.71
EC	1.10.3.-	Oxidoreductases. Acting on diphenols and related substa	Tfu_0638	Tfu_0638 putative cytochrome oxidase subunit I			19.89	19.95	23.08	
EC	1.10.3.-	Oxidoreductases. Acting on diphenols and related substa	Tfu_0766	Tfu_0766 highly similar to cytochrome D ubiquinol oxidase subunit I						
EC	1.11.1.10	Chloride peroxidase.	Tfu_1653	Tfu_1653 chloride peroxidase						
EC	1.11.1.15	Peroxiredoxin.	Tfu_2360	Tfu_2360 bacterioferritin comigratory protein	17.08	16.37	18.22	18.06	22.15	1.027
EC	1.11.1.19	Dye decolorizing peroxidase.	Tfu_3078	Tfu_3078 hypothetical protein						
EC	1.11.1.6	Catalase.	Tfu_1649	Tfu_1649 catalase	20.13	19.98	21.56	21.24	24.73	0.727
EC	1.11.1.9	Glutathione peroxidase.	Tfu_2759	Tfu_2759 similar to Glutathione peroxidase		15.24			20.7	1.126
EC	1.13.11.11	Tryptophan 2,3-dioxygenase.	Tfu_0921	Tfu_0921 putative tryptophan 2,3-dioxygenase	13.54	14.16			17.35	
EC	1.14.11.-	Oxidoreductases. Acting on paired donors, with incorpo	Tfu_1427	Tfu_1427 putative DNA repair protein						
EC	1.14.12.17	Nitric oxide dioxygenase.	Tfu_0423	Tfu_0423 flavohemoprotein						
EC	1.14.13.22	Cyclohexanone monooxygenase.	Tfu_1490	Tfu_1490 putative monooxygenase					16.06	
EC	1.14.13.83	Precorrin-3B synthase.	Tfu_0318	Tfu_0318 cobalamin biosynthesis protein CobG, precorrin-3B synthase						
EC	1.14.14.-	Oxidoreductases. Acting on paired donors, with incorpo	Tfu_1234	Tfu_1234 putative hydrolase			13.82	13	20.38	
EC	1.14.14.5	Alkanesulfonate monooxygenase.	Tfu_1497	Tfu_1497 alkanesulfonate monooxygenase						
EC	1.14.14.5	Alkanesulfonate monooxygenase.	Tfu_1500	Tfu_1500 alkanesulfonate monooxygenase						
EC	1.14.14.5	Alkanesulfonate monooxygenase.	Tfu_1502	Tfu_1502 alkanesulfonate monooxygenase						
EC	1.14.19.1	Stearoyl-CoA 9-desaturase.	Tfu_0413	Tfu_0413 stearoyl-CoA 9-desaturase						
EC	1.14.99.3	Heme oxygenase.	Tfu_2345	Tfu_2345 heme oxygenase (decyclizing)						
EC	1.15.1.1	Superoxide dismutase.	Tfu_0957	Tfu_0957 superoxide dismutase	22.64	22.53	22.08	22.69	25.05	0.848
EC	1.15.1.1	Superoxide dismutase.	Tfu_2766	Tfu_2766 hypothetical protein	17.21	16.85	15.75	15.26	19.61	
EC	1.17.1.2	4-hydroxy-3-methylbut-2-enyl diphosphate reductase.	Tfu_0471	Tfu_0471 4-hydroxy-3-methylbut-2-enyl diphosphate reductase					19.27	
EC	1.17.4.1	Ribonucleoside-diphosphate reductase.	Tfu_2149	Tfu_2149 ribonucleotide-diphosphate reductase alpha subunit	14.41		17.19	15.02	21.83	0.68
EC	1.17.4.1	Ribonucleoside-diphosphate reductase.	Tfu_3001	Tfu_3001 ribonucleoside-diphosphate reductase	13.73	13.7	18.55	18.52	22.84	1.196
EC	1.17.4.1	Ribonucleoside-diphosphate reductase.	Tfu_3002	Tfu_3002 ribonucleoside-diphosphate reductase			18.75	18.62	22.88	0.758
EC	1.17.7.1	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthas	Tfu_0749	Tfu_0749 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase					16.63	
EC	1.18.1.2	Ferredoxin--NADP(+) reductase.	Tfu_1915	Tfu_1915 ferredoxin/ferredoxin--NADP reductase, putative		13.93			20	
EC	1.18.1.3	Ferredoxin--NAD(+) reductase.	Tfu_1273	Tfu_1273 putative oxidoreductase						
EC	1.2.1.11	Aspartate-semialdehyde dehydrogenase.	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1 related	18.57	18.71	20.61	20.33	23.82	0.982
EC	1.2.1.12	Glyceraldehyde-3-phosphate dehydrogenase (phosphor	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, type I	23.03	22.77	25.37	25.33	28.17	1.113
EC	1.2.1.16	Succinate-semialdehyde dehydrogenase (NAD(P)(+)).	Tfu_2949	Tfu_2949 succinate-semialdehyde dehydrogenase (NAD(P)+)	16.8	17.18	15.55	15.98	20.6	
EC	1.2.1.18	Malonate-semialdehyde dehydrogenase (acetylating).	Tfu_0687	Tfu_0687 methylmalonate-semialdehyde dehydrogenase	18.43	17.24	18.03	18.14	22.37	1.017
EC	1.2.1.2	Formate dehydrogenase.	Tfu_1737	Tfu_1737 oxidoreductase alpha (molybdopterin) subunit			14.39	13.79	19.93	
EC	1.2.1.27	Methylmalonate-semialdehyde dehydrogenase (acylatin	Tfu_0687	Tfu_0687 methylmalonate-semialdehyde dehydrogenase	18.43	17.24	18.03	18.14	22.37	1.017
EC	1.2.1.3	Aldehyde dehydrogenase (NAD(+)).	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
EC	1.2.1.3	Aldehyde dehydrogenase (NAD(+)).	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
EC	1.2.1.3	Aldehyde dehydrogenase (NAD(+)).	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
EC	1.2.1.38	N-acetyl-gamma-glutamyl-phosphate reductase.	Tfu_2057	Tfu_2057 N-acetyl-gamma-glutamyl-phosphate reductase					20.33	
EC	1.2.1.4	Aldehyde dehydrogenase (NADP(+)).	Tfu_1706	Tfu_1706 putative aldehyde dehydrogenase					17.58	
EC	1.2.1.41	Glutamate-5-semialdehyde dehydrogenase.	Tfu_2175	Tfu_2175 gamma-glutamyl phosphate reductase GPR	16.65	16.53	17.82	17.26	21.71	
EC	1.2.1.46	Formaldehyde dehydrogenase.	Tfu_3025	Tfu_3025 putative alcohol dehydrogenase	18.7	19.04	16.64	17.19	21.72	
EC	1.2.1.70	Glutamyl-tRNA reductase.	Tfu_2733	Tfu_2733 glutamyl-tRNA reductase						
EC	1.2.1.8	Betaine-aldehyde dehydrogenase.	Tfu_0279	Tfu_0279 betaine-aldehyde dehydrogenase	21.7	21.51	19.8	20.02	23.9	0.958
EC	1.2.1.8	Betaine-aldehyde dehydrogenase.	Tfu_1287	Tfu_1287 betaine-aldehyde dehydrogenase					18.53	
EC	1.2.1.8	Betaine-aldehyde dehydrogenase.	Tfu_1471	Tfu_1471 betaine-aldehyde dehydrogenase					16.26	
EC	1.2.1.8	Betaine-aldehyde dehydrogenase.	Tfu_1776	Tfu_1776 betaine-aldehyde dehydrogenase	16	15.03			18.4	
EC	1.2.4.1	Pyruvate dehydrogenase (acetyl-transferring).	Tfu_0180	Tfu_0180 pyruvate dehydrogenase (lipoamide)	20.47	20.54	21.95	22.05	25.45	0.974
EC	1.2.4.1	Pyruvate dehydrogenase (acetyl-transferring).	Tfu_0181	Tfu_0181 putative branched-chain alpha keto acid dehydrogenase E1 beta subunit	21.52	21.2	22.35	22.16	25.65	0.999
EC	1.2.4.1	Pyruvate dehydrogenase (acetyl-transferring).	Tfu_3049	Tfu_3049 pyruvate dehydrogenase (lipoamide)	20.31	19.75	20.61	20.78	24.41	1.167
EC	1.2.4.1	Pyruvate dehydrogenase (acetyl-transferring).	Tfu_3050	Tfu_3050 dehydrogenase complex, E1 component, beta subunit	20.68	20.22	21.86	21.38	24.75	1.231
EC	1.2.4.2	Oxoglutarate dehydrogenase (succinyl-transferring).	Tfu_0566	Tfu_0566 alpha-ketoglutarate decarboxylase	22.63	22.08	23.34	23.51	26.75	1.555

EC	1.2.7.3	2-oxoglutarate synthase.	Tfu_2674	Tfu_2674 2-oxoglutarate ferredoxin oxidoreductase, alpha subunit	14.55		17.74	18.16	22.74	1.656
EC	1.2.7.3	2-oxoglutarate synthase.	Tfu_2675	Tfu_2675 ferrodoxin oxidoreductase beta subunit			17.01	16.7	21.8	
EC	1.2.99.2	Carbon-monoxide dehydrogenase (acceptor).	Tfu_2586	Tfu_2586 carbon monoxide dehydrogenase						
EC	1.2.99.2	Carbon-monoxide dehydrogenase (acceptor).	Tfu_2587	Tfu_2587 molybdopterin dehydrogenase						
EC	1.20.4.1	Arsenate reductase (glutaredoxin).	Tfu_1521	Tfu_1521 similar to Arsenate reductase and related proteins glutaredoxin family					17.85	
EC	1.20.4.1	Arsenate reductase (glutaredoxin).	Tfu_1554	Tfu_1554 Low molecular weight phosphotyrosine protein phosphatase	12.56	12.64	14.42	12.86	16.39	
EC	1.3.1.12	Prephenate dehydrogenase.	Tfu_1208	Tfu_1208 prephenate dehydrogenase						
EC	1.3.1.26	Dihydrodipicolinate reductase.	Tfu_0786	Tfu_0786 dihydrodipicolinate reductase	18.87	17.45	19.64	18.4	23.22	0.825
EC	1.3.1.28	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase.	Tfu_1873	Tfu_1873 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase					14.76	
EC	1.3.1.54	Precorrin-6A reductase.	Tfu_0310	Tfu_0310 precorrin-6x reductase CbiJ/CobK					14.55	
EC	1.3.1.76	Precorrin-2 dehydrogenase.	Tfu_2221	Tfu_2221 uroporphyrin-III C-methyltransferase, C-terminal:Siroheme synthase, N-terminal	17.11	16.52	17.24	16.23	21.37	0.99
EC	1.3.1.9	Enoyl-[acyl-carrier-protein] reductase (NADH).	Tfu_1842	Tfu_1842 enoyl-(acyl carrier protein) reductase	20.49	19.93	21.16	21.07	24.76	1.053
EC	1.3.3.4	Protoporphyrinogen oxidase.	Tfu_1897	Tfu_1897 protoporphyrinogen oxidase			14.61		20.74	1.244
EC	1.3.3.6	Acyl-CoA oxidase.	Tfu_2239	Tfu_2239 hypothetical protein	17.58	17.57	18.21	17.62	22.75	0.874
EC	1.3.5.3	Protoporphyrinogen IX dehydrogenase (menaquinone).	Tfu_3023	Tfu_3023 similar to Flavodoxin						
EC	1.3.8.1	Butyryl-CoA dehydrogenase.	Tfu_0946	Tfu_0946 putative acyl-CoA dehydrogenase	20.62	20.44	21.21	21.21	24.67	0.91
EC	1.3.8.1	Butyryl-CoA dehydrogenase.	Tfu_1281	Tfu_1281 butyryl-CoA dehydrogenase						
EC	1.3.98.1	Dihydroorotate oxidase (fumarate).	Tfu_0927	Tfu_0927 dihydroorotate dehydrogenase	17.12	17.21	17.52	17.43	21.74	
EC	1.3.98.1	Dihydroorotate oxidase (fumarate).	Tfu_1059	Tfu_1059 dihydroorotate dehydrogenase 1						
EC	1.3.98.1	Dihydroorotate oxidase (fumarate).	Tfu_2378	Tfu_2378 hypothetical protein					16.58	
EC	1.3.99.1	Succinate dehydrogenase.	Tfu_2451	Tfu_2451 succinate dehydrogenase	19.35	19.39	20.29	20.56	23.66	1.002
EC	1.3.99.1	Succinate dehydrogenase.	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
EC	1.3.99.22	Coproporphyrinogen dehydrogenase.	Tfu_0739	Tfu_0739 coproporphyrinogen III oxidase						
EC	1.3.99.22	Coproporphyrinogen dehydrogenase.	Tfu_0835	Tfu_0835 putative oxygen-independent coproporphyrinogen III oxidase						
EC	1.3.99.3	Acyl-CoA dehydrogenase.	Tfu_1282	Tfu_1282 putative acyl-CoA dehydrogenase					18.17	
EC	1.3.99.3	Acyl-CoA dehydrogenase.	Tfu_1284	Tfu_1284 putative acyl-CoA dehydrogenase						
EC	1.3.99.3	Acyl-CoA dehydrogenase.	Tfu_1512	Tfu_1512 putative acyl-CoA dehydrogenase	14.16	14.11		14.03	20.64	
EC	1.3.99.3	Acyl-CoA dehydrogenase.	Tfu_1647	Tfu_1647 acyl-CoA dehydrogenase	19.93	19.53	19.07	19.09	22.67	1.416
EC	1.3.99.3	Acyl-CoA dehydrogenase.	Tfu_1999	Tfu_1999 acyl-CoA dehydrogenase						
EC	1.3.99.3	Acyl-CoA dehydrogenase.	Tfu_2485	Tfu_2485 acyl-CoA dehydrogenase	14.3		15.52	15.96	21.16	
EC	1.3.99.7	Glutaryl-CoA dehydrogenase.	Tfu_1068	Tfu_1068 glutaryl-CoA dehydrogenase	15.85	16.25	15.59	15.48	20.62	0.775
EC	1.4.1.1	Alanine dehydrogenase.	Tfu_0961	Tfu_0961 alanine dehydrogenase and pyridine nucleotide transhydrogenase			19.5	19.59	23.05	1.544
EC	1.4.1.13	Glutamate synthase (NADPH).	Tfu_1173	Tfu_1173 glutamate synthase (ferredoxin)					19.09	
EC	1.4.1.13	Glutamate synthase (NADPH).	Tfu_1174	Tfu_1174 glutamate synthase, NADH/NADPH, small subunit 1						
EC	1.4.1.14	Glutamate synthase (NADH).	Tfu_1173	Tfu_1173 glutamate synthase (ferredoxin)					19.09	
EC	1.4.1.14	Glutamate synthase (NADH).	Tfu_1174	Tfu_1174 glutamate synthase, NADH/NADPH, small subunit 1						
EC	1.4.1.2	Glutamate dehydrogenase.	Tfu_2481	Tfu_2481 putative NAD-glutamate dehydrogenase	20.96	20.83	21.88	21.73	25.49	1.153
EC	1.4.1.4	Glutamate dehydrogenase (NADP(+)).	Tfu_1371	Tfu_1371 glutamate dehydrogenase	13.87		17.06	16.78	21.17	1.233
EC	1.4.3.16	L-aspartate oxidase.	Tfu_2883	Tfu_2883 L-aspartate oxidase			15.62	16.95	20.84	
EC	1.4.3.19	Glycine oxidase.	Tfu_1044	Tfu_1044 thiamine biosynthesis oxidoreductase ThiO	14.05				17.56	0.833
EC	1.4.3.5	Pyridoxal 5'-phosphate synthase.	Tfu_0248	Tfu_0248 pyridoxamine 5'-phosphate oxidase	15.34	14.98		14.89	18.71	
EC	1.4.4.2	Glycine dehydrogenase (decarboxylating).	Tfu_1398	Tfu_1398 glycine dehydrogenase	19.26	19.25	19.62	19.33	23.73	1.358
EC	1.4.99.1	D-amino-acid dehydrogenase.	Tfu_2797	Tfu_2797 d-amino-acid dehydrogenase	19.11	19.07	21.99	22	24.93	1.927
EC	1.5.1.12	1-pyrroline-5-carboxylate dehydrogenase.	Tfu_0433	Tfu_0433 delta-1-pyrroline-5-carboxylate dehydrogenase 1	20.87	20.52	20.5	20.22	24.05	1.051
EC	1.5.1.2	Pyrroline-5-carboxylate reductase.	Tfu_2708	Tfu_2708 delta 1-pyrroline-5-carboxylate reductase	17.73	17.16	18.03	17.57	21.11	
EC	1.5.1.20	Methylenetetrahydrofolate reductase (NAD(P)H).	Tfu_1050	Tfu_1050 5,10-methylenetetrahydrofolate reductase						
EC	1.5.1.5	Methylenetetrahydrofolate dehydrogenase (NADP(+)).	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
EC	1.5.99.8	Proline dehydrogenase.	Tfu_0434	Tfu_0434 proline dehydrogenase	18.28	18.4	17.73	16.85	22.15	1.304
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2682	Tfu_2682 NADH dehydrogenase subunit N	15.55	15.11	17.89	15.78	21.55	1.549
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2683	Tfu_2683 NADH dehydrogenase subunit M	15.96	15.61	18.67	18.21	22.04	1.217
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2684	Tfu_2684 NADH dehydrogenase subunit L	16.72	16.18	19.09	19.32	22.49	1.313

EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2685	Tfu_2685 NADH dehydrogenase kappa subunit	15.96	16.12	17.42	17.06	21.01	1.226
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2686	Tfu_2686 NADH dehydrogenase subunit J	14.57		19.26	18.19	22.25	
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2687	Tfu_2687 NADH-quinone oxidoreductase, chain I	17.42	17.05	19.49	19.25	23.17	1.344
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2688	Tfu_2688 NADH dehydrogenase subunit H	16.85	15.81	18.1	18.62	22.74	1.366
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2689	Tfu_2689 NADH dehydrogenase gamma subunit	19.85	19.4	22.2	22.17	25.89	1.474
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2690	Tfu_2690 NADH-quinone oxidoreductase, F subunit	18.4	18.59	21.04	20.94	24.09	1.696
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2691	Tfu_2691 ATP synthase subunit E	18.11	17.48	19.19	19.38	23.19	
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2692	Tfu_2692 NADH dehydrogenase delta subunit	17.85	17.37	21.19	20.56	24.79	1.513
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2693	Tfu_2693 NADH dehydrogenase subunit C	17.89	18.01	20.34	20.17	23.82	1.361
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2694	Tfu_2694 NADH dehydrogenase beta subunit	17.52	17.43	19.51	19.02	23.25	1.847
EC	1.6.5.3	NADH:ubiquinone reductase (H(+)-translocating).	Tfu_2695	Tfu_2695 NADH dehydrogenase alpha subunit	15.61	15.66	16.21	16.57	20.39	
EC	1.6.5.5	NADPH:quinone reductase.	Tfu_0360	Tfu_0360 putative oxidoreductase					16.95	
EC	1.6.5.5	NADPH:quinone reductase.	Tfu_2228	Tfu_2228 putative quinone oxidoreductase	18.91	19.37	18.34	18.58	21.72	0.952
EC	1.6.99.3	NADH dehydrogenase.	Tfu_0432	Tfu_0432 NADH dehydrogenase					14.78	
EC	1.6.99.3	NADH dehydrogenase.	Tfu_0950	Tfu_0950 NADH dehydrogenase	16.94	16.44	15.12	16.14	21.41	
EC	1.7.2.1	Nitrite reductase (NO-forming).	Tfu_2794	Tfu_2794 hypothetical protein						
EC	1.7.2.3	Trimethylamine-N-oxide reductase (cytochrome c).	Tfu_0340	Tfu_0340 trimethylamine-N-oxide reductase (cytochrome c)	16.72	15.79	15.16		21.33	
EC	1.7.7.1	Ferredoxin--nitrite reductase.	Tfu_1888	Tfu_1888 putative nitrite/sulphite reductase	16.01	13.98	17.79	17.82	22.36	1.384
EC	1.8.1.4	Dihydrolipoyl dehydrogenase.	Tfu_0994	Tfu_0994 dihydrolipoamide dehydrogenase	23.87	23.67	23.96	23.71	27.03	1.154
EC	1.8.1.4	Dihydrolipoyl dehydrogenase.	Tfu_2559	Tfu_2559 dihydrolipoamide dehydrogenase	17.62	17.97	18.6	18.7	23.28	1.063
EC	1.8.1.9	Thioredoxin-disulfide reductase.	Tfu_3108	Tfu_3108 thioredoxin reductase	16.25	15.17	16.88	17.34	22.36	1.054
EC	1.8.4.11	Peptide-methionine (S)-S-oxide reductase.	Tfu_2678	Tfu_2678 methionine sulfoxide reductase A					16.73	
EC	1.8.4.12	Peptide-methionine (R)-S-oxide reductase.	Tfu_1893	Tfu_1893 methionine sulfoxide reductase B	15.65	15.39		14.71	18.99	
EC	1.8.4.8	Phosphoadenylyl-sulfate reductase (thioredoxin).	Tfu_1889	Tfu_1889 phosphoadenosine phosphosulfate reductase						
EC	1.8.7.1	Sulfite reductase (ferredoxin).	Tfu_1888	Tfu_1888 putative nitrite/sulphite reductase	16.01	13.98	17.79	17.82	22.36	1.384
EC	1.9.3.1	Cytochrome-c oxidase.	Tfu_0881	Tfu_0881 cytochrome-c oxidase			17.98	18.28	22.45	
EC	1.9.3.1	Cytochrome-c oxidase.	Tfu_1015	Tfu_1015 hypothetical protein	20.5	19.96	19.7	20.09	23.2	1.256
EC	1.9.3.1	Cytochrome-c oxidase.	Tfu_1016	Tfu_1016 cytochrome-c oxidase					20.91	1.146
EC	1.9.3.1	Cytochrome-c oxidase.	Tfu_1022	Tfu_1022 cytochrome c oxidase subunit III						
EC	1.9.3.1	Cytochrome-c oxidase.	Tfu_1695	Tfu_1695 cytochrome-c oxidase						
EC	2.-	Transferases.	Tfu_0538	Tfu_0538 molybdenum cofactor biosynthesis protein E					15.59	
EC	2.1.1.-	Transferases. Transferring one-carbon groups. Methyltr	Tfu_1089	Tfu_1089 hypothetical protein						
EC	2.1.1.-	Transferases. Transferring one-carbon groups. Methyltr	Tfu_2418	Tfu_2418 modification methylase HemK						
EC	2.1.1.104	Caffeoyl-CoA O-methyltransferase.	Tfu_0966	Tfu_0966 caffeoyl-CoA O-methyltransferase		13.62			16.15	
EC	2.1.1.107	Uroporphyrinogen-III C-methyltransferase.	Tfu_2221	Tfu_2221 uroporphyrin-III C-methyltransferase, C-terminal:Siroheme synthase, N-terminal	17.11	16.52	17.24	16.23	21.37	0.99
EC	2.1.1.107	Uroporphyrinogen-III C-methyltransferase.	Tfu_2731	Tfu_2731 putative uroporphyrin-III C-methyltransferase/uroporphyrinogen-III synthase	19.75	19.58	19.91	19.51	24.15	1.231
EC	2.1.1.13	Methionine synthase.	Tfu_1825	Tfu_1825 5-methyltetrahydrofolate--homocysteine methyltransferase					15.39	
EC	2.1.1.130	Precorrin-2 C(20)-methyltransferase.	Tfu_0316	Tfu_0316 precorrin-3B C17-methyltransferase region:Precorrin-2 C20-methyltransferase						
EC	2.1.1.131	Precorrin-3B C(17)-methyltransferase.	Tfu_0316	Tfu_0316 precorrin-3B C17-methyltransferase region:Precorrin-2 C20-methyltransferase						
EC	2.1.1.132	Precorrin-6Y C(5,15)-methyltransferase (decarboxylati	Tfu_0314	Tfu_0314 SAM (and some other nucleotide) binding motif						
EC	2.1.1.133	Precorrin-4 C(11)-methyltransferase.	Tfu_0315	Tfu_0315 precorrin-4 C11-methyltransferase region					19.46	0.814
EC	2.1.1.148	Thymidylate synthase (FAD).	Tfu_1387	Tfu_1387 thymidylate synthase complementing protein ThyX			16.01	15.73	20.7	0.764
EC	2.1.1.152	Precorrin-6A synthase (deacetylating).	Tfu_0320	Tfu_0320 putative cobF protein, precorrin-6A synthase						
EC	2.1.1.163	Demethylmenaquinone methyltransferase.	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
EC	2.1.1.17	Phosphatidylethanolamine N-methyltransferase.	Tfu_0735	Tfu_0735 ubiquinone/menaquinone biosynthesis methyltransferase						
EC	2.1.1.170	16S rRNA (guanine(527)-N(7))-methyltransferase.	Tfu_3112	Tfu_3112 glucose-inhibited division protein B					18.58	
EC	2.1.1.172	16S rRNA (guanine(1207)-N(2))-methyltransferase.	Tfu_1683	Tfu_1683 hypothetical protein						
EC	2.1.1.176	16S rRNA (cytosine(967)-C(5))-methyltransferase.	Tfu_1076	Tfu_1076 putative RNA-binding Sun protein					19.48	0.765
EC	2.1.1.182	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-d	Tfu_0405	Tfu_0405 dimethyladenosine transferase	13.75	15.29		12.82	19.01	
EC	2.1.1.185	23S rRNA (guanine(2251)-2'-O)-methyltransferase.	Tfu_0213	Tfu_0213 RNA methyltransferase TrmH, group 3	14.34	15.23	17.16	16.99	21.69	0.777
EC	2.1.1.187	23S rRNA (guanine(745)-N(1))-methyltransferase.	Tfu_1634	Tfu_1634 putative ribosomal RNA methyltransferase						

EC	2.1.1.192	23S rRNA (adenine(2503)-C(2))-methyltransferase.	Tfu_0683	Tfu_0683 Conserved hypothetical protein 48						
EC	2.1.1.193	16S rRNA (uracil(1498)-N(3))-methyltransferase.	Tfu_0840	Tfu_0840 Conserved hypothetical protein 46					18.56	
EC	2.1.1.198	16S rRNA (cytidine(1402)-2'-O)-methyltransferase.	Tfu_0386	Tfu_0386 hypothetical protein					18.93	
EC	2.1.1.199	16S rRNA (cytosine(1402)-N(4))-methyltransferase.	Tfu_1102	Tfu_1102 bacterial methyltransferase	16.91	16.77	14.4		20.21	0.758
EC	2.1.1.201	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase.	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
EC	2.1.1.34	tRNA guanosine-2'-O-methyltransferase.	Tfu_1684	Tfu_1684 probable tRNA/rRNA methyltransferase					18.25	
EC	2.1.1.63	Methylated-DNA--[protein]-cysteine S-methyltransferas	Tfu_0366	Tfu_0366 methylated-DNA (protein)-cysteine S-methyltransferase						
EC	2.1.1.71	Phosphatidyl-N-methylethanolamine N-methyltransfera	Tfu_0735	Tfu_0735 ubiquinone/menaquinone biosynthesis methyltransferase						
EC	2.1.1.77	Protein-L-isoaspartate(D-aspartate) O-methyltransferas	Tfu_1808	Tfu_1808 putative methyltransferase					14.61	
EC	2.1.1.79	Cyclopropane-fatty-acyl-phospholipid synthase.	Tfu_2160	Tfu_2160 putative cyclopropane fatty acid synthase	20.23	19.76	18.57	18.29	22.69	1.518
EC	2.1.2.1	Glycine hydroxymethyltransferase.	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
EC	2.1.2.10	Aminomethyltransferase.	Tfu_2351	Tfu_2351 aminomethyltransferase	17.24	17.22	16.2	16.08	20.82	0.867
EC	2.1.2.11	3-methyl-2-oxobutanoate hydroxymethyltransferase.	Tfu_0981	Tfu_0981 3-methyl-2-oxobutanoate hydroxymethyltransferase	18.23	17.36	19.12	19.31	23.68	0.787
EC	2.1.2.2	Phosphoribosylglycinamide formyltransferase.	Tfu_2573	Tfu_2573 phosphoribosylglycinamide formyltransferase	14.49	14.7	17.07	16.78	21.38	
EC	2.1.2.3	Phosphoribosylaminoimidazolecarboxamide formyltran	Tfu_2572	Tfu_2572 bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohy	19.86	19.04	20.76	20.79	24.53	0.912
EC	2.1.2.9	Methionyl-tRNA formyltransferase.	Tfu_1075	Tfu_1075 methionyl-tRNA formyltransferase	18.3	17.78	18.03	17.53	22.14	1.153
EC	2.1.3.2	Aspartate carbamoyltransferase.	Tfu_1054	Tfu_1054 aspartate carbamoyltransferase catalytic subunit					19.72	1.183
EC	2.1.3.3	Ornithine carbamoyltransferase.	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
EC	2.2.1.1	Transketolase.	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
EC	2.2.1.2	Transaldolase.	Tfu_2003	Tfu_2003 transaldolase	20.04	20.08	21.54	21.1	24.47	1.211
EC	2.2.1.6	Acetolactate synthase.	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
EC	2.2.1.6	Acetolactate synthase.	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	
EC	2.2.1.6	Acetolactate synthase.	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
EC	2.2.1.7	1-deoxy-D-xylulose-5-phosphate synthase.	Tfu_1917	Tfu_1917 1-deoxy-D-xylulose-5-phosphate synthase					16.98	
EC	2.2.1.9	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-c	Tfu_1411	Tfu_1411 Menaquinone biosynthesis protein					16.81	
EC	2.3.1.-	Transferases. Acyltransferases. Transferring groups oth	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
EC	2.3.1.-	Transferases. Acyltransferases. Transferring groups oth	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
EC	2.3.1.-	Transferases. Acyltransferases. Transferring groups oth	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
EC	2.3.1.-	Transferases. Acyltransferases. Transferring groups oth	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
EC	2.3.1.1	Amino-acid N-acetyltransferase.	Tfu_2056	Tfu_2056 bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	17.05	16.43	18.49	17.65	22.7	
EC	2.3.1.1	Amino-acid N-acetyltransferase.	Tfu_2879	Tfu_2879 hypothetical protein	13.85	13.58			19.82	
EC	2.3.1.117	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succiny	Tfu_0494	Tfu_0494 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	20.98	20.36	20.57	20.17	24.7	0.791
EC	2.3.1.12	Dihydrolipoyllysine-residue acetyltransferase.	Tfu_0182	Tfu_0182 putative dihydrolipoamide acyltransferase component	22.33	22.24	22.85	22.66	25.78	1.092
EC	2.3.1.12	Dihydrolipoyllysine-residue acetyltransferase.	Tfu_3051	Tfu_3051 pyruvate dehydrogenase complex, E2 component, dihydrolipoamide acetyltransferase	21.68	21.7	22.67	22.41	25.66	1.062
EC	2.3.1.128	Ribosomal-protein-alanine N-acetyltransferase.	Tfu_0377	Tfu_0377 ribosomal-protein-alanine N-acetyltransferase						
EC	2.3.1.128	Ribosomal-protein-alanine N-acetyltransferase.	Tfu_2603	Tfu_2603 Ribosomal-protein-alanine acetyltransferase		13.04		14.23	19.75	
EC	2.3.1.15	Glycerol-3-phosphate O-acyltransferase.	Tfu_0271	Tfu_0271 Fatty acid synthesis plsX protein		15.01			17.65	
EC	2.3.1.157	Glucosamine-1-phosphate N-acetyltransferase.	Tfu_0414	Tfu_0414 UDP-N-acetylglucosamine pyrophosphorylase	19.4	19.37	19.9	19.97	23.72	1.114
EC	2.3.1.16	Acetyl-CoA C-acyltransferase.	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
EC	2.3.1.16	Acetyl-CoA C-acyltransferase.	Tfu_1278	Tfu_1278 thiolase						
EC	2.3.1.16	Acetyl-CoA C-acyltransferase.	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
EC	2.3.1.178	Diaminobutyrate acetyltransferase.	Tfu_0300	Tfu_0300 putative acetyltransferase						
EC	2.3.1.179	Beta-ketoacyl-acyl-carrier-protein synthase II.	Tfu_1976	Tfu_1976 putative 3-oxoacyl-ACP synthase II	18.39	18.02	19.63	19.4	22.79	0.718
EC	2.3.1.180	Beta-ketoacyl-acyl-carrier-protein synthase III.	Tfu_1229	Tfu_1229 putative 3-oxoacyl-ACP synthase III						
EC	2.3.1.180	Beta-ketoacyl-acyl-carrier-protein synthase III.	Tfu_1974	Tfu_1974 3-oxoacyl-(acyl carrier protein) synthase	14.7	15.5	19.86	19.55	23.27	0.869
EC	2.3.1.181	Lipoyl(octanoyl) transferase.	Tfu_0992	Tfu_0992 lipoyltransferase					18.24	
EC	2.3.1.189	Mycothiol synthase.	Tfu_2739	Tfu_2739 putative acetyltransferase	18.06	18.1	17.74	17.44	21.61	
EC	2.3.1.31	Homoserine O-acetyltransferase.	Tfu_2822	Tfu_2822 homoserine O-acetyltransferase	15.5	15.63		15.19	19.08	
EC	2.3.1.35	Glutamate N-acetyltransferase.	Tfu_2056	Tfu_2056 bifunctional ornithine acetyltransferase/N-acetylglutamate synthase protein	17.05	16.43	18.49	17.65	22.7	
EC	2.3.1.39	[Acyl-carrier-protein] S-malonyltransferase.	Tfu_1973	Tfu_1973 acyl-carrier-protein S-malonyltransferase	18.46	18.27	20.02	20.23	23.66	0.61
EC	2.3.1.51	1-acylglycerol-3-phosphate O-acyltransferase.	Tfu_1036	Tfu_1036 phospholipid/glycerol acyltransferase	18.2	17.54	17.83	17.5	21.56	

EC	2.3.1.51	1-acylglycerol-3-phosphate O-acyltransferase.	Tfu_1417	Tfu_1417 phospholipid/glycerol acyltransferase	13.91	13.6		12.45	17.58	
EC	2.3.1.61	Dihydrolipoyllysine-residue succinyltransferase.	Tfu_0993	Tfu_0993 dihydrolipoamide S-succinyltransferase	21.69	21.57	21.99	21.46	25.01	1.46
EC	2.3.1.79	Maltose O-acetyltransferase.	Tfu_1260	Tfu_1260 maltose O-acetyltransferase	17.34	17.54		16.06	20.06	
EC	2.3.1.9	Acetyl-CoA C-acetyltransferase.	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
EC	2.3.1.9	Acetyl-CoA C-acetyltransferase.	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
EC	2.3.1.9	Acetyl-CoA C-acetyltransferase.	Tfu_1520	Tfu_1520 thiolase					15.67	
EC	2.3.1.9	Acetyl-CoA C-acetyltransferase.	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
EC	2.3.3.1	Citrate (Si)-synthase.	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
EC	2.3.3.13	2-isopropylmalate synthase.	Tfu_0617	Tfu_0617 2-isopropylmalate synthase	16.51	16.22	15.8	13.84	20.9	
EC	2.3.3.13	2-isopropylmalate synthase.	Tfu_0850	Tfu_0850 2-isopropylmalate synthase	16.67	16.9	16.57	16.17	21.98	
EC	2.3.3.9	Malate synthase.	Tfu_0819	Tfu_0819 malate synthase	20.71	20.65	20.77	20.84	24.52	0.986
EC	2.4.1.-	Transferases. Glycosyltransferases. Hexosyltransferases	Tfu_1730	Tfu_1730 hypothetical protein						
EC	2.4.1.-	Transferases. Glycosyltransferases. Hexosyltransferases	Tfu_1732	Tfu_1732 hypothetical protein						
EC	2.4.1.-	Transferases. Glycosyltransferases. Hexosyltransferases	Tfu_1764	Tfu_1764 putative glycosyl transferase						
EC	2.4.1.1	Phosphorylase.	Tfu_0586	Tfu_0586 alpha-glucan phosphorylase					15.86	
EC	2.4.1.129	Peptidoglycan glycosyltransferase.	Tfu_1104	Tfu_1104 peptidoglycan glycosyltransferase						
EC	2.4.1.129	Peptidoglycan glycosyltransferase.	Tfu_3064	Tfu_3064 hypothetical protein	17.05	16.02	15.7	15.59	20.75	
EC	2.4.1.15	Alpha,alpha-trehalose-phosphate synthase (UDP-formin	Tfu_0225	Tfu_0225 alpha,alpha-trehalose-phosphate synthase (UDP-forming)	19.68	19.62	20.81	20.85	24.46	1.199
EC	2.4.1.18	1,4-alpha-glucan branching enzyme.	Tfu_0582	Tfu_0582 1,4-alpha-glucan branching enzyme					16.55	
EC	2.4.1.227	Undecaprenyldiphospho-muramoylpentapeptide beta-N	Tfu_1110	Tfu_1110 N-acetylglucosaminyl transferase	19.15	18.71	18.79	18.53	22.9	0.735
EC	2.4.1.25	4-alpha-glucanotransferase.	Tfu_2205	Tfu_2205 glycoside hydrolase, family 77					15.25	
EC	2.4.1.250	D-inositol-3-phosphate glycosyltransferase.	Tfu_2913	Tfu_2913 putative glycosyltransferase						
EC	2.4.1.57	Phosphatidylinositol alpha-mannosyltransferase.	Tfu_2101	Tfu_2101 phosphatidyl-myo-inositol alpha-mannosyltransferase						
EC	2.4.1.83	Dolichyl-phosphate beta-D-mannosyltransferase.	Tfu_1850	Tfu_1850 dolichyl-phosphate beta-D-mannosyltransferase	17.8	17.7	16.81	17.93	21.31	0.842
EC	2.4.2.-	Transferases. Glycosyltransferases. Pentosyltransferase	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
EC	2.4.2.1	Purine-nucleoside phosphorylase.	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
EC	2.4.2.10	Orotate phosphoribosyltransferase.	Tfu_3008	Tfu_3008 orotate phosphoribosyltransferase	17.41	17.4	17.96	17.05	22.2	0.852
EC	2.4.2.11	Nicotinate phosphoribosyltransferase.	Tfu_2373	Tfu_2373 nicotinate phosphoribosyltransferase	14.96		15.9	12.14	20.35	
EC	2.4.2.14	Amidophosphoribosyltransferase.	Tfu_2747	Tfu_2747 amidophosphoribosyltransferase						
EC	2.4.2.17	ATP phosphoribosyltransferase.	Tfu_0174	Tfu_0174 ATP phosphoribosyltransferase	19.33	18.84	19.91	18.99	23.24	1.037
EC	2.4.2.18	Anthranilate phosphoribosyltransferase.	Tfu_1024	Tfu_1024 anthranilate phosphoribosyltransferase						
EC	2.4.2.19	Nicotinate-nucleotide diphosphorylase (carboxylating).	Tfu_2883	Tfu_2883 L-aspartate oxidase			15.62	16.95	20.84	
EC	2.4.2.21	Nicotinate-nucleotide--dimethylbenzimidazole phospho	Tfu_2222	Tfu_2222 nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase subtype	15.06		15.97	15.99	20.79	0.7
EC	2.4.2.7	Adenine phosphoribosyltransferase.	Tfu_2091	Tfu_2091 adenine phosphoribosyltransferase		14.26			19.51	0.761
EC	2.4.2.8	Hypoxanthine phosphoribosyltransferase.	Tfu_2896	Tfu_2896 hypoxanthine phosphoribosyl transferase		16.7	16.94	16.58	21.76	0.668
EC	2.4.2.9	Uracil phosphoribosyltransferase.	Tfu_1053	Tfu_1053 pyrimidine regulatory protein PyrR	17.14	17.38	18.18	18.29	22.2	0.824
EC	2.5.1.-	Transferases. Transferring alkyl or aryl groups, other th	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
EC	2.5.1.-	Transferases. Transferring alkyl or aryl groups, other th	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
EC	2.5.1.-	Transferases. Transferring alkyl or aryl groups, other th	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
EC	2.5.1.1	Dimethylallyltranstransferase.	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
EC	2.5.1.10	(2E,6E)-farnesyl diphosphate synthase.	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
EC	2.5.1.15	Dihydropteroate synthase.	Tfu_1314	Tfu_1314 dihydropteroate synthase	16.71	16.84	17.22	16.91	22.57	1.071
EC	2.5.1.15	Dihydropteroate synthase.	Tfu_2893	Tfu_2893 dihydropteroate synthase	18.01	17.46	18.35	17.82	21.56	1.133
EC	2.5.1.16	Spermidine synthase.	Tfu_2234	Tfu_2234 spermidine synthase						
EC	2.5.1.17	Cob(I)yrinic acid a,c-diamide adenosyltransferase.	Tfu_0312	Tfu_0312 cob(I)yrinic acid a,c-diamide adenosyltransferase					16.96	
EC	2.5.1.19	3-phosphoshikimate 1-carboxyvinyltransferase.	Tfu_0544	Tfu_0544 3-phosphoshikimate 1-carboxyvinyltransferase						
EC	2.5.1.29	Farnesyltranstransferase.	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
EC	2.5.1.3	Thiamine-phosphate diphosphorylase.	Tfu_1046	Tfu_1046 thiamine-phosphate pyrophosphorylase		14.35			19.31	
EC	2.5.1.30	Heptaprenyl diphosphate synthase.	Tfu_2681	Tfu_2681 trans-hexaprenyltranstransferase					20.84	0.581
EC	2.5.1.31	Di-trans,poly-cis-undecaprenyl-diphosphate synthase ((	Tfu_0853	Tfu_0853 di-trans-poly-cis-decaprenylcistransferase	16.33	16.31	16	16.58	20.43	0.931
EC	2.5.1.32	Phytoene synthase.	Tfu_3076	Tfu_3076 putative phytoene synthase						

EC	2.5.1.47	Cysteine synthase.	Tfu_2368	Tfu_2368 cysteine synthase K/M		14.5	14.44		19.69	
EC	2.5.1.48	Cystathionine gamma-synthase.	Tfu_0440	Tfu_0440 cystathionine gamma-synthase					17.4	
EC	2.5.1.48	Cystathionine gamma-synthase.	Tfu_0632	Tfu_0632 cystathionine gamma-synthase					15.55	0.471
EC	2.5.1.49	O-acetylhomoserine aminocarboxypropyltransferase.	Tfu_2823	Tfu_2823 O-acetylhomoserine sulfhydrylase	22.33	21.67	21.43	21.62	25.14	0.779
EC	2.5.1.54	3-deoxy-7-phosphoheptulonate synthase.	Tfu_1039	Tfu_1039 phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 2						
EC	2.5.1.54	3-deoxy-7-phosphoheptulonate synthase.	Tfu_2350	Tfu_2350 phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1			14.88	13.66	19.21	
EC	2.5.1.56	N-acetylneuraminate synthase.	Tfu_0010	Tfu_0010 n-acetylneuraminate synthase						
EC	2.5.1.6	Methionine adenosyltransferase.	Tfu_1065	Tfu_1065 S-adenosylmethionine synthetase	15.28	15.32	15.74	16.4	20.99	0.962
EC	2.5.1.61	Hydroxymethylbilane synthase.	Tfu_2732	Tfu_2732 porphobilinogen deaminase	13.44				19.8	
EC	2.5.1.68	(2Z,6E)-farnesyl diphosphate synthase.	Tfu_0456	Tfu_0456 di-trans-poly-cis-decaprenylcistransferase					16.85	
EC	2.5.1.7	UDP-N-acetylglucosamine 1-carboxyvinyltransferase.	Tfu_3016	Tfu_3016 UDP-N-acetylglucosamine 1-carboxyvinyltransferase		14.48	17.9	17.73	22.19	1.204
EC	2.5.1.72	Quinolinate synthase.	Tfu_0575	Tfu_0575 quinolinate synthetase						
EC	2.5.1.74	1,4-dihydroxy-2-naphthoate polyprenyltransferase.	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
EC	2.5.1.75	tRNA dimethylallyltransferase.	Tfu_0815	Tfu_0815 tRNA delta(2)-isopentenylpyrophosphate transferase					18.28	
EC	2.5.1.78	6,7-dimethyl-8-ribityllumazine synthase.	Tfu_1081	Tfu_1081 6,7-dimethyl-8-ribityllumazine synthase	15.97	15.69	16.33	16.62	21.62	
EC	2.5.1.9	Riboflavin synthase.	Tfu_1078	Tfu_1078 Lumazine-binding protein		13.92	16.4	17.05	20.31	
EC	2.6.-	Transferases. Transferring nitrogenous groups.	Tfu_2097	Tfu_2097 putative glutamine amidotransferase					15.71	
EC	2.6.1.11	Acetylornithine transaminase.	Tfu_2054	Tfu_2054 acetylornithine and succinylornithine aminotransferase	16.33	18.16	18.68	18.83	22.2	1.056
EC	2.6.1.13	Ornithine aminotransferase.	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
EC	2.6.1.16	Glutamine--fructose-6-phosphate transaminase (isomer	Tfu_2611	Tfu_2611 D-fructose-6-phosphate amidotransferase	16.46	16.09	18.53	18.54	22.75	1.101
EC	2.6.1.17	Succinyldiaminopimelate transaminase.	Tfu_0568	Tfu_0568 hypothetical protein					18.2	
EC	2.6.1.19	4-aminobutyrate transaminase.	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
EC	2.6.1.22	(S)-3-amino-2-methylpropionate transaminase.	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
EC	2.6.1.42	Branched-chain-amino-acid transaminase.	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
EC	2.6.1.42	Branched-chain-amino-acid transaminase.	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
EC	2.6.1.52	Phosphoserine transaminase.	Tfu_0246	Tfu_0246 phosphoserine aminotransferase	19.59	19.46	22.48	21.91	25.76	1.096
EC	2.6.1.76	Diaminobutyrate--2-oxoglutarate transaminase.	Tfu_0301	Tfu_0301 diaminobutyrate--2-oxoglutarate aminotransferase						
EC	2.6.1.85	Aminodeoxychorismate synthase.	Tfu_1666	Tfu_1666 para-aminobenzoate synthase, component I:Glutamine amidotransferase of anthranilate synthase						
EC	2.6.1.9	Histidinol-phosphate transaminase.	Tfu_1151	Tfu_1151 histidinol-phosphate aminotransferase					19.66	1.354
EC	2.6.1.9	Histidinol-phosphate transaminase.	Tfu_2223	Tfu_2223 putative aminotransferase					16.25	
EC	2.6.1.9	Histidinol-phosphate transaminase.	Tfu_3018	Tfu_3018 putative aminotransferase					19.29	1.473
EC	2.7.-	Transferases. Transferring phosphorous-containing gro	Tfu_2763	Tfu_2763 arginine/ornithine transport system ATPase	16.2	15.51	14.39	14.55	18.73	
EC	2.7.1.12	Gluconokinase.	Tfu_2114	Tfu_2114 carbohydrate kinase, thermoresistant glucokinase	15.34		15.45	14.87	18.89	
EC	2.7.1.148	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kina	Tfu_0407	Tfu_0407 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase					17.64	
EC	2.7.1.15	Ribokinase.	Tfu_0259	Tfu_0259 ribokinase, bacterial					17.88	
EC	2.7.1.156	Adenosylcobinamide kinase.	Tfu_0997	Tfu_0997 adenosylcobinamide kinase / adenosylcobinamide-phosphate guanylyltransferase		15.35		15.47	20.21	
EC	2.7.1.17	Xylulokinase.	Tfu_1575	Tfu_1575 putative sugar kinase protein						
EC	2.7.1.17	Xylulokinase.	Tfu_1604	Tfu_1604 xylulokinase	16.69	16.85	17.01	17.12	22.06	
EC	2.7.1.2	Glucokinase.	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
EC	2.7.1.2	Glucokinase.	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
EC	2.7.1.20	Adenosine kinase.	Tfu_1012	Tfu_1012 putative carbohydrate kinase				14.19	20.45	
EC	2.7.1.23	NAD(+) kinase.	Tfu_2033	Tfu_2033 inorganic polyphosphate/ATP-NAD kinase	16.3	16.08	15.21	15.52	19.8	
EC	2.7.1.24	Dephospho-CoA kinase.	Tfu_1192	Tfu_1192 dephospho-CoA kinase	17.51	17.36	16.73	16.92	20.12	
EC	2.7.1.26	Riboflavin kinase.	Tfu_0782	Tfu_0782 Cytidyltransferase-related		13.35	14.92	14.18	20.03	
EC	2.7.1.29	Glycerone kinase.	Tfu_1716	Tfu_1716 glycerone kinase	16	15.49	13.71		18.65	
EC	2.7.1.30	Glycerol kinase.	Tfu_0787	Tfu_0787 glycerol kinase	18.54	18.3	17.06	16.96	21.42	0.925
EC	2.7.1.31	Glycerate kinase.	Tfu_1010	Tfu_1010 glycerate kinase			14.48		20.4	
EC	2.7.1.33	Pantothenate kinase.	Tfu_2610	Tfu_2610 pantothenate kinase			14.28		19	
EC	2.7.1.33	Pantothenate kinase.	Tfu_2882	Tfu_2882 Bvg accessory factor	15.79	15.26	16.09	15.65	20.23	
EC	2.7.1.39	Homoserine kinase.	Tfu_2422	Tfu_2422 homoserine kinase					19.33	0.823
EC	2.7.1.4	Fructokinase.	Tfu_0928	Tfu_0928 fructokinase	18.37	17.96	18.63	18.42	22.16	0.898

EC	2.7.1.40	Pyruvate kinase.	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
EC	2.7.1.45	2-dehydro-3-deoxygluconokinase.	Tfu_0189	Tfu_0189 putative PfkB-family carbohydrate kinase						
EC	2.7.1.49	Hydroxymethylpyrimidine kinase.	Tfu_2250	Tfu_2250 phosphomethylpyrimidine kinase	16.07	16.41	14.97		19.92	1.225
EC	2.7.1.56	1-phosphofructokinase.	Tfu_0696	Tfu_0696 putative 6-phosphofructokinase : 1-phosphofructokinase						
EC	2.7.1.6	Galactokinase.	Tfu_2566	Tfu_2566 galactokinase						
EC	2.7.1.63	Polyphosphate--glucose phosphotransferase.	Tfu_1811	Tfu_1811 polyphosphate glucokinase/transcriptional regulator						
EC	2.7.1.69	Protein-N(pi)-phosphohistidine--sugar phosphotransfer	Tfu_2489	Tfu_2489 putative phosphoenolpyruvate-dependent sugar phosphotransferase					16.36	
EC	2.7.1.71	Shikimate kinase.	Tfu_1091	Tfu_1091 shikimate kinase					19.23	
EC	2.7.1.90	Diphosphate--fructose-6-phosphate 1-phosphotransfera	Tfu_1037	Tfu_1037 phosphofructokinase	21.14	20.73	24.02	23.83	26.57	0.842
EC	2.7.11.1	Non-specific serine/threonine protein kinase.	Tfu_0177	Tfu_0177 hypothetical protein					15.64	
EC	2.7.11.1	Non-specific serine/threonine protein kinase.	Tfu_1041	Tfu_1041 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA		13.51			20.01	
EC	2.7.11.1	Non-specific serine/threonine protein kinase.	Tfu_1195	Tfu_1195 putative regulator					17.25	
EC	2.7.11.1	Non-specific serine/threonine protein kinase.	Tfu_3065	Tfu_3065 Tyrosine protein kinase:Serine/threonine protein kinase					18.02	
EC	2.7.11.1	Non-specific serine/threonine protein kinase.	Tfu_3066	Tfu_3066 Tyrosine protein kinase:Serine/threonine protein kinase:PASTA	19.07	19.31	18.37	17.91	22.14	0.98
EC	2.7.13.3	Histidine kinase.	Tfu_0256	Tfu_0256 hypothetical protein	15.31	14.78			18.74	
EC	2.7.13.3	Histidine kinase.	Tfu_0289	Tfu_0289 hypothetical protein						
EC	2.7.13.3	Histidine kinase.	Tfu_0344	Tfu_0344 signal transduction histidine kinase					18.04	
EC	2.7.13.3	Histidine kinase.	Tfu_2495	Tfu_2495 ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histidine kinase A, N-terminal					17.64	
EC	2.7.13.3	Histidine kinase.	Tfu_2857	Tfu_2857 ATP-binding region, ATPase-like					15.54	
EC	2.7.13.3	Histidine kinase.	Tfu_2909	Tfu_2909 ATP-binding region, ATPase-like:Histidine kinase A, N-terminal					18.74	
EC	2.7.2.1	Acetate kinase.	Tfu_2971	Tfu_2971 acetate kinase					13.64	
EC	2.7.2.11	Glutamate 5-kinase.	Tfu_2179	Tfu_2179 gamma-glutamyl kinase					17.69	
EC	2.7.2.3	Phosphoglycerate kinase.	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
EC	2.7.2.4	Aspartate kinase.	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
EC	2.7.2.8	Acetylglutamate kinase.	Tfu_2055	Tfu_2055 acetylglutamate kinase		13.89	16.85	16.6	21.88	1.485
EC	2.7.3.9	Phosphoenolpyruvate--protein phosphotransferase.	Tfu_2765	Tfu_2765 Phosphoenolpyruvate-protein phosphotransferase	14.84	14.48			19.67	
EC	2.7.4.1	Polyphosphate kinase.	Tfu_0323	Tfu_0323 polyphosphate kinase	15.85	16.25	15.92	15.14	20.75	1.02
EC	2.7.4.14	UMP/CMP kinase.	Tfu_1209	Tfu_1209 cytidylate kinase	15.69	15.43		14.19	19.62	
EC	2.7.4.16	Thiamine-phosphate kinase.	Tfu_0643	Tfu_0643 thiamine monophosphate kinase					14.5	
EC	2.7.4.22	UMP kinase.	Tfu_0678	Tfu_0678 uridylate kinase	18.09	18.05	17.82	18.33	22.01	1.02
EC	2.7.4.3	Adenylate kinase.	Tfu_2625	Tfu_2625 adenylate kinase, subfamily	19.36	20.27	22.16	21.48	24.95	0.736
EC	2.7.4.6	Nucleoside-diphosphate kinase.	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
EC	2.7.4.7	Phosphomethylpyrimidine kinase.	Tfu_2250	Tfu_2250 phosphomethylpyrimidine kinase	16.07	16.41	14.97		19.92	1.225
EC	2.7.4.8	Guanylate kinase.	Tfu_1062	Tfu_1062 guanylate kinase			14.95	15.22	19.61	
EC	2.7.4.9	dTMP kinase.	Tfu_2783	Tfu_2783 thymidylate kinase	19.41	19.13	18.67	18.47	22.51	0.962
EC	2.7.6.1	Ribose-phosphate diphosphokinase.	Tfu_0415	Tfu_0415 ribose-phosphate pyrophosphokinase	18.35	17.7	20.22	20.21	23.7	1.099
EC	2.7.6.3	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine (	Tfu_2890	Tfu_2890 7, 8-Dihydro-6-hydroxymethylpterin-pyrophosphokinase, HPPK					15.52	
EC	2.7.6.5	GTP diphosphokinase.	Tfu_2090	Tfu_2090 RelA/SpoT protein	12.76			12.64	18.41	
EC	2.7.7.-	Transferases. Transferring phosphorous-containing gro	Tfu_0866	Tfu_0866 DNA primase					16.49	
EC	2.7.7.13	Mannose-1-phosphate guanylyltransferase.	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / phosphomannomutase	19.06	18.82	21.97	21.81	25.49	1.131
EC	2.7.7.18	Nicotinate-nucleotide adenylyltransferase.	Tfu_2171	Tfu_2171 nicotinic acid mononucleotide adenyltransferase					18.95	
EC	2.7.7.19	Polynucleotide adenylyltransferase.	Tfu_3102	Tfu_3102 metal-dependent phosphohydrolase		14.3	17.01	16.42	21.49	
EC	2.7.7.2	FAD synthetase.	Tfu_0782	Tfu_0782 Cytidyltransferase-related		13.35	14.92	14.18	20.03	
EC	2.7.7.23	UDP-N-acetylglucosamine diphosphorylase.	Tfu_0414	Tfu_0414 UDP-N-acetylglucosamine pyrophosphorylase	19.4	19.37	19.9	19.97	23.72	1.114
EC	2.7.7.3	Pantetheine-phosphate adenylyltransferase.	Tfu_0648	Tfu_0648 coenzyme A biosynthesis protein:Cytidyltransferase-related	18.01	16.72	17.97	17.55	22.5	1.132
EC	2.7.7.4	Sulfate adenylyltransferase.	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
EC	2.7.7.4	Sulfate adenylyltransferase.	Tfu_0420	Tfu_0420 Small GTP-binding protein domain:Sulfate adenylyltransferase, large subunit			14.13		18.76	0.81
EC	2.7.7.4	Sulfate adenylyltransferase.	Tfu_0425	Tfu_0425 adenylylsulfate kinase					17.66	
EC	2.7.7.41	Phosphatidate cytidylyltransferase.	Tfu_0680	Tfu_0680 phosphatidate cytidylyltransferase	15.69	15.29	15.87	15.37	19.59	
EC	2.7.7.42	[Glutamate--ammonia-ligase] adenylyltransferase.	Tfu_0986	Tfu_0986 glutamate-ammonia-ligase adenylyltransferase					18.95	
EC	2.7.7.43	N-acylneuraminate cytidylyltransferase.	Tfu_0009	Tfu_0009 putative transferase						

EC	2.7.7.56	tRNA nucleotidyltransferase.	Tfu_2365	Tfu_2365 ribonuclease PH	18.55	18.11	18.5	18.13	22.43	
EC	2.7.7.58	(2,3-dihydroxybenzoyl)adenylate synthase.	Tfu_1871	Tfu_1871 2,3-dihydroxybenzoate-AMP ligase			14.18	14.93	21.25	0.737
EC	2.7.7.6	DNA-directed RNA polymerase.	Tfu_1063	Tfu_1063 DNA-directed RNA polymerase omega subunit						
EC	2.7.7.6	DNA-directed RNA polymerase.	Tfu_2618	Tfu_2618 DNA-directed RNA polymerase alpha subunit	20.3	20.33	21.62	21.41	24.58	1.11
EC	2.7.7.6	DNA-directed RNA polymerase.	Tfu_2653	Tfu_2653 DNA-directed RNA polymerase beta' subunit	20.69	20.49	21.52	21.3	25.54	1.261
EC	2.7.7.6	DNA-directed RNA polymerase.	Tfu_2654	Tfu_2654 DNA-directed RNA polymerase beta subunit	20.88	20.63	21.68	21.31	25.36	1.169
EC	2.7.7.62	Adenosylcobinamide-phosphate guanylyltransferase.	Tfu_0997	Tfu_0997 adenosylcobinamide kinase / adenosylcobinamide-phosphate guanylyltransferase		15.35		15.47	20.21	
EC	2.7.7.68	2-phospho-L-lactate guanylyltransferase.	Tfu_0629	Tfu_0629 hypothetical protein						
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_0002	Tfu_0002 DNA polymerase III subunit beta			14.09		20.64	
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_0047	Tfu_0047 DNA polymerase III subunit alpha					14.78	
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_0051	Tfu_0051 DNA polymerase III subunits gamma and tau					16.27	
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_0086	Tfu_0086 DNA polymerase III subunit beta	14.58			14.38	19.46	
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_0183	Tfu_0183 DNA polymerase III subunit epsilon					16.34	
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_0714	Tfu_0714 exonuclease	20.07	19.91	16.25	15.46	21.16	1.005
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_0823	Tfu_0823 DNA polymerase III, delta subunit					18.6	
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_0902	Tfu_0902 DNA polymerase III, epsilon subunit						
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_1027	Tfu_1027 hypothetical protein						
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_1096	Tfu_1096 DNA-directed DNA polymerase						
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_1189	Tfu_1189 DNA polymerase I	20.07	19.68	19.65	19.77	23.74	0.917
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_2347	Tfu_2347 exonuclease					16.03	
EC	2.7.7.7	DNA-directed DNA polymerase.	Tfu_2782	Tfu_2782 DNA polymerase III delta prime subunit					15.08	
EC	2.7.7.8	Polyribonucleotide nucleotidyltransferase.	Tfu_0784	Tfu_0784 polyribonucleotide nucleotidyltransferase	20.08	19.88	21.21	21.25	24.81	1.127
EC	2.7.7.9	UTP--glucose-1-phosphate uridylyltransferase.	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase, bacterial and archaeal type	16.85	15	17.24	17.46	22.15	
EC	2.7.8.-	Transferases. Transferring phosphorous-containing gro	Tfu_1855	Tfu_1855 4'-phosphopantetheinyl transferase						
EC	2.7.8.-	Transferases. Transferring phosphorous-containing gro	Tfu_2817	Tfu_2817 hypothetical protein					18.27	
EC	2.7.8.12	CDP-glycerol glycerophosphotransferase.	Tfu_2178	Tfu_2178 similar to Putative glycosyl/glycerophosphate transferase involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC						
EC	2.7.8.13	Phospho-N-acetylmuramoyl-pentapeptide-transferase.	Tfu_1107	Tfu_1107 phospho-N-acetylmuramoyl-pentapeptide- transferase					17.98	
EC	2.7.8.26	Adenosylcobinamide-GDP ribazoletransferase.	Tfu_0996	Tfu_0996 putative cobalamin (5'-phosphate) synthase : adenosylcobinamide-GDP ribazoletransferase						
EC	2.7.8.28	2-phospho-L-lactate transferase.	Tfu_2517	Tfu_2517 LPPG:Fo 2-phospho-L-lactate transferase			14.64	15.51	20.71	
EC	2.7.8.5	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatid	Tfu_0796	Tfu_0796 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase					15.36	
EC	2.7.8.5	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatid	Tfu_1393	Tfu_1393 putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase					15.45	
EC	2.7.8.5	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatid	Tfu_2103	Tfu_2103 putative membrane transferase		14.75	15	14.79	18.49	
EC	2.7.8.8	CDP-diacylglycerol--serine O-phosphatidyltransferase.	Tfu_1895	Tfu_1895 putative phosphatidylserine synthase						
EC	2.7.9.1	Pyruvate, phosphate dikinase.	Tfu_0863	Tfu_0863 pyruvate phosphate dikinase	17.84	17.11	21.38	21.45	25.04	1.455
EC	2.8.1.-	Transferases. Transferring sulfur-containing groups. Su	Tfu_0597	Tfu_0597 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase						
EC	2.8.1.-	Transferases. Transferring sulfur-containing groups. Su	Tfu_1014	Tfu_1014 putative aminotransferase						
EC	2.8.1.1	Thiosulfate sulfurtransferase.	Tfu_0354	Tfu_0354 3-mercaptopyruvate sulfurtransferase					18.69	
EC	2.8.1.1	Thiosulfate sulfurtransferase.	Tfu_2719	Tfu_2719 thiosulfate sulfurtransferase	22.47	22.41	22.74	22.62	25.34	0.79
EC	2.8.1.2	3-mercaptopyruvate sulfurtransferase.	Tfu_0354	Tfu_0354 3-mercaptopyruvate sulfurtransferase					18.69	
EC	2.8.1.2	3-mercaptopyruvate sulfurtransferase.	Tfu_2719	Tfu_2719 thiosulfate sulfurtransferase	22.47	22.41	22.74	22.62	25.34	0.79
EC	2.8.1.7	Cysteine desulfurase.	Tfu_0595	Tfu_0595 putative pyridoxal-phosphate-dependent aminotransferase					16.06	
EC	2.8.1.7	Cysteine desulfurase.	Tfu_1983	Tfu_1983 cysteine desulphurases, SufS	14.11			13.91	18.52	0.647
EC	2.8.1.8	Lipoyl synthase.	Tfu_0991	Tfu_0991 lipoyl synthase					17.9	1.46
EC	2.8.3.15	Succinyl-CoA:(R)-benzylsuccinate CoA-transferase.	Tfu_1480	Tfu_1480 subunit of CoA-transferase of family III						
EC	2.8.3.16	Formyl-CoA transferase.	Tfu_1069	Tfu_1069 CaiB/BaiF family protein					17.39	0.688
EC	3.1.-	Hydrolases. Acting on ester bonds.	Tfu_0792	Tfu_0792 putative hydrolase of the metallo-beta-lactamase superfamily	19.38	19.05	18.75	18.41	22.78	1.171
EC	3.1.-	Hydrolases. Acting on ester bonds.	Tfu_2069	Tfu_2069 Holliday junction resolvase YqgF					17.3	
EC	3.1.-	Hydrolases. Acting on ester bonds.	Tfu_2269	Tfu_2269 oligoribonuclease	16.91	16.6	17.83	17.13	21.66	
EC	3.1.-	Hydrolases. Acting on ester bonds.	Tfu_2922	Tfu_2922 D-tyrosyl-tRNA deacylase					20.07	
EC	3.1.1.-	Hydrolases. Acting on ester bonds. Carboxylic ester hyd	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
EC	3.1.1.1	Carboxylesterase.	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567

EC	3.1.1.24	3-oxoadipate enol-lactonase.	Tfu_0162	Tfu_0162 b-ketoadipate enol-lactone hydrolase				14.37	20.07	
EC	3.1.1.24	3-oxoadipate enol-lactonase.	Tfu_0874	Tfu_0874 Alpha/beta hydrolase	16.84	15.52	17.31	18.48	22.22	0.937
EC	3.1.1.29	Aminoacyl-tRNA hydrolase.	Tfu_0417	Tfu_0417 peptidyl-tRNA hydrolase	16.17	14.6	16.64	16.59	20.35	
EC	3.1.1.3	Triacylglycerol lipase.	Tfu_0155	Tfu_0155 esterase / lipase						
EC	3.1.1.3	Triacylglycerol lipase.	Tfu_0882	Tfu_0882 hypothetical protein						
EC	3.1.1.3	Triacylglycerol lipase.	Tfu_0883	Tfu_0883 hypothetical protein						
EC	3.1.1.31	6-phosphogluconolactonase.	Tfu_2007	Tfu_2007 6-phosphogluconolactonase	18.7	19.13	18.21	17.98	22.37	0.913
EC	3.1.1.41	Cephalosporin-C deacetylase.	Tfu_1462	Tfu_1462 similar to Acetyl esterase (deacetylase)	17.67	15.79	15.84	16.11	21.76	0.85
EC	3.1.1.56	Methylumbelliferyl-acetate deacetylase.	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
EC	3.1.1.73	Feruloyl esterase.	Tfu_0082	Tfu_0082 hypothetical protein		13.31			15.38	
EC	3.1.1.84	Cocaine esterase.	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
EC	3.1.11.2	Exodeoxyribonuclease III.	Tfu_0258	Tfu_0258 AP endonuclease, family 1:Exodeoxyribonuclease III xth		15.38	17.28	16.99	20.99	
EC	3.1.11.2	Exodeoxyribonuclease III.	Tfu_1541	Tfu_1541 AP endonuclease, family 1:Exodeoxyribonuclease III xth					16.85	
EC	3.1.11.5	Exodeoxyribonuclease V.	Tfu_1753	Tfu_1753 helicase RecD/TraA					15.31	
EC	3.1.11.5	Exodeoxyribonuclease V.	Tfu_1840	Tfu_1840 hypothetical protein					19.33	
EC	3.1.11.6	Exodeoxyribonuclease VII.	Tfu_0467	Tfu_0467 exodeoxyribonuclease VII small subunit	15.19	15.36			16.56	
EC	3.1.11.6	Exodeoxyribonuclease VII.	Tfu_0468	Tfu_0468 exodeoxyribonuclease VII large subunit	16.38	16.62		14.75	20.3	
EC	3.1.13.5	Ribonuclease D.	Tfu_1901	Tfu_1901 HRDC:3'-5' exonuclease	14.88		15.41	14.88	21.2	1.409
EC	3.1.2.-	Hydrolases. Acting on ester bonds. Thiolester hydrolase	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
EC	3.1.2.-	Hydrolases. Acting on ester bonds. Thiolester hydrolase	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
EC	3.1.2.-	Hydrolases. Acting on ester bonds. Thiolester hydrolase	Tfu_2213	Tfu_2213 hypothetical protein						
EC	3.1.21.-	Hydrolases. Acting on ester bonds. Endodeoxyribonucle	Tfu_0398	Tfu_0398 TatD-related deoxyribonuclease					18.88	
EC	3.1.21.2	Deoxyribonuclease IV (phage-T(4)-induced).	Tfu_1956	Tfu_1956 AP endonuclease, family 2			12.75	12.58	17.8	
EC	3.1.21.7	Deoxyribonuclease V.	Tfu_1400	Tfu_1400 putative endonuclease						
EC	3.1.22.4	Crossover junction endodeoxyribonuclease.	Tfu_2095	Tfu_2095 Holliday junction resolvase						
EC	3.1.26.11	Ribonuclease Z.	Tfu_1526	Tfu_1526 ribonuclease Z					18.58	
EC	3.1.26.12	Ribonuclease E.	Tfu_2183	Tfu_2183 ribonuclease E and G	15.17	14.73	17.43	17.22	22.5	1.093
EC	3.1.26.3	Ribonuclease III.	Tfu_0651	Tfu_0651 ribonuclease III	19.19	19.06	19.23	19.28	23.05	0.694
EC	3.1.26.4	Ribonuclease H.	Tfu_2145	Tfu_2145 ribonuclease HII						
EC	3.1.26.5	Ribonuclease P.	Tfu_3116	Tfu_3116 ribonuclease P protein	14.64	14.28	14.15	13.87	18.19	
EC	3.1.3.-	Hydrolases. Acting on ester bonds. Phosphoric monoest	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
EC	3.1.3.1	Alkaline phosphatase.	Tfu_1673	Tfu_1673 hypothetical protein						
EC	3.1.3.11	Fructose-bisphosphatase.	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
EC	3.1.3.12	Trehalose-phosphatase.	Tfu_0224	Tfu_0224 trehalose-phosphatase:HAD-superfamily hydrolase subfamily IIB	14.64	15.78	17.3	17.76	22.74	0.78
EC	3.1.3.15	Histidinol-phosphatase.	Tfu_0542	Tfu_0542 histidinol-phosphate phosphatase, putative, inositol monophosphatase	18.79	18.37	16.97	17.19	21.21	
EC	3.1.3.16	Phosphoprotein phosphatase.	Tfu_0297	Tfu_0297 Protein phosphatase 2C-like	14.85		14.32		19.33	0.687
EC	3.1.3.16	Phosphoprotein phosphatase.	Tfu_2592	Tfu_2592 putative phosphatase	13.93	15.27	14.31		19.57	
EC	3.1.3.16	Phosphoprotein phosphatase.	Tfu_3062	Tfu_3062 Protein phosphatase 2C-like	19.97	19.61	19.68	19.29	23.44	1.296
EC	3.1.3.25	Inositol-phosphate phosphatase.	Tfu_1212	Tfu_1212 archaeal fructose-1 6-bisphosphatase and related enzyme of inositol monophosphatase fa	14.95	15.73	15.51	15.72	20.15	0.894
EC	3.1.3.25	Inositol-phosphate phosphatase.	Tfu_1943	Tfu_1943 inositol-1(or 4)-monophosphatase	16.16	15.99			19.17	0.652
EC	3.1.3.3	Phosphoserine phosphatase.	Tfu_0136	Tfu_0136 phosphoserine phosphatase SerB:HAD-superfamily hydrolase subfamily IB, PSPase-like					16.25	
EC	3.1.3.48	Protein-tyrosine-phosphatase.	Tfu_2341	Tfu_2341 Protein-tyrosine-phosphatase				13.75	19	
EC	3.1.3.7	3'(2'),5'-bisphosphate nucleotidase.	Tfu_0418	Tfu_0418 3'-Phosphoadenosine 5'-phosphosulfate (PAPS) 3'-phosphatase					17.11	
EC	3.1.4.46	Glycerophosphodiester phosphodiesterase.	Tfu_0245	Tfu_0245 glycerophosphoryl diester phosphodiesterase	13.34	13.18		14.83	20.82	
EC	3.1.4.46	Glycerophosphodiester phosphodiesterase.	Tfu_1757	Tfu_1757 putative glycerophosphoryl diester phosphodiesterase						
EC	3.1.4.46	Glycerophosphodiester phosphodiesterase.	Tfu_2540	Tfu_2540 glycerophosphoryl diester phosphodiesterase, putative					18.74	
EC	3.1.5.1	dGTPase.	Tfu_0865	Tfu_0865 deoxyguanosinetriphosphate triphosphohydrolase-like protein	15.92	16.87			18.37	
EC	3.2.-	Hydrolases. Glycosylases.	Tfu_1178	Tfu_1178 peptidase C56, PfpI					15.89	
EC	3.2.-	Hydrolases. Glycosylases.	Tfu_2828	Tfu_2828 peptidase C56, PfpI						0.636
EC	3.2.1.-	Hydrolases. Glycosylases. Glycosidases, i.e. enzymes hyd	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
EC	3.2.1.1	Alpha-amylase.	Tfu_0584	Tfu_0584 alpha amylase, catalytic subdomain						

EC	3.2.1.1	Alpha-amylase.	Tfu_0985	Tfu_0985 hypothetical protein						
EC	3.2.1.14	Chitinase.	Tfu_0580	Tfu_0580 chitinase II	17.05	17.75	15.71	15.95	21.45	
EC	3.2.1.14	Chitinase.	Tfu_0868	Tfu_0868 hypothetical protein					16.11	
EC	3.2.1.20	Alpha-glucosidase.	Tfu_0833	Tfu_0833 alpha amylase, catalytic subdomain	15.71	15.55	14.92	15.54	20.77	0.845
EC	3.2.1.21	Beta-glucosidase.	Tfu_0937	Tfu_0937 beta-glucosidase	16.92	16.79	21.22	20.91	23.7	2.426
EC	3.2.1.21	Beta-glucosidase.	Tfu_1607	Tfu_1607 beta-glucosidase						
EC	3.2.1.21	Beta-glucosidase.	Tfu_1629	Tfu_1629 beta-glucosidase	20.15	19.64	19.92	19.43	23.45	1.12
EC	3.2.1.23	Beta-galactosidase.	Tfu_1615	Tfu_1615 beta-galactosidase					16.26	
EC	3.2.1.25	Beta-mannosidase.	Tfu_0915	Tfu_0915 beta-mannosidase	16.19	15.87	19.77	19.48	24.11	
EC	3.2.1.37	Xylan 1,4-beta-xylosidase.	Tfu_1616	Tfu_1616 alpha-L-arabinofuranosidase	18.6	18.38			20.92	1.664
EC	3.2.1.4	Cellulase.	Tfu_0901	Tfu_0901 hypothetical protein						
EC	3.2.1.4	Cellulase.	Tfu_1074	Tfu_1074 hypothetical protein						
EC	3.2.1.4	Cellulase.	Tfu_1627	Tfu_1627 hypothetical protein						
EC	3.2.1.4	Cellulase.	Tfu_2176	Tfu_2176 hypothetical protein						
EC	3.2.1.4	Cellulase.	Tfu_2712	Tfu_2712 hypothetical protein						
EC	3.2.1.52	Beta-N-acetylhexosaminidase.	Tfu_2486	Tfu_2486 hypothetical protein	16.26	16.75		15.08	20.28	
EC	3.2.1.55	Alpha-N-arabinofuranosidase.	Tfu_1616	Tfu_1616 alpha-L-arabinofuranosidase	18.6	18.38			20.92	1.664
EC	3.2.1.78	Mannan endo-1,4-beta-mannosidase.	Tfu_0900	Tfu_0900 hypothetical protein						
EC	3.2.1.8	Endo-1,4-beta-xylanase.	Tfu_1213	Tfu_1213 hypothetical protein						
EC	3.2.1.8	Endo-1,4-beta-xylanase.	Tfu_2791	Tfu_2791 hypothetical protein						
EC	3.2.1.8	Endo-1,4-beta-xylanase.	Tfu_2923	Tfu_2923 hypothetical protein						
EC	3.2.1.86	6-phospho-beta-glucosidase.	Tfu_2768	Tfu_2768 6-phospho-beta-glucosidase	16.59	15.79	14.95	14.18	20.38	0.664
EC	3.2.1.91	Cellulose 1,4-beta-cellobiosidase.	Tfu_0620	Tfu_0620 hypothetical protein						
EC	3.2.1.91	Cellulose 1,4-beta-cellobiosidase.	Tfu_1627	Tfu_1627 hypothetical protein						
EC	3.2.1.91	Cellulose 1,4-beta-cellobiosidase.	Tfu_1959	Tfu_1959 hypothetical protein					15.56	
EC	3.2.2.-	Hydrolases. Glycosylases. Hydrolyzing N-glycosyl compo	Tfu_0694	Tfu_0694 putative DNA repair hydrolase						
EC	3.2.2.-	Hydrolases. Glycosylases. Hydrolyzing N-glycosyl compo	Tfu_1918	Tfu_1918 putative DNA glycosylase						
EC	3.2.2.-	Hydrolases. Glycosylases. Hydrolyzing N-glycosyl compo	Tfu_2875	Tfu_2875 HhH-GPD:Iron-sulfur cluster loop						
EC	3.2.2.1	Purine nucleosidase.	Tfu_2581	Tfu_2581 inosine-uridine preferring nucleoside hydrolase	16.93	16.72	16.96	15.37	21.32	
EC	3.2.2.20	DNA-3-methyladenine glycosylase I.	Tfu_0498	Tfu_0498 DNA-3-methyladenine glycosylase I					15.85	
EC	3.2.2.23	DNA-formamidopyrimidine glycosylase.	Tfu_0652	Tfu_0652 formamidopyrimidine-DNA glycosylase						
EC	3.2.2.27	Uracil-DNA glycosylase.	Tfu_1341	Tfu_1341 uracil-DNA glycosylase	17.73	18.1	16.87	17.48	21.34	0.623
EC	3.3.1.1	Adenosylhomocysteinase.	Tfu_2505	Tfu_2505 S-adenosyl-L-homocysteine hydrolase	18.66	19.01	19.8	19.23	23.56	1.126
EC	3.3.2.1	Isochorismatase.	Tfu_1870	Tfu_1870 isochorismatase						
EC	3.4.-	Hydrolases. Acting on peptide bonds (peptide hydrolase	Tfu_2961	Tfu_2961 peptidase S26B, eukaryotic signal peptidase						
EC	3.4.11.1	Leucyl aminopeptidase.	Tfu_0503	Tfu_0503 leucyl aminopeptidase	19.88	19.54	19.89	19.71	24.09	0.912
EC	3.4.11.1	Leucyl aminopeptidase.	Tfu_0995	Tfu_0995 leucyl aminopeptidase	22.3	22.22	21.93	22.33	25.29	1.048
EC	3.4.11.15	Aminopeptidase Y.	Tfu_2403	Tfu_2403 hypothetical protein	19.38	19.42	15.52		20.8	
EC	3.4.11.18	Methionyl aminopeptidase.	Tfu_0968	Tfu_0968 methionine aminopeptidase	15.07			15	21.26	
EC	3.4.11.18	Methionyl aminopeptidase.	Tfu_2624	Tfu_2624 peptidase M24A, methionine aminopeptidase, subfamily 1	15.62	14.46	17.87	17.48	22.13	1.234
EC	3.4.11.2	Membrane alanyl aminopeptidase.	Tfu_2204	Tfu_2204 peptidase M, neutral zinc metallopeptidase, zinc-binding site	19.26	19.22	19.6	18.89	23.54	1.255
EC	3.4.11.5	Prolyl aminopeptidase.	Tfu_2349	Tfu_2349 peptidase S33, proline iminopeptidase 1	16.69	17.1	17.23	15.65	21	1.063
EC	3.4.11.9	Xaa-Pro aminopeptidase.	Tfu_1744	Tfu_1744 xaa-Pro aminopeptidase	17.01	17.42	17.27	18.16	22.27	1.008
EC	3.4.14.5	Dipeptidyl-peptidase IV.	Tfu_0485	Tfu_0485 putative peptidase	17.73	17.6	18.42	18.1	22.9	0.789
EC	3.4.16.4	Serine-type D-Ala-D-Ala carboxypeptidase.	Tfu_2903	Tfu_2903 hypothetical protein					17.09	
EC	3.4.21.-	Hydrolases. Acting on peptide bonds (peptide hydrolase	Tfu_0353	Tfu_0353 trypsin-like serine protease typically periplasmic contain C-terminal PDZ domain						
EC	3.4.21.-	Hydrolases. Acting on peptide bonds (peptide hydrolase	Tfu_0507	Tfu_0507 trypsin-like serine protease typically periplasmic contain C-terminal PDZ domain					16.4	
EC	3.4.21.-	Hydrolases. Acting on peptide bonds (peptide hydrolase	Tfu_0579	Tfu_0579 peptidase S49, protease IV:Peptidase S49, SppA	21.99	21.86	21.35	20.93	25.08	1.204
EC	3.4.21.-	Hydrolases. Acting on peptide bonds (peptide hydrolase	Tfu_2903	Tfu_2903 hypothetical protein					17.09	
EC	3.4.21.26	Prolyl oligopeptidase.	Tfu_1856	Tfu_1856 prolyl oligopeptidase					19.55	
EC	3.4.21.26	Prolyl oligopeptidase.	Tfu_2212	Tfu_2212 prolyl oligopeptidase						

EC	3.4.21.88	Repressor lexA.	Tfu_2152	Tfu_2152 peptidase S24, LexA repressor	16.53	15.15	15.32		20.68	
EC	3.4.21.89	Signal peptidase I.	Tfu_0667	Tfu_0667 peptidase S26A, signal peptidase I						
EC	3.4.21.92	Endopeptidase Clp.	Tfu_2193	Tfu_2193 ATP-dependent Clp protease proteolytic subunit	20.29	20.62	21.31	20.84	24.1	0.798
EC	3.4.21.92	Endopeptidase Clp.	Tfu_2194	Tfu_2194 endopeptidase Clp	21.36	21.68	21.56	21.35	24.71	1.134
EC	3.4.22.70	Sortase A.	Tfu_2383	Tfu_2383 peptidase C60, sortase A and B					17.58	
EC	3.4.23.36	Signal peptidase II.	Tfu_1122	Tfu_1122 signal peptidase II					18.28	
EC	3.4.23.43	Prepilin peptidase.	Tfu_1089	Tfu_1089 hypothetical protein						
EC	3.4.24.-	Hydrolases. Acting on peptide bonds (peptide hydrolase	Tfu_1008	Tfu_1008 heat shock protein HtpX						
EC	3.4.24.-	Hydrolases. Acting on peptide bonds (peptide hydrolase	Tfu_2673	Tfu_2673 putative peptidase						
EC	3.4.24.-	Hydrolases. Acting on peptide bonds (peptide hydrolase	Tfu_2895	Tfu_2895 hypothetical protein	18.74	18.46	19.98	19.65	23.82	1.538
EC	3.4.24.57	O-sialoglycoprotein endopeptidase.	Tfu_2602	Tfu_2602 peptidase M22, glycoprotease	14.17		16.74	16.68	20.36	
EC	3.4.24.64	Mitochondrial processing peptidase.	Tfu_0785	Tfu_0785 mitochondrial processing peptidase					18.09	0.986
EC	3.4.25.1	Proteasome endopeptidase complex.	Tfu_1789	Tfu_1789 putative 20S proteasome alpha-subunit	21.35	20.72	20.29	20.07	23.84	0.978
EC	3.4.25.1	Proteasome endopeptidase complex.	Tfu_1790	Tfu_1790 Proteasome endopeptidase complex	20.83	20.83	21.11	21.18	24.64	1.164
EC	3.5.1.-	Hydrolases. Acting on carbon-nitrogen bonds, other tha	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
EC	3.5.1.-	Hydrolases. Acting on carbon-nitrogen bonds, other tha	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
EC	3.5.1.10	Formyltetrahydrofolate deformylase.	Tfu_2356	Tfu_2356 formyltetrahydrofolate deformylase					15.81	
EC	3.5.1.103	N-acetyl-1-D-myo-inositol-2-amino-2-deoxy-alpha-D-gl	Tfu_0486	Tfu_0486 hypothetical protein	15.4	16.4	16.51	15.88	21.61	0.747
EC	3.5.1.11	Penicillin amidase.	Tfu_1644	Tfu_1644 hypothetical protein	20.36	20.05	18.51	17.42	23.26	
EC	3.5.1.18	Succinyl-diaminopimelate desuccinylase.	Tfu_0495	Tfu_0495 succinyl-diaminopimelate desuccinylase	16.35	16.43	16.49	16.87	20.83	0.501
EC	3.5.1.19	Nicotinamidase.	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
EC	3.5.1.25	N-acetylglucosamine-6-phosphate deacetylase.	Tfu_2473	Tfu_2473 n-acetylglucosamine-6-phosphate deacetylase	14.21				17.55	
EC	3.5.1.28	N-acetylmuramoyl-L-alanine amidase.	Tfu_2753	Tfu_2753 cell wall hydrolase/autolysin						
EC	3.5.1.32	Hippurate hydrolase.	Tfu_2437	Tfu_2437 peptidase M20D, amidohydrolase	19.51	19.04	18.35	17.96	22.85	0.958
EC	3.5.1.32	Hippurate hydrolase.	Tfu_2564	Tfu_2564 peptidase M20D, amidohydrolase					20.11	
EC	3.5.1.4	Amidase.	Tfu_2207	Tfu_2207 amidase					14.6	
EC	3.5.1.87	N-carbamoyl-L-amino-acid hydrolase.	Tfu_2012	Tfu_2012 N-carbamoyl-L-amino acid amidohydrolase	13.88	14.26	13.69	13.1	19.27	
EC	3.5.1.88	Peptide deformylase.	Tfu_1726	Tfu_1726 formylmethionine deformylase		16.72	17.51	16.93	21.31	
EC	3.5.1.88	Peptide deformylase.	Tfu_2433	Tfu_2433 formylmethionine deformylase						
EC	3.5.1.9	Arylformamidase.	Tfu_1418	Tfu_1418 hypothetical protein	18.89	18.42	20.57	20.44	23.75	0.572
EC	3.5.1.9	Arylformamidase.	Tfu_1722	Tfu_1722 hypothetical protein					14.24	
EC	3.5.2.3	Dihydroorotase.	Tfu_0962	Tfu_0962 allantoinase						
EC	3.5.2.3	Dihydroorotase.	Tfu_1055	Tfu_1055 dihydroorotase	13.79		18.6	18.17	22.62	
EC	3.5.2.7	Imidazolonepropionase.	Tfu_0821	Tfu_0821 imidazolonepropionase					17.2	
EC	3.5.3.1	Arginase.	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
EC	3.5.3.11	Agmatinase.	Tfu_0058	Tfu_0058 putative agmatinase	15.19	15.1			18.15	1.47
EC	3.5.3.6	Arginine deiminase.	Tfu_1993	Tfu_1993 arginine deiminase	17.46	16.86	15.61	15.61	20.88	1.353
EC	3.5.4.1	Cytosine deaminase.	Tfu_0027	Tfu_0027 putative deaminase					17.96	0.99
EC	3.5.4.10	IMP cyclohydrolase.	Tfu_2572	Tfu_2572 bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohy	19.86	19.04	20.76	20.79	24.53	0.912
EC	3.5.4.13	dCTP deaminase.	Tfu_2932	Tfu_2932 deoxycytidine triphosphate deaminase					19.21	
EC	3.5.4.16	GTP cyclohydrolase I.	Tfu_2894	Tfu_2894 GTP cyclohydrolase I		15.85	17.62	17.38	21.27	0.628
EC	3.5.4.19	Phosphoribosyl-AMP cyclohydrolase.	Tfu_1159	Tfu_1159 phosphoribosyl-AMP cyclohydrolase					16.88	
EC	3.5.4.25	GTP cyclohydrolase II.	Tfu_1080	Tfu_1080 bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein						
EC	3.5.4.26	Diaminohydroxyphosphoribosylaminopyrimidine deam	Tfu_0877	Tfu_0877 hypothetical protein					17.13	
EC	3.5.4.4	Adenosine deaminase.	Tfu_2563	Tfu_2563 adenosine deaminase					16.67	
EC	3.5.4.4	Adenosine deaminase.	Tfu_2662	Tfu_2662 adenosine deaminase				13.97	19.93	1.018
EC	3.5.4.9	Methenyltetrahydrofolate cyclohydrolase.	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
EC	3.5.99.2	Thiaminase.	Tfu_2953	Tfu_2953 putative transcriptional regulator	15.38	15.61	16.42	14.9	19.48	1.394
EC	3.6.1.-	Hydrolases. Acting on acid anhydrides. In phosphorous-	Tfu_0543	Tfu_0543 hypothetical protein			13.59	14.81	19.36	
EC	3.6.1.-	Hydrolases. Acting on acid anhydrides. In phosphorous-	Tfu_0576	Tfu_0576 hypothetical protein					17.31	
EC	3.6.1.-	Hydrolases. Acting on acid anhydrides. In phosphorous-	Tfu_2457	Tfu_2457 putative mutT-like protein						

EC	3.6.1.1	Inorganic diphosphatase.	Tfu_0134	Tfu_0134 inorganic H+ pyrophosphatase	23.51	23.41	21.68	21.58	25.23	0.963
EC	3.6.1.1	Inorganic diphosphatase.	Tfu_2902	Tfu_2902 inorganic diphosphatase	14.95		16.63	16.62	20.87	
EC	3.6.1.11	Exopolyphosphatase.	Tfu_0431	Tfu_0431 putative hydrolase					20.26	
EC	3.6.1.13	ADP-ribose diphosphatase.	Tfu_1200	Tfu_1200 hypothetical protein			14.4	14.71	20.54	
EC	3.6.1.19	Nucleoside-triphosphate diphosphatase.	Tfu_0426	Tfu_0426 MazG, bacterial			13.43		19.98	
EC	3.6.1.19	Nucleoside-triphosphate diphosphatase.	Tfu_2364	Tfu_2364 Ham1-like protein	17.27	15.22	18.89	17.92	22.35	0.853
EC	3.6.1.22	NAD(+) diphosphatase.	Tfu_0527	Tfu_0527 hypothetical protein					16.28	
EC	3.6.1.23	dUTP diphosphatase.	Tfu_1935	Tfu_1935 deoxyUTP pyrophosphatase subfamily 1					16.91	
EC	3.6.1.27	Undecaprenyl-diphosphatase.	Tfu_1838	Tfu_1838 undecaprenyl pyrophosphate phosphatase	17.56	17.35	17.39	17.14	20.29	0.764
EC	3.6.1.31	Phosphoribosyl-ATP diphosphatase.	Tfu_0175	Tfu_0175 phosphoribosyl-ATP pyrophosphatase	17.66	17.21	14.18	15.95	21.68	0.868
EC	3.6.1.40	Guanosine-5'-triphosphate,3'-diphosphate diphosphata	Tfu_0431	Tfu_0431 putative hydrolase					20.26	
EC	3.6.1.7	Acylphosphatase.	Tfu_0653	Tfu_0653 acylphosphatase					17.12	
EC	3.6.3.-	Hydrolases. Acting on acid anhydrides. Acting on acid ar	Tfu_0810	Tfu_0810 ABC-type polar amino acid transport system ATPase component	20.65	20.47	19.17	19	22.36	1.163
EC	3.6.3.-	Hydrolases. Acting on acid anhydrides. Acting on acid ar	Tfu_0858	Tfu_0858 ABC-type Mn/Zn transport systems ATPase component						
EC	3.6.3.-	Hydrolases. Acting on acid anhydrides. Acting on acid ar	Tfu_1100	Tfu_1100 putative regulatory protein						
EC	3.6.3.-	Hydrolases. Acting on acid anhydrides. Acting on acid ar	Tfu_1676	Tfu_1676 MoxR-like ATPase					16.26	
EC	3.6.3.-	Hydrolases. Acting on acid anhydrides. Acting on acid ar	Tfu_2500	Tfu_2500 ATPase	18.85	18.12	18.16	18.37	22.96	1.114
EC	3.6.3.14	H(+)-transporting two-sector ATPase.	Tfu_2406	Tfu_2406 H+-transporting two-sector ATPase, delta/epsilon subunit	17.61	17.4	18.54	18.5	21.47	
EC	3.6.3.14	H(+)-transporting two-sector ATPase.	Tfu_2407	Tfu_2407 ATP synthase F1, beta subunit	21.37	21.44	23.04	22.88	26.22	1.194
EC	3.6.3.14	H(+)-transporting two-sector ATPase.	Tfu_2408	Tfu_2408 H+-transporting two-sector ATPase, gamma subunit	20.11	19.39	21.19	20.62	23.67	
EC	3.6.3.14	H(+)-transporting two-sector ATPase.	Tfu_2409	Tfu_2409 ATP synthase subunit A	21.64	21.69	23.06	22.63	26.34	1.138
EC	3.6.3.14	H(+)-transporting two-sector ATPase.	Tfu_2410	Tfu_2410 H+-transporting two-sector ATPase, delta (OSCP) subunit	20.66	20.14	21.77	21.25	24.88	0.912
EC	3.6.3.14	H(+)-transporting two-sector ATPase.	Tfu_2411	Tfu_2411 ATP synthase F0, subunit B	20.75	20.59	21	21.14	24.9	0.695
EC	3.6.3.14	H(+)-transporting two-sector ATPase.	Tfu_2412	Tfu_2412 ATP synthase F0, C subunit						
EC	3.6.3.14	H(+)-transporting two-sector ATPase.	Tfu_2413	Tfu_2413 H+-transporting two-sector ATPase, A subunit						
EC	3.6.3.16	Arsenite-transporting ATPase.	Tfu_1391	Tfu_1391 arsenite-transporting ATPase						
EC	3.6.3.17	Monosaccharide-transporting ATPase.	Tfu_1921	Tfu_1921 ABC-type sugar transport system ATPase component	16.87	16.94	19.92	20.01	23.32	0.871
EC	3.6.3.21	Polar-amino-acid-transporting ATPase.	Tfu_0306	Tfu_0306 ABC-type polar amino acid transport system ATPase component					16.25	
EC	3.6.3.27	Phosphate-transporting ATPase.	Tfu_2743	Tfu_2743 Phosphate transport system permease protein 1	15.49	15.5	16.86	15.14	21.63	
EC	3.6.3.29	Molybdate-transporting ATPase.	Tfu_0326	Tfu_0326 ABC-type spermidine/putrescine transport systems ATPase components						
EC	3.6.3.30	Fe(3+)-transporting ATPase.	Tfu_1308	Tfu_1308 ABC-type spermidine/putrescine transport systems ATPase components						
EC	3.6.3.31	Polyamine-transporting ATPase.	Tfu_0280	Tfu_0280 spermidine/putrescine ABC transporter ATP-binding subunit	16.15	16.84	16.09	16.49	21.27	
EC	3.6.3.32	Quaternary-amine-transporting ATPase.	Tfu_2930	Tfu_2930 glycine betaine/L-proline transport ATP-binding subunit			14.84		19.59	
EC	3.6.3.34	Iron-chelate-transporting ATPase.	Tfu_0139	Tfu_0139 ABC transporter, ATP-binding protein			14.9	15.05	20.84	
EC	3.6.3.34	Iron-chelate-transporting ATPase.	Tfu_0336	Tfu_0336 ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components					15.18	
EC	3.6.3.34	Iron-chelate-transporting ATPase.	Tfu_1494	Tfu_1494 ABC-type cobalamin/Fe3+-siderophores transport systems ATPase components						
EC	3.6.3.34	Iron-chelate-transporting ATPase.	Tfu_2384	Tfu_2384 ABC-type hemin transport system ATPase component						
EC	3.6.3.4	Copper-exporting ATPase.	Tfu_2848	Tfu_2848 ATPase, E1-E2 type:Copper-translocating P-type ATPase:Heavy metal translocating P-type ATPase					14.11	
EC	3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid ar	Tfu_0061	Tfu_0061 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal					17.56	
EC	3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid ar	Tfu_0424	Tfu_0424 transcription-repair coupling factor					18.09	
EC	3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid ar	Tfu_0712	Tfu_0712 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal					12.98	
EC	3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid ar	Tfu_1073	Tfu_1073 primosome assembly protein PriA					16.49	0.882
EC	3.6.4.-	Hydrolases. Acting on acid anhydrides. Acting on acid ar	Tfu_1765	Tfu_1765 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal	14.16		17.46	17.45	22.14	0.919
EC	3.6.4.12	DNA helicase.	Tfu_0019	Tfu_0019 DnaB helicase					15.82	
EC	3.6.4.12	DNA helicase.	Tfu_0524	Tfu_0524 putative DNA helicase					16.97	
EC	3.6.4.12	DNA helicase.	Tfu_0530	Tfu_0530 superfamily I DNA and RNA helicases						
EC	3.6.4.12	DNA helicase.	Tfu_0646	Tfu_0646 ATP-dependent DNA helicase RecG					20.26	
EC	3.6.4.12	DNA helicase.	Tfu_2093	Tfu_2093 Holliday junction DNA helicase RuvB						
EC	3.6.4.12	DNA helicase.	Tfu_2094	Tfu_2094 DNA recombination protein, RuvA					18.24	
EC	3.6.4.12	DNA helicase.	Tfu_2167	Tfu_2167 helicase c2:DEAD/DEAH box helicase, N-terminal						
EC	3.6.4.12	DNA helicase.	Tfu_2580	Tfu_2580 ATP-dependent DNA helicase PcrA					19.8	

EC	3.6.4.13	RNA helicase.	Tfu_1440	Tfu_1440 helicase, C-terminal:DEAD/DEAH box helicase, N-terminal			11.04		19.52	
EC	3.6.4.13	RNA helicase.	Tfu_2317	Tfu_2317 ATP-dependent helicase HrpA					19.03	
EC	3.7.1.3	Kynureninase.	Tfu_0922	Tfu_0922 kynureninase	16.91	15.34	13.9	14.63	19.53	1.172
EC	4.-	Lyases.	Tfu_2099	Tfu_2099 pyridoxine biosynthesis protein	20.72	20.99	21.71	21.88	24.97	0.901
EC	4.1.1.11	Aspartate 1-decarboxylase.	Tfu_1862	Tfu_1862 aspartate 1-decarboxylase precursor			14.98		19.99	
EC	4.1.1.20	Diaminopimelate decarboxylase.	Tfu_2425	Tfu_2425 diaminopimelate decarboxylase					18.01	
EC	4.1.1.23	Orotidine-5'-phosphate decarboxylase.	Tfu_1060	Tfu_1060 orotidine 5'-phosphate decarboxylase	17.31	17.43	16.58	16.96	22.37	0.988
EC	4.1.1.31	Phosphoenolpyruvate carboxylase.	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
EC	4.1.1.32	Phosphoenolpyruvate carboxykinase (GTP).	Tfu_0083	Tfu_0083 phosphoenolpyruvate carboxykinase (GTP)	18.4	18.56	20.72	20.61	24.19	1.846
EC	4.1.1.36	Phosphopantothenoylcysteine decarboxylase.	Tfu_1064	Tfu_1064 phosphopantothenoylcysteine synthase/decarboxylase	18.49	18.47	18.49	18.95	22.74	1.103
EC	4.1.1.37	Uroporphyrinogen decarboxylase.	Tfu_1899	Tfu_1899 uroporphyrinogen decarboxylase HemE		14.37	15.41	15.99	20.69	0.856
EC	4.1.1.48	Indole-3-glycerol-phosphate synthase.	Tfu_1164	Tfu_1164 indole-3-glycerol-phosphate synthase					20.46	1.072
EC	4.1.1.65	Phosphatidylserine decarboxylase.	Tfu_1894	Tfu_1894 phosphatidylserine decarboxylase	16.99	15.03	17.14	16.9	21.01	1.091
EC	4.1.2.13	Fructose-bisphosphate aldolase.	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
EC	4.1.2.14	2-dehydro-3-deoxy-phosphogluconate aldolase.	Tfu_0188	Tfu_0188 2-dehydro-3-deoxyphosphogluconate aldolase / 4-hydroxy-2-oxoglutarate aldolase	14.36				15.14	
EC	4.1.2.22	Fructose-6-phosphate phosphoketolase.	Tfu_2970	Tfu_2970 putative phosphoketolase						
EC	4.1.2.25	Dihydroneopterin aldolase.	Tfu_2891	Tfu_2891 dihydroneopterin aldolase family:Dihydroneopterin aldolase	14.95	14.62	16	15.74	20.08	
EC	4.1.3.-	Lyases. Carbon-carbon lyases. Oxo-acid-lyases.	Tfu_1156	Tfu_1156 histidine biosynthesis protein HisF	14.6	14.45	14.77	14.57	20.69	
EC	4.1.3.1	Isocitrate lyase.	Tfu_1377	Tfu_1377 isocitrate lyase	17.24	15.99	17.23	17.21	21.54	
EC	4.1.3.16	4-hydroxy-2-oxoglutarate aldolase.	Tfu_0188	Tfu_0188 2-dehydro-3-deoxyphosphogluconate aldolase / 4-hydroxy-2-oxoglutarate aldolase	14.36				15.14	
EC	4.1.3.27	Anthranilate synthase.	Tfu_1386	Tfu_1386 glutamine amidotransferase of anthranilate synthase:Anthranilate synthase, alpha protec	14.29	15.3	14.48	14.83	21.47	1.207
EC	4.1.3.34	Citryl-CoA lyase.	Tfu_0341	Tfu_0341 citryl-CoA lyase	17.85	17.79	17.74	17.05	21.43	
EC	4.1.3.34	Citryl-CoA lyase.	Tfu_1285	Tfu_1285 citryl-CoA lyase						
EC	4.1.3.34	Citryl-CoA lyase.	Tfu_1313	Tfu_1313 putative citrate lyase beta subunit	20.71	20.33	20.94	21.03	24.43	1.292
EC	4.1.3.36	1,4-dihydroxy-2-naphthoyl-CoA synthase.	Tfu_1409	Tfu_1409 naphthoate synthase	16.03	15.45	18.71	18.23	22.53	
EC	4.1.3.6	Citrate (pro-3S)-lyase.	Tfu_0341	Tfu_0341 citryl-CoA lyase	17.85	17.79	17.74	17.05	21.43	
EC	4.1.3.6	Citrate (pro-3S)-lyase.	Tfu_1285	Tfu_1285 citryl-CoA lyase						
EC	4.1.3.6	Citrate (pro-3S)-lyase.	Tfu_1313	Tfu_1313 putative citrate lyase beta subunit	20.71	20.33	20.94	21.03	24.43	1.292
EC	4.1.99.12	3,4-dihydroxy-2-butanone-4-phosphate synthase.	Tfu_1080	Tfu_1080 bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein						
EC	4.1.99.3	Deoxyribodipyrimidine photo-lyase.	Tfu_0534	Tfu_0534 deoxyribodipyrimidine photolyase						
EC	4.2.1.-	Lyases. Carbon-oxygen lyases. Hydro-lyases.	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
EC	4.2.1.1	Carbonate dehydratase.	Tfu_2132	Tfu_2132 carbonic anhydrase, putative					20.01	
EC	4.2.1.10	3-dehydroquinate dehydratase.	Tfu_1635	Tfu_1635 dehydroquinase, class II					16.28	
EC	4.2.1.108	Ectoine synthase.	Tfu_0302	Tfu_0302 putative condensing enzyme					17.04	
EC	4.2.1.11	Phosphopyruvate hydratase.	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
EC	4.2.1.113	o-succinylbenzoate synthase.	Tfu_0960	Tfu_0960 n-acylamino acid racemase : O-succinylbenzoate-CoA synthase					19.49	
EC	4.2.1.113	o-succinylbenzoate synthase.	Tfu_1410	Tfu_1410 O-succinylbenzoate synthase					15.48	
EC	4.2.1.17	Enoyl-CoA hydratase.	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
EC	4.2.1.17	Enoyl-CoA hydratase.	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
EC	4.2.1.17	Enoyl-CoA hydratase.	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
EC	4.2.1.17	Enoyl-CoA hydratase.	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
EC	4.2.1.17	Enoyl-CoA hydratase.	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
EC	4.2.1.17	Enoyl-CoA hydratase.	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
EC	4.2.1.17	Enoyl-CoA hydratase.	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
EC	4.2.1.19	Imidazoleglycerol-phosphate dehydratase.	Tfu_1152	Tfu_1152 imidazoleglycerol-phosphate dehydratase					17.24	
EC	4.2.1.2	Fumarate hydratase.	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
EC	4.2.1.20	Tryptophan synthase.	Tfu_1165	Tfu_1165 tryptophan synthase, beta chain					18.55	
EC	4.2.1.20	Tryptophan synthase.	Tfu_1166	Tfu_1166 tryptophan synthase subunit alpha					18.24	
EC	4.2.1.22	Cystathionine beta-synthase.	Tfu_0438	Tfu_0438 cystathionine beta-synthase	13		14.49	12.98	20.18	
EC	4.2.1.24	Porphobilinogen synthase.	Tfu_2730	Tfu_2730 porphobilinogen synthase					18.56	
EC	4.2.1.3	Aconitate hydratase.	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403

EC	4.2.1.33	3-isopropylmalate dehydratase.	Tfu_0626	Tfu_0626 isopropylmalate isomerase large subunit			15.08	14.46	19.36	
EC	4.2.1.33	3-isopropylmalate dehydratase.	Tfu_0627	Tfu_0627 isopropylmalate isomerase small subunit	13.33				18.83	
EC	4.2.1.35	(R)-2-methylmalate dehydratase.	Tfu_0626	Tfu_0626 isopropylmalate isomerase large subunit			15.08	14.46	19.36	
EC	4.2.1.35	(R)-2-methylmalate dehydratase.	Tfu_0627	Tfu_0627 isopropylmalate isomerase small subunit	13.33				18.83	
EC	4.2.1.41	5-dehydro-4-deoxyglucarate dehydratase.	Tfu_1718	Tfu_1718 putative 5-dehydro-4-deoxyglucarate dehydratase						
EC	4.2.1.51	Prephenate dehydratase.	Tfu_3053	Tfu_3053 prephenate dehydratase					16.06	
EC	4.2.1.52	Dihydrodipicolinate synthase.	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844
EC	4.2.1.52	Dihydrodipicolinate synthase.	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
EC	4.2.1.6	Galactonate dehydratase.	Tfu_1786	Tfu_1786 mandelate racemase/muconate lactonizing enzyme family	16.66	16.7	15.07	15.62	20.33	1.311
EC	4.2.1.75	Uroporphyrinogen-III synthase.	Tfu_2731	Tfu_2731 putative uroporphyrin-III C-methyltransferase/uroporphyrinogen-III synthase	19.75	19.58	19.91	19.51	24.15	1.231
EC	4.2.1.9	Dihydroxy-acid dehydratase.	Tfu_2209	Tfu_2209 dihydroxy-acid dehydratase	14.66	14.56	15.67	16.08	21.64	
EC	4.2.1.96	4a-hydroxytetrahydrobiopterin dehydratase.	Tfu_1547	Tfu_1547 pterin-4-alpha-carbinolamine dehydratase						
EC	4.2.2.2	Pectate lyase.	Tfu_0153	Tfu_0153 hypothetical protein						
EC	4.2.3.1	Threonine synthase.	Tfu_0226	Tfu_0226 threonine synthase	15.9	15.94	18.57	18.65	22.91	1.385
EC	4.2.3.1	Threonine synthase.	Tfu_2423	Tfu_2423 threonine synthase	13.86				17.31	
EC	4.2.3.4	3-dehydroquinate synthase.	Tfu_1092	Tfu_1092 3-dehydroquinate synthase	18.86	18.36	19.22	18.34	23.14	1.077
EC	4.2.3.5	Chorismate synthase.	Tfu_1090	Tfu_1090 chorismate synthase	19.19	18.56	19.76	19.46	23.47	
EC	4.2.99.18	DNA-(apurinic or apyrimidinic site) lyase.	Tfu_0118	Tfu_0118 hypothetical protein					16.68	
EC	4.2.99.18	DNA-(apurinic or apyrimidinic site) lyase.	Tfu_0652	Tfu_0652 formamidopyrimidine-DNA glycosylase						
EC	4.2.99.18	DNA-(apurinic or apyrimidinic site) lyase.	Tfu_0694	Tfu_0694 putative DNA repair hydrolase						
EC	4.3.1.19	Threonine ammonia-lyase.	Tfu_1741	Tfu_1741 threonine dehydratase					16.86	
EC	4.3.2.1	Argininosuccinate lyase.	Tfu_2051	Tfu_2051 argininosuccinate lyase	15.68	16.51	18.68	18.9	22.79	
EC	4.3.2.2	Adenylosuccinate lyase.	Tfu_3014	Tfu_3014 adenylosuccinate lyase	18.68	18.68	20.17	19.69	23.57	0.954
EC	4.4.1.16	Selenocysteine lyase.	Tfu_1983	Tfu_1983 cysteine desulphurases, SufS	14.11			13.91	18.52	0.647
EC	4.6.1.1	Adenylate cyclase.	Tfu_2552	Tfu_2552 adenylyl cyclase class-3/4/guanylyl cyclase	15.46	15.87		14.57	19.3	
EC	4.6.1.12	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase.	Tfu_2906	Tfu_2906 MECDP-synthase	14.67		15.37		18.41	0.633
EC	4.99.1.1	Ferrochelatase.	Tfu_1945	Tfu_1945 ferrochelatase		13.87	18.69	18.79	22.82	1.023
EC	4.99.1.4	Sirohydrochlorin ferrochelatase.	Tfu_2221	Tfu_2221 uroporphyrin-III C-methyltransferase, C-terminal:Siroheme synthase, N-terminal	17.11	16.52	17.24	16.23	21.37	0.99
EC	5.1.1.1	Alanine racemase.	Tfu_2606	Tfu_2606 alanine racemase region	16.31	14.93	16.54	16.55	20.86	
EC	5.1.1.3	Glutamate racemase.	Tfu_2162	Tfu_2162 glutamate racemase						
EC	5.1.1.7	Diaminopimelate epimerase.	Tfu_0816	Tfu_0816 diaminopimelate epimerase					18.06	
EC	5.1.3.1	Ribulose-phosphate 3-epimerase.	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
EC	5.1.3.2	UDP-glucose 4-epimerase.	Tfu_0169	Tfu_0169 nucleoside-diphosphate-sugar epimerase (UDP-glucose 4-epimerase)	14.49	16.6	18.84	18.16	22.51	0.845
EC	5.1.3.2	UDP-glucose 4-epimerase.	Tfu_1622	Tfu_1622 UDP-glucose 4-epimerase						
EC	5.1.3.2	UDP-glucose 4-epimerase.	Tfu_2591	Tfu_2591 UDP-glucose 4-epimerase					14.83	
EC	5.1.3.2	UDP-glucose 4-epimerase.	Tfu_2723	Tfu_2723 putative epimerase						
EC	5.1.99.1	Methylmalonyl-CoA epimerase.	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
EC	5.1.99.4	Alpha-methylacyl-CoA racemase.	Tfu_0399	Tfu_0399 putative fatty acid-CoA racemase	16.76	16.16	14.76	15.27	19.11	
EC	5.2.1.8	Peptidylprolyl isomerase.	Tfu_1773	Tfu_1773 similar to FKBP-type peptidyl-prolyl cis-trans isomerase 1	18.39	18.19	17.36	17.39	22.49	
EC	5.2.1.8	Peptidylprolyl isomerase.	Tfu_2285	Tfu_2285 similar to FKBP-type peptidyl-prolyl cis-trans isomerase 1					18.88	
EC	5.2.1.8	Peptidylprolyl isomerase.	Tfu_2820	Tfu_2820 hypothetical protein	17.27	18.07	15.39	15.23	20.65	
EC	5.2.1.8	Peptidylprolyl isomerase.	Tfu_3069	Tfu_3069 peptidylprolyl isomerase	14.49		16.71	16.23	20.71	0.843
EC	5.3.1.1	Triose-phosphate isomerase.	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
EC	5.3.1.16	1-(5-phosphoribosyl)-5- ((5-phosphoribosylamino)met	Tfu_1155	Tfu_1155 1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomer			15.7	16.67	21.72	
EC	5.3.1.24	Phosphoribosylanthranilate isomerase.	Tfu_1155	Tfu_1155 1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomer			15.7	16.67	21.72	
EC	5.3.1.5	Xylose isomerase.	Tfu_1603	Tfu_1603 xylose isomerase	19.44	19.38	19.81	20.12	23.3	1.128
EC	5.3.1.6	Ribose-5-phosphate isomerase.	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
EC	5.3.1.8	Mannose-6-phosphate isomerase.	Tfu_0016	Tfu_0016 mannose-6-phosphate isomerase, type I						
EC	5.3.1.8	Mannose-6-phosphate isomerase.	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
EC	5.3.1.9	Glucose-6-phosphate isomerase.	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
EC	5.3.1.9	Glucose-6-phosphate isomerase.	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	

EC	5.4.1.2	Precorrin-8X methylmutase.	Tfu_0317	Tfu_0317 precorrin-8X methylmutase						
EC	5.4.2.1	Phosphoglycerate mutase.	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
EC	5.4.2.1	Phosphoglycerate mutase.	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
EC	5.4.2.1	Phosphoglycerate mutase.	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
EC	5.4.2.1	Phosphoglycerate mutase.	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
EC	5.4.2.10	Phosphoglucosamine mutase.	Tfu_2612	Tfu_2612 phosphoglucosamine mutase		12.2	15.38	14.97	20.13	0.827
EC	5.4.2.2	Phosphoglucomutase.	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
EC	5.4.2.8	Phosphomannomutase.	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / phosphomannomutase	19.06	18.82	21.97	21.81	25.49	1.131
EC	5.4.2.8	Phosphomannomutase.	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
EC	5.4.3.2	Lysine 2,3-aminomutase.	Tfu_0272	Tfu_0272 DUF160	17.82	17.78	20.43	19.91	24.03	1.174
EC	5.4.3.8	Glutamate-1-semialdehyde 2,1-aminomutase.	Tfu_2726	Tfu_2726 glutamate-1-semialdehyde aminotransferase	17.89	17.41	18.76	18.54	22.7	
EC	5.4.4.2	Isochorismate synthase.	Tfu_1413	Tfu_1413 isochorismate synthase						
EC	5.4.4.2	Isochorismate synthase.	Tfu_1872	Tfu_1872 isochorismate synthase					17.85	
EC	5.4.99.12	tRNA pseudouridine(38-40) synthase.	Tfu_2616	Tfu_2616 tRNA pseudouridine synthase A			15.6	16.26	20.01	
EC	5.4.99.16	Maltose alpha-D-glucosyltransferase.	Tfu_0584	Tfu_0584 alpha amylase, catalytic subdomain						
EC	5.4.99.18	5-(carboxyamino)imidazole ribonucleotide mutase.	Tfu_2546	Tfu_2546 1-(5-Phosphoribosyl)-5-amino-4-imidazole- carboxylate (AIR) carboxylase	17.46	17.22	17.98	17.21	21.62	
EC	5.4.99.19	16S rRNA pseudouridine(516) synthase.	Tfu_1206	Tfu_1206 pseudouridine synthase, Rsu					18.38	
EC	5.4.99.2	Methylmalonyl-CoA mutase.	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
EC	5.4.99.2	Methylmalonyl-CoA mutase.	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
EC	5.4.99.2	Methylmalonyl-CoA mutase.	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
EC	5.4.99.23	23S rRNA pseudouridine(1911/1915/1917) synthase.	Tfu_1123	Tfu_1123 pseudouridine synthase, RluD					18.53	
EC	5.4.99.25	tRNA pseudouridine(55) synthase.	Tfu_0781	Tfu_0781 tRNA pseudouridine synthase B					18.04	
EC	5.4.99.5	Chorismate mutase.	Tfu_1207	Tfu_1207 chorismate mutase of the AroH class						
EC	5.5.1.4	Inositol-3-phosphate synthase.	Tfu_3099	Tfu_3099 myo-inositol-1-phosphate synthase	16.21	15.62	18.24	18.23	23.01	0.924
EC	5.99.1.2	DNA topoisomerase.	Tfu_2784	Tfu_2784 bacterial DNA topoisomerase I	18.89	18.47	19.13	18.7	23.17	1.366
EC	5.99.1.3	DNA topoisomerase (ATP-hydrolyzing).	Tfu_0006	Tfu_0006 DNA topoisomerase IV subunit B	17.12	17.69	18.92	18.55	22.87	1.181
EC	5.99.1.3	DNA topoisomerase (ATP-hydrolyzing).	Tfu_0007	Tfu_0007 DNA gyrase, subunit A	19.16	19.14	20.72	20.43	24.43	1.156
EC	5.99.1.3	DNA topoisomerase (ATP-hydrolyzing).	Tfu_2131	Tfu_2131 DNA gyrase subunit A			14.33		20.22	
EC	5.99.1.3	DNA topoisomerase (ATP-hydrolyzing).	Tfu_2134	Tfu_2134 DNA gyrase subunit B		13.06			19.19	
EC	6.1.1.1	Tyrosine--tRNA ligase.	Tfu_2043	Tfu_2043 tyrosyl-tRNA synthetase, class Ib	16.28	16.71	18.6	18.54	22.47	1.194
EC	6.1.1.10	Methionine--tRNA ligase.	Tfu_0389	Tfu_0389 methionyl-tRNA synthetase	18.09	18	20.33	20.35	23.82	1.106
EC	6.1.1.11	Serine--tRNA ligase.	Tfu_0031	Tfu_0031 seryl-tRNA synthetase	19.71	19.5	20.47	20.38	23.8	0.939
EC	6.1.1.12	Aspartate--tRNA ligase.	Tfu_2086	Tfu_2086 aspartyl-tRNA synthetase	18.54	17.59	19.9	19.59	23.67	1.015
EC	6.1.1.14	Glycine--tRNA ligase.	Tfu_0861	Tfu_0861 glycyl-tRNA synthetase	18.27	17.66	19.58	19.58	23.56	1.154
EC	6.1.1.15	Proline--tRNA ligase.	Tfu_0772	Tfu_0772 prolyl-tRNA synthetase	19.32	19.13	19.74	19.37	23.57	1.007
EC	6.1.1.16	Cysteine--tRNA ligase.	Tfu_0212	Tfu_0212 cysteinyl-tRNA synthetase	16.41	14.49	18.9	18.08	23.01	1.169
EC	6.1.1.16	Cysteine--tRNA ligase.	Tfu_1832	Tfu_1832 cysteinyl-tRNA synthetase	15.91	16.04	18.24	17.09	22.24	1.186
EC	6.1.1.17	Glutamate--tRNA ligase.	Tfu_0623	Tfu_0623 glutamyl-tRNA synthetase bacterial/mitochondrial	18.5	17.36	18.79	19.22	23.34	0.908
EC	6.1.1.19	Arginine--tRNA ligase.	Tfu_0269	Tfu_0269 arginyl-tRNA synthetase, class Ic	17.72	17.49	20.13	19.85	24.16	1.223
EC	6.1.1.19	Arginine--tRNA ligase.	Tfu_2426	Tfu_2426 similar to Arginyl-tRNA synthetase					16.36	
EC	6.1.1.2	Tryptophan--tRNA ligase.	Tfu_2376	Tfu_2376 tryptophanyl-tRNA synthetase, class Ib	15.16		16.88	16.16	20.45	
EC	6.1.1.20	Phenylalanine--tRNA ligase.	Tfu_2060	Tfu_2060 phenylalanyl-tRNA synthetase beta subunit	19.74	19.67	20.55	20.4	24.66	1.059
EC	6.1.1.20	Phenylalanine--tRNA ligase.	Tfu_2061	Tfu_2061 phenylalanyl-tRNA synthetase alpha subunit	16.56	17.28	19.09	18.91	22.49	0.719
EC	6.1.1.21	Histidine--tRNA ligase.	Tfu_0759	Tfu_0759 histidine--tRNA ligase	16.98	16.75	18.26	18.29	22.52	0.925
EC	6.1.1.3	Threonine--tRNA ligase.	Tfu_2108	Tfu_2108 threonyl-tRNA synthetase	18.4	18.24	19.7	19.43	23.68	1.178
EC	6.1.1.4	Leucine--tRNA ligase.	Tfu_2156	Tfu_2156 leucyl-tRNA synthetase bacterial/mitochondrial, class Ia	20.17	20.38	21.64	21.31	25.2	1.161
EC	6.1.1.5	Isoleucine--tRNA ligase.	Tfu_1120	Tfu_1120 isoleucyl-tRNA synthetase, class Ia	16.68	16.31	19.54	19.65	23.84	1.694
EC	6.1.1.6	Lysine--tRNA ligase.	Tfu_2881	Tfu_2881 lysyl-tRNA synthetase, class-2	16.6	16.7	19.01	18.9	23.54	0.997
EC	6.1.1.7	Alanine--tRNA ligase.	Tfu_2070	Tfu_2070 alanyl-tRNA synthetase	18.51	18.11	19.5	19.52	23.9	1.221
EC	6.1.1.9	Valine--tRNA ligase.	Tfu_1936	Tfu_1936 valyl-tRNA synthetase	17.79	17.98	19.77	19.27	23.94	1.167
EC	6.2.1.-	Ligases. Forming carbon-sulfur bonds. Acid--thiol ligase	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly related to diterpenoid metabolism	16.49	15.45			20.78	

EC	6.2.1.-	Ligases. Forming carbon-sulfur bonds. Acid--thiol ligase	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
EC	6.2.1.1	Acetate--CoA ligase.	Tfu_1546	Tfu_1546 putative acyl-CoA synthetase					20.01	
EC	6.2.1.1	Acetate--CoA ligase.	Tfu_2808	Tfu_2808 putative acetyl-coenzyme A synthetase			16.12	15.88	21.7	
EC	6.2.1.1	Acetate--CoA ligase.	Tfu_2856	Tfu_2856 acetyl-coenzyme A synthetase	24.08	23.76	23.99	23.94	27	1.638
EC	6.2.1.14	6-carboxyhexanoate--CoA ligase.	Tfu_1302	Tfu_1302 probable 6-carboxyhexanoate--COA ligase					15.64	
EC	6.2.1.16	Acetoacetate--CoA ligase.	Tfu_2245	Tfu_2245 acetoacetyl-CoA synthase	21.88	21.42	21.12	20.91	24.4	0.895
EC	6.2.1.26	o-succinylbenzoate--CoA ligase.	Tfu_1408	Tfu_1408 putative ortho-succinylbenzoate-CoA synthetase						
EC	6.2.1.3	Long-chain-fatty-acid--CoA ligase.	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
EC	6.2.1.3	Long-chain-fatty-acid--CoA ligase.	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
EC	6.2.1.3	Long-chain-fatty-acid--CoA ligase.	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
EC	6.2.1.3	Long-chain-fatty-acid--CoA ligase.	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
EC	6.2.1.5	Succinate--CoA ligase (ADP-forming).	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
EC	6.2.1.5	Succinate--CoA ligase (ADP-forming).	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
EC	6.3.-	Ligases. Forming carbon-nitrogen bonds.	Tfu_2565	Tfu_2565 Enzymatic protein of unknown function	15.64	15.14	17.69	15.59	21.46	1.452
EC	6.3.1.10	Adenosylcobinamide-phosphate synthase.	Tfu_2224	Tfu_2224 cobalamin biosynthesis protein						
EC	6.3.1.13	L-cysteine:1D-myo-inositol 2-amino-2-deoxy-alpha-D-g	Tfu_1832	Tfu_1832 cysteinyl-tRNA synthetase	15.91	16.04	18.24	17.09	22.24	1.186
EC	6.3.1.2	Glutamate--ammonia ligase.	Tfu_0982	Tfu_0982 glutamine synthetase type I	16.36	15.34	14.3	15.33	20.84	1.147
EC	6.3.1.2	Glutamate--ammonia ligase.	Tfu_0988	Tfu_0988 glutamine synthetase type I		16.24	19.93	19.87	23.49	1.247
EC	6.3.2.-	Ligases. Forming carbon-nitrogen bonds. Acid--D-amino	Tfu_1788	Tfu_1788 hypothetical protein	19.06	18.7	19.67	19.63	23.68	1.295
EC	6.3.2.-	Ligases. Forming carbon-nitrogen bonds. Acid--D-amino	Tfu_1796	Tfu_1796 putative proteasome component	14.51	14.96	17.7	16.83	22.14	
EC	6.3.2.1	Pantoate--beta-alanine ligase.	Tfu_2884	Tfu_2884 pantoate-beta-alanine ligase	18.94	18.13	19.39	18.92	22.68	1.137
EC	6.3.2.10	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine	Tfu_1106	Tfu_1106 UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase		13.98	15.35	14.44	21.31	0.824
EC	6.3.2.12	Dihydrofolate synthase.	Tfu_2190	Tfu_2190 folylpolyglutamate synthetase					19.35	
EC	6.3.2.13	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-dian	Tfu_1105	Tfu_1105 UDP-N-acetylmuramyl-tripeptide synthetase	15.32	14.97	16.06	15.77	20.43	0.647
EC	6.3.2.17	Tetrahydrofolate synthase.	Tfu_2190	Tfu_2190 folylpolyglutamate synthetase					19.35	
EC	6.3.2.31	Coenzyme F420-0:L-glutamate ligase.	Tfu_2518	Tfu_2518 hypothetical protein			14.93		19.68	
EC	6.3.2.34	Coenzyme F420-1:gamma-L-glutamate ligase.	Tfu_2518	Tfu_2518 hypothetical protein			14.93		19.68	
EC	6.3.2.4	D-alanine--D-alanine ligase.	Tfu_0633	Tfu_0633 D-alanylalanine synthetase	15.85	14.68	13.91		19.95	0.685
EC	6.3.2.4	D-alanine--D-alanine ligase.	Tfu_1640	Tfu_1640 D-alanine--D-alanine ligase					15.9	
EC	6.3.2.5	Phosphopantothenate--cysteine ligase.	Tfu_1064	Tfu_1064 phosphopantothenoylcysteine synthase/decarboxylase	18.49	18.47	18.49	18.95	22.74	1.103
EC	6.3.2.6	Phosphoribosylaminoimidazolesuccinocarboxamide syn	Tfu_3015	Tfu_3015 phosphoribosylaminoimidazole-succinocarboxamide synthase	17.2	16.06	17.97	17.67	21.89	0.805
EC	6.3.2.8	UDP-N-acetylmuramate--L-alanine ligase.	Tfu_1111	Tfu_1111 UDP-N-acetylmuramate--alanine ligase			14.68	15.53	20.38	1.128
EC	6.3.2.9	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase.	Tfu_1108	Tfu_1108 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase					18.55	
EC	6.3.3.1	Phosphoribosylformylglycinamidine cyclo-ligase.	Tfu_2748	Tfu_2748 phosphoribosylaminoimidazole synthetase	14.77		17.56	17.33	20.81	0.689
EC	6.3.3.2	5-formyltetrahydrofolate cyclo-ligase.	Tfu_0372	Tfu_0372 hypothetical protein						
EC	6.3.4.13	Phosphoribosylamine--glycine ligase.	Tfu_3013	Tfu_3013 phosphoribosylglycinamide synthetase			17.63	17.26	21.77	
EC	6.3.4.14	Biotin carboxylase.	Tfu_0947	Tfu_0947 putative acetyl/propionyl CoA carboxylase alpha subunit: biotin carboxylase	20.64	20.68	21.06	20.9	24.61	1.056
EC	6.3.4.14	Biotin carboxylase.	Tfu_1228	Tfu_1228 putative acyl-CoA carboxylase complex A subunit						
EC	6.3.4.14	Biotin carboxylase.	Tfu_2557	Tfu_2557 putative acyl-CoA carboxylase, alpha subunit	16.42	15.3	17.56	17.37	22.48	
EC	6.3.4.15	Biotin--[acetyl-CoA-carboxylase] ligase.	Tfu_2553	Tfu_2553 biotin--acetyl-CoA-carboxylase ligase						
EC	6.3.4.18	5-(carboxyamino)imidazole ribonucleotide synthase.	Tfu_2547	Tfu_2547 phosphoribosylaminoimidazole carboxylase, ATPase subunit					18.27	
EC	6.3.4.2	CTP synthase.	Tfu_1199	Tfu_1199 CTP synthetase	15.21	15.76	18.58	17.89	22.8	1.201
EC	6.3.4.4	Adenylosuccinate synthase.	Tfu_3012	Tfu_3012 adenylosuccinate synthetase	15.75	15.57	18.76	18.61	22.25	0.954
EC	6.3.4.5	Argininosuccinate synthase.	Tfu_2052	Tfu_2052 argininosuccinate synthase	13.3		18.49	17.16	22.53	
EC	6.3.5.1	NAD(+) synthase (glutamine-hydrolyzing).	Tfu_0983	Tfu_0983 NAD+ synthase	16.91	16.85	17.72	17.22	22.21	0.82
EC	6.3.5.10	Adenosylcobyric acid synthase (glutamine-hydrolyzing)	Tfu_0309	Tfu_0309 cobyric acid synthase					19.41	
EC	6.3.5.11	Cobyrinate a,c-diamide synthase (glutamine-hydrolyzin	Tfu_0311	Tfu_0311 cobyrinic acid a,c-diamide synthase CbiA					16.36	
EC	6.3.5.2	GMP synthase (glutamine-hydrolyzing).	Tfu_2589	Tfu_2589 bifunctional GMP synthase/glutamine amidotransferase protein	14.94		18.4	18.53	23.34	1.278
EC	6.3.5.3	Phosphoribosylformylglycinamidine synthase.	Tfu_0156	Tfu_0156 phosphoribosylformylglycinamidine synthase I			15.57	15.14	21.14	0.902
EC	6.3.5.3	Phosphoribosylformylglycinamidine synthase.	Tfu_0158	Tfu_0158 phosphoribosylformylglycinamidine synthase subunit II	13.89	15.06	17.93	18.1	22.88	0.924
EC	6.3.5.3	Phosphoribosylformylglycinamidine synthase.	Tfu_0178	Tfu_0178 phosphoribosylformylglycinamidine synthase					17.74	

EC	6.3.5.4	Asparagine synthase (glutamine-hydrolyzing).	Tfu_1145	Tfu_1145 hypothetical protein						
EC	6.3.5.5	Carbamoyl-phosphate synthase (glutamine-hydrolyzing	Tfu_1056	Tfu_1056 carbamoyl-phosphate synthase, small subunit		15.52	17.25	17.26	22.56	0.884
EC	6.3.5.5	Carbamoyl-phosphate synthase (glutamine-hydrolyzing	Tfu_1057	Tfu_1057 carbamoyl-phosphate synthase, large subunit, glutamine-dependent	16.53	16.24	19.8	19.69	24.13	0.99
EC	6.3.5.6	Asparaginyl-tRNA synthase (glutamine-hydrolyzing).	Tfu_0605	Tfu_0605 aspartyl/glutamyl-tRNA amidotransferase subunit C				14.86	18.24	
EC	6.3.5.6	Asparaginyl-tRNA synthase (glutamine-hydrolyzing).	Tfu_0606	Tfu_0606 glutamyl-tRNA amidotransferase subunit A	15.37		19.4	18.8	23.02	0.99
EC	6.3.5.6	Asparaginyl-tRNA synthase (glutamine-hydrolyzing).	Tfu_0609	Tfu_0609 aspartyl/glutamyl-tRNA amidotransferase subunit B	15.46	16.45	19.76	19.56	23.81	
EC	6.3.5.7	Glutaminyl-tRNA synthase (glutamine-hydrolyzing).	Tfu_0605	Tfu_0605 aspartyl/glutamyl-tRNA amidotransferase subunit C				14.86	18.24	
EC	6.3.5.7	Glutaminyl-tRNA synthase (glutamine-hydrolyzing).	Tfu_0606	Tfu_0606 glutamyl-tRNA amidotransferase subunit A	15.37		19.4	18.8	23.02	0.99
EC	6.3.5.7	Glutaminyl-tRNA synthase (glutamine-hydrolyzing).	Tfu_0609	Tfu_0609 aspartyl/glutamyl-tRNA amidotransferase subunit B	15.46	16.45	19.76	19.56	23.81	
EC	6.3.5.9	Hydrogenobyrinic acid a,c-diamide synthase (glutamine	Tfu_0311	Tfu_0311 cobyrinic acid a,c-diamide synthase CbiA					16.36	
EC	6.4.1.3	Propionyl-CoA carboxylase.	Tfu_2555	Tfu_2555 propionyl-CoA carboxylase complex B subunit	18.59	18.29	18.47	17.99	22.37	0.744
EC	6.4.1.4	Methylcrotonoyl-CoA carboxylase.	Tfu_0948	Tfu_0948 propionyl-CoA carboxylase	20.47	20.23	20.41	20.19	24.8	
EC	6.5.1.-	Ligases. Forming phosphoric ester bonds. Ligases that f	Tfu_0243	Tfu_0243 hypothetical protein					16.84	
EC	6.5.1.2	DNA ligase (NAD(+)).	Tfu_0603	Tfu_0603 DNA ligase	17.51	17.99	18.58	17.99	22.94	
EC	6.5.1.3	RNA ligase (ATP).	Tfu_1357	Tfu_1357 hypothetical protein						
EC	6.6.1.1	Magnesium chelatase.	Tfu_0313	Tfu_0313 Mg-chelatase subunit ChlI	16.96	16.73	17.38	16.55	20.43	
EC	6.6.1.1	Magnesium chelatase.	Tfu_0443	Tfu_0443 magnesium chelatase subunit ChlI					17.16	
EC	6.6.1.2	Cobaltochelatase.	Tfu_0319	Tfu_0319 cobaltochelatase	18.14	17.88	19.25	19.28	23.66	1.195

Appendix - E - Proteomics Data HOV: MetaCyc

CLASS	HOV	HOV-description	locus	locus-description	AV	AVR	CB	CBR	CB2D	iTRAQ
METACYC	LYSDEGII-PWY	lysine degradation III	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	LYSDEGII-PWY	lysine degradation III	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	LYSDEGII-PWY	lysine degradation III	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	LYSDEGII-PWY	lysine degradation III	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6000	γ-linolenate biosynthesis II (animals)	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-6000	γ-linolenate biosynthesis II (animals)	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-6000	γ-linolenate biosynthesis II (animals)	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6000	γ-linolenate biosynthesis II (animals)	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-5284	shisonin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5284	shisonin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5284	shisonin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5284	shisonin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5284	shisonin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5284	shisonin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5284	shisonin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	SUCSYN-PWY	sucrose biosynthesis	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase,	16.85	15	17.24	17.46	22.15	
METACYC	SUCSYN-PWY	sucrose biosynthesis	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
METACYC	SUCSYN-PWY	sucrose biosynthesis	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	SUCSYN-PWY	sucrose biosynthesis	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	SUCSYN-PWY	sucrose biosynthesis	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	SUCSYN-PWY	sucrose biosynthesis	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	SUCSYN-PWY	sucrose biosynthesis	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	SUCSYN-PWY	sucrose biosynthesis	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-6728	methylaspartate cycle	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	PWY-6728	methylaspartate cycle	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	PWY-6728	methylaspartate cycle	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	PWY-6728	methylaspartate cycle	Tfu_0819	Tfu_0819 malate synthase	20.71	20.65	20.77	20.84	24.52	0.986
METACYC	PWY-6728	methylaspartate cycle	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	PWY-6728	methylaspartate cycle	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
METACYC	PWY-6728	methylaspartate cycle	Tfu_2481	Tfu_2481 putative NAD-glutamate dehydrogenase	20.96	20.83	21.88	21.73	25.49	1.153
METACYC	PWY-6728	methylaspartate cycle	Tfu_2555	Tfu_2555 propionyl-CoA carboxylase complex B subunit	18.59	18.29	18.47	17.99	22.37	0.744
METACYC	PWY-6728	methylaspartate cycle	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
METACYC	PWY-6728	methylaspartate cycle	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
METACYC	PWY-6728	methylaspartate cycle	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
METACYC	PWY-6728	methylaspartate cycle	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
METACYC	PWY-6728	methylaspartate cycle	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
METACYC	PWY-6728	methylaspartate cycle	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
METACYC	PWY-981	salicylate biosynthesis II	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-981	salicylate biosynthesis II	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-981	salicylate biosynthesis II	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY-241	C4 photosynthetic carbon assimilation cycle	Tfu_0863	Tfu_0863 pyruvate phosphate dikinase	17.84	17.11	21.38	21.45	25.04	1.455
METACYC	PWY-241	C4 photosynthetic carbon assimilation cycle	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	PWY-6624	salicylate glucosides biosynthesis III	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6624	salicylate glucosides biosynthesis III	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6624	salicylate glucosides biosynthesis III	Tfu_1764	Tfu_1764 putative glycosyl transferase						

METACYC	PWY-1121	suberin biosynthesis	Tfu_0966	Tfu_0966 caffeoyl-CoA O-methyltransferase		13.62			16.15	
METACYC	PWY-1121	suberin biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-1121	suberin biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6608	guanosine nucleotides degradation III	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY-5871	ubiquinol-9 biosynthesis (eukaryotic)	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-6890	4-amino-2-methyl-5-diphosphomethylpyrimidine bi	Tfu_2250	Tfu_2250 phosphomethylpyrimidine kinase	16.07	16.41	14.97		19.92	1.225
METACYC	LARABITOLUTIL-PWY	xylitol degradation	Tfu_1575	Tfu_1575 putative sugar kinase protein						
METACYC	LARABITOLUTIL-PWY	xylitol degradation	Tfu_1604	Tfu_1604 xylulokinase	16.69	16.85	17.01	17.12	22.06	
METACYC	GLYOXDEG-PWY	glycolate and glyoxylate degradation II	Tfu_0819	Tfu_0819 malate synthase	20.71	20.65	20.77	20.84	24.52	0.986
METACYC	PWY-6148	tetrahydromethanopterin biosynthesis	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
METACYC	PWY-5773	gossypol biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5773	gossypol biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	P121-PWY	adenine and adenosine salvage I	Tfu_2091	Tfu_2091 adenine phosphoribosyltransferase		14.26			19.51	0.761
METACYC	P121-PWY	adenine and adenosine salvage I	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY-6477	gibberellin inactivation II (methylation)	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6477	gibberellin inactivation II (methylation)	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6854	ethylene biosynthesis III (microbes)	Tfu_0957	Tfu_0957 superoxide dismutase	22.64	22.53	22.08	22.69	25.05	0.848
METACYC	PWY-6854	ethylene biosynthesis III (microbes)	Tfu_2766	Tfu_2766 hypothetical protein	17.21	16.85	15.75	15.26	19.61	
METACYC	PWY-6805	cellulose degradation I (cellulosome)	Tfu_0620	Tfu_0620 hypothetical protein						
METACYC	PWY-6805	cellulose degradation I (cellulosome)	Tfu_0901	Tfu_0901 hypothetical protein						
METACYC	PWY-6805	cellulose degradation I (cellulosome)	Tfu_1074	Tfu_1074 hypothetical protein						
METACYC	PWY-6805	cellulose degradation I (cellulosome)	Tfu_1627	Tfu_1627 hypothetical protein						
METACYC	PWY-6805	cellulose degradation I (cellulosome)	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6805	cellulose degradation I (cellulosome)	Tfu_1959	Tfu_1959 hypothetical protein					15.56	
METACYC	PWY-6805	cellulose degradation I (cellulosome)	Tfu_2176	Tfu_2176 hypothetical protein						
METACYC	PWY-6805	cellulose degradation I (cellulosome)	Tfu_2712	Tfu_2712 hypothetical protein						
METACYC	PWY0-321	phenylacetate degradation I (aerobic)	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	PWY0-321	phenylacetate degradation I (aerobic)	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	PWY0-321	phenylacetate degradation I (aerobic)	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
METACYC	PWY0-321	phenylacetate degradation I (aerobic)	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	PWY0-321	phenylacetate degradation I (aerobic)	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
METACYC	PWY0-321	phenylacetate degradation I (aerobic)	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
METACYC	PWY0-321	phenylacetate degradation I (aerobic)	Tfu_1278	Tfu_1278 thiolase						
METACYC	PWY0-321	phenylacetate degradation I (aerobic)	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	PWY0-321	phenylacetate degradation I (aerobic)	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	PWY0-321	phenylacetate degradation I (aerobic)	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
METACYC	ACETOACETATE-DEG-PWY	acetoacetate degradation (to acetyl CoA)	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	ACETOACETATE-DEG-PWY	acetoacetate degradation (to acetyl CoA)	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	ACETOACETATE-DEG-PWY	acetoacetate degradation (to acetyl CoA)	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	ACETOACETATE-DEG-PWY	acetoacetate degradation (to acetyl CoA)	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	TRPSYN-PWY	tryptophan biosynthesis	Tfu_1024	Tfu_1024 anthranilate phosphoribosyltransferase						
METACYC	TRPSYN-PWY	tryptophan biosynthesis	Tfu_1155	Tfu_1155 1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylidene			15.7	16.67	21.72	
METACYC	TRPSYN-PWY	tryptophan biosynthesis	Tfu_1164	Tfu_1164 indole-3-glycerol-phosphate synthase					20.46	1.072
METACYC	TRPSYN-PWY	tryptophan biosynthesis	Tfu_1386	Tfu_1386 glutamine amidotransferase of anthranilate syr	14.29	15.3	14.48	14.83	21.47	1.207
METACYC	SOPHOROSYLOXYDOCOSANOATE-SYN-PWY	sophorosyloxydocosanoate biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	SOPHOROSYLOXYDOCOSANOATE-SYN-PWY	sophorosyloxydocosanoate biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	SOPHOROSYLOXYDOCOSANOATE-SYN-PWY	sophorosyloxydocosanoate biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	SOPHOROSYLOXYDOCOSANOATE-SYN-PWY	sophorosyloxydocosanoate biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6986	alginate degradation	Tfu_0189	Tfu_0189 putative PfkB-family carbohydrate kinase						
METACYC	PWY-6411	ginsenoside degradation I	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						

METACYC	PWY-6411	ginsenoside degradation I	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6411	ginsenoside degradation I	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6411	ginsenoside degradation I	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6930	phenolic malonylglucosides biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6930	phenolic malonylglucosides biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6930	phenolic malonylglucosides biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6930	phenolic malonylglucosides biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-1801	formaldehyde oxidation II (glutathione-dependent)	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-1801	formaldehyde oxidation II (glutathione-dependent)	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-5856	ubiquinol-9 biosynthesis (prokaryotic)	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-3341	proline biosynthesis III	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
METACYC	PWY-3341	proline biosynthesis III	Tfu_2708	Tfu_2708 delta 1-pyrroline-5-carboxylate reductase	17.73	17.16	18.03	17.57	21.11	
METACYC	PWY-6124	inosine-5'-phosphate biosynthesis II	Tfu_2572	Tfu_2572 bifunctional phosphoribosylaminoimidazolecar	19.86	19.04	20.76	20.79	24.53	0.912
METACYC	PWY-6124	inosine-5'-phosphate biosynthesis II	Tfu_3014	Tfu_3014 adenylosuccinate lyase	18.68	18.68	20.17	19.69	23.57	0.954
METACYC	PWY-6124	inosine-5'-phosphate biosynthesis II	Tfu_3015	Tfu_3015 phosphoribosylaminoimidazole-succinocarbox	17.2	16.06	17.97	17.67	21.89	0.805
METACYC	PWY-5759	saponin biosynthesis III	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5759	saponin biosynthesis III	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5759	saponin biosynthesis III	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6442	spermidine hydroxycinnamic acid conjugates biosyn	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6442	spermidine hydroxycinnamic acid conjugates biosyn	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6442	spermidine hydroxycinnamic acid conjugates biosyn	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6442	spermidine hydroxycinnamic acid conjugates biosyn	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6442	spermidine hydroxycinnamic acid conjugates biosyn	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6442	spermidine hydroxycinnamic acid conjugates biosyn	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	TREDEGLOW-PWY	trehalose degradation I (low osmolarity)	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	TREDEGLOW-PWY	trehalose degradation I (low osmolarity)	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	PWY-5642	2,4-dinitrotoluene degradation	Tfu_0687	Tfu_0687 methylmalonate-semialdehyde dehydrogenase	18.43	17.24	18.03	18.14	22.37	1.017
METACYC	DARABCAT-PWY	D-arabinose degradation II	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
METACYC	PWY0-1297	purine deoxyribonucleosides degradation	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY-1861	formaldehyde assimilation II (RuMP Cycle)	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
METACYC	PWY-1861	formaldehyde assimilation II (RuMP Cycle)	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
METACYC	PWY-1861	formaldehyde assimilation II (RuMP Cycle)	Tfu_2003	Tfu_2003 transaldolase	20.04	20.08	21.54	21.1	24.47	1.211
METACYC	PWY-1861	formaldehyde assimilation II (RuMP Cycle)	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
METACYC	PWY-1861	formaldehyde assimilation II (RuMP Cycle)	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-6837	fatty acid beta-oxidation V (unsaturated, odd numbe	Tfu_2239	Tfu_2239 hypothetical protein	17.58	17.57	18.21	17.62	22.75	0.874
METACYC	PWY-7043	11-cis-3-hydroxyretinal biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-7043	11-cis-3-hydroxyretinal biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5338	galactosylcyclitol biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5338	galactosylcyclitol biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5338	galactosylcyclitol biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY490-3	nitrate reduction VI (assimilatory)	Tfu_0982	Tfu_0982 glutamine synthetase type I	16.36	15.34	14.3	15.33	20.84	1.147
METACYC	PWY490-3	nitrate reduction VI (assimilatory)	Tfu_0988	Tfu_0988 glutamine synthetase type I		16.24	19.93	19.87	23.49	1.247
METACYC	PWY490-3	nitrate reduction VI (assimilatory)	Tfu_1371	Tfu_1371 glutamate dehydrogenase	13.87		17.06	16.78	21.17	1.233
METACYC	PWY490-3	nitrate reduction VI (assimilatory)	Tfu_1888	Tfu_1888 putative nitrite/sulphite reductase	16.01	13.98	17.79	17.82	22.36	1.384
METACYC	PWY-5	canavanine biosynthesis	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
METACYC	PWY-5	canavanine biosynthesis	Tfu_2051	Tfu_2051 argininosuccinate lyase	15.68	16.51	18.68	18.9	22.79	
METACYC	PWY-5	canavanine biosynthesis	Tfu_2052	Tfu_2052 argininosuccinate synthase	13.3		18.49	17.16	22.53	
METACYC	PWY-5737	(5R)-carbapenem biosynthesis	Tfu_0434	Tfu_0434 proline dehydrogenase	18.28	18.4	17.73	16.85	22.15	1.304
METACYC	PWY-6739	pinitol biosynthesis II	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6739	pinitol biosynthesis II	Tfu_2418	Tfu_2418 modification methylase HemK						

METACYC	PWY-5176	coumarin biosynthesis (via 2-coumarate)	Tfu_0937	Tfu_0937 beta-glucosidase	16.92	16.79	21.22	20.91	23.7	2.426
METACYC	PWY-5176	coumarin biosynthesis (via 2-coumarate)	Tfu_1607	Tfu_1607 beta-glucosidase						
METACYC	PWY-5176	coumarin biosynthesis (via 2-coumarate)	Tfu_1629	Tfu_1629 beta-glucosidase	20.15	19.64	19.92	19.43	23.45	1.12
METACYC	ALACAT2-PWY	alanine degradation II (to D-lactate)	Tfu_2481	Tfu_2481 putative NAD-glutamate dehydrogenase	20.96	20.83	21.88	21.73	25.49	1.153
METACYC	VALDEG-PWY	valine degradation I	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	VALDEG-PWY	valine degradation I	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	VALDEG-PWY	valine degradation I	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
METACYC	VALDEG-PWY	valine degradation I	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	VALDEG-PWY	valine degradation I	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	VALDEG-PWY	valine degradation I	Tfu_0687	Tfu_0687 methylmalonate-semialdehyde dehydrogenase	18.43	17.24	18.03	18.14	22.37	1.017
METACYC	VALDEG-PWY	valine degradation I	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
METACYC	VALDEG-PWY	valine degradation I	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
METACYC	VALDEG-PWY	valine degradation I	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	VALDEG-PWY	valine degradation I	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	VALDEG-PWY	valine degradation I	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	PWY-1061	homogalacturonan biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-1061	homogalacturonan biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6164	3-dehydroquinate biosynthesis I	Tfu_1039	Tfu_1039 phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 2						
METACYC	PWY-6164	3-dehydroquinate biosynthesis I	Tfu_1092	Tfu_1092 3-dehydroquinate synthase	18.86	18.36	19.22	18.34	23.14	1.077
METACYC	PWY-6164	3-dehydroquinate biosynthesis I	Tfu_2350	Tfu_2350 phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1			14.88	13.66	19.21	
METACYC	PWY-84	resveratrol biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-84	resveratrol biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-84	resveratrol biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-84	resveratrol biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6105	botryococcenes and methylated squalene biosynthes	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-6105	botryococcenes and methylated squalene biosynthes	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6105	botryococcenes and methylated squalene biosynthes	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-6105	botryococcenes and methylated squalene biosynthes	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6105	botryococcenes and methylated squalene biosynthes	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6588	pyruvate fermentation to acetone	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-6588	pyruvate fermentation to acetone	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-6588	pyruvate fermentation to acetone	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-6588	pyruvate fermentation to acetone	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	UDPNACETYLGALSYN-PWY	UDP-N-acetyl-D-glucosamine biosynthesis II	Tfu_0414	Tfu_0414 UDP-N-acetylglucosamine pyrophosphorylase	19.4	19.37	19.9	19.97	23.72	1.114
METACYC	UDPNACETYLGALSYN-PWY	UDP-N-acetyl-D-glucosamine biosynthesis II	Tfu_2611	Tfu_2611 D-fructose-6-phosphate amidotransferase	16.46	16.09	18.53	18.54	22.75	1.101
METACYC	PWY-5082	methionine degradation III	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-5082	methionine degradation III	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-5082	methionine degradation III	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-5082	methionine degradation III	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-181	photorespiration	Tfu_1010	Tfu_1010 glycerate kinase			14.48		20.4	
METACYC	PWY-181	photorespiration	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
METACYC	PWY-181	photorespiration	Tfu_2980	Tfu_2980 (S)-2-hydroxy-acid oxidase					14.64	
METACYC	ANARESP1-PWY	respiration (anaerobic)	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	ANARESP1-PWY	respiration (anaerobic)	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	ANARESP1-PWY	respiration (anaerobic)	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	ANARESP1-PWY	respiration (anaerobic)	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	ANARESP1-PWY	respiration (anaerobic)	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	ANARESP1-PWY	respiration (anaerobic)	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	ANARESP1-PWY	respiration (anaerobic)	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	ANARESP1-PWY	respiration (anaerobic)	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131

METACYC	PWY-5958	acridone alkaloid biosynthesis	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-5958	acridone alkaloid biosynthesis	Tfu_1386	Tfu_1386 glutamine amidotransferase of anthranilate syr	14.29	15.3	14.48	14.83	21.47	1.207
METACYC	PWY-5958	acridone alkaloid biosynthesis	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6282	palmitoleate biosynthesis I	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWY-6282	palmitoleate biosynthesis I	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWY-6282	palmitoleate biosynthesis I	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWY-6282	palmitoleate biosynthesis I	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	PWY-6383	mono-trans, poly-cis decaprenyl phos	Tfu_0456	Tfu_0456 di-trans-poly-cis-decaprenylcistransferase					16.85	
METACYC	PWY-6383	mono-trans, poly-cis decaprenyl phos	Tfu_0543	Tfu_0543 hypothetical protein			13.59	14.81	19.36	
METACYC	PWY-6383	mono-trans, poly-cis decaprenyl phos	Tfu_0576	Tfu_0576 hypothetical protein					17.31	
METACYC	PWY-6383	mono-trans, poly-cis decaprenyl phos	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
METACYC	PWY-6383	mono-trans, poly-cis decaprenyl phos	Tfu_2457	Tfu_2457 putative mutT-like protein						
METACYC	ANAEROFRUCAT-PWY	homolactic fermentation	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	ANAEROFRUCAT-PWY	homolactic fermentation	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	ANAEROFRUCAT-PWY	homolactic fermentation	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	ANAEROFRUCAT-PWY	homolactic fermentation	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	NAD-BIOSYNTHESIS-II	NAD salvage pathway II	Tfu_0527	Tfu_0527 hypothetical protein					16.28	
METACYC	P108-PWY	pyruvate fermentation to propionate I	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	P108-PWY	pyruvate fermentation to propionate I	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	P108-PWY	pyruvate fermentation to propionate I	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
METACYC	P108-PWY	pyruvate fermentation to propionate I	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
METACYC	P108-PWY	pyruvate fermentation to propionate I	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
METACYC	P108-PWY	pyruvate fermentation to propionate I	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
METACYC	PWY-5154	arginine biosynthesis III	Tfu_1056	Tfu_1056 carbamoyl-phosphate synthase, small subunit		15.52	17.25	17.26	22.56	0.884
METACYC	PWY-5154	arginine biosynthesis III	Tfu_1057	Tfu_1057 carbamoyl-phosphate synthase, large subunit,	16.53	16.24	19.8	19.69	24.13	0.99
METACYC	PWY-5154	arginine biosynthesis III	Tfu_2051	Tfu_2051 argininosuccinate lyase	15.68	16.51	18.68	18.9	22.79	
METACYC	PWY-5154	arginine biosynthesis III	Tfu_2052	Tfu_2052 argininosuccinate synthase	13.3		18.49	17.16	22.53	
METACYC	PWY-5154	arginine biosynthesis III	Tfu_2054	Tfu_2054 acetylornithine and succinylornithine aminotra	16.33	18.16	18.68	18.83	22.2	1.056
METACYC	PWY-5154	arginine biosynthesis III	Tfu_2055	Tfu_2055 acetylglutamate kinase		13.89	16.85	16.6	21.88	1.485
METACYC	PWY-5154	arginine biosynthesis III	Tfu_2056	Tfu_2056 bifunctional ornithine acetyltransferase/N-ace	17.05	16.43	18.49	17.65	22.7	
METACYC	PWY-5154	arginine biosynthesis III	Tfu_2057	Tfu_2057 N-acetyl-gamma-glutamyl-phosphate reductase					20.33	
METACYC	PWY-5154	arginine biosynthesis III	Tfu_2879	Tfu_2879 hypothetical protein	13.85	13.58			19.82	
METACYC	PWY-4942	cyclopropane and cyclopropene fatty acid biosynthes	Tfu_2160	Tfu_2160 putative cyclopropane fatty acid synthase	20.23	19.76	18.57	18.29	22.69	1.518
METACYC	PROPIONMET-PWY	methylmalonyl pathway	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
METACYC	PROPIONMET-PWY	methylmalonyl pathway	Tfu_2555	Tfu_2555 propionyl-CoA carboxylase complex B subunit	18.59	18.29	18.47	17.99	22.37	0.744
METACYC	PROPIONMET-PWY	methylmalonyl pathway	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
METACYC	PROPIONMET-PWY	methylmalonyl pathway	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
METACYC	PROPIONMET-PWY	methylmalonyl pathway	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
METACYC	P122-PWY	heterolactic fermentation	Tfu_0003	Tfu_0003 6-phosphogluconate dehydrogenase	20.18	20.31	19.92	19.72	23.9	0.655
METACYC	P122-PWY	heterolactic fermentation	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	P122-PWY	heterolactic fermentation	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	P122-PWY	heterolactic fermentation	Tfu_0928	Tfu_0928 fructokinase	18.37	17.96	18.63	18.42	22.16	0.898
METACYC	P122-PWY	heterolactic fermentation	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	P122-PWY	heterolactic fermentation	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
METACYC	P122-PWY	heterolactic fermentation	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	P122-PWY	heterolactic fermentation	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	P122-PWY	heterolactic fermentation	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	P122-PWY	heterolactic fermentation	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	P122-PWY	heterolactic fermentation	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	P122-PWY	heterolactic fermentation	Tfu_1953	Tfu_1953 hypothetical protein					16.39	

METACYC	P122-PWY	heterolactic fermentation	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	P122-PWY	heterolactic fermentation	Tfu_2005	Tfu_2005 glucose-6-phosphate 1-dehydrogenase	16.6	15.74	16.81	16.27	21.46	
METACYC	P122-PWY	heterolactic fermentation	Tfu_2007	Tfu_2007 6-phosphogluconolactonase	18.7	19.13	18.21	17.98	22.37	0.913
METACYC	P122-PWY	heterolactic fermentation	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	P122-PWY	heterolactic fermentation	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	P122-PWY	heterolactic fermentation	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	P122-PWY	heterolactic fermentation	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	P122-PWY	heterolactic fermentation	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	P122-PWY	heterolactic fermentation	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	RIBITOLUTIL-PWY	ribitol degradation	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
METACYC	PWY-5036	gibberellin biosynthesis II (early C-3 hydroxylation)	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-6537	4-aminobutyrate degradation II	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
METACYC	PWY-6333	acetaldehyde biosynthesis I	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-6333	acetaldehyde biosynthesis I	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-6333	acetaldehyde biosynthesis I	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-6333	acetaldehyde biosynthesis I	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY4FS-3	phosphatidylcholine biosynthesis III	Tfu_0735	Tfu_0735 ubiquinone/menaquinone biosynthesis methyltransferase						
METACYC	PWY4FS-3	phosphatidylcholine biosynthesis III	Tfu_1855	Tfu_1855 4'-phosphopantetheinyl transferase						
METACYC	PWY4FS-3	phosphatidylcholine biosynthesis III	Tfu_2817	Tfu_2817 hypothetical protein					18.27	
METACYC	PWY-6951	docosahexanoate biosynthesis	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-6951	docosahexanoate biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6951	docosahexanoate biosynthesis	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWY-6951	docosahexanoate biosynthesis	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-6951	docosahexanoate biosynthesis	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWY-6951	docosahexanoate biosynthesis	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWY-6951	docosahexanoate biosynthesis	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6951	docosahexanoate biosynthesis	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-6951	docosahexanoate biosynthesis	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	PWY-5915	phycoerythrobilin biosynthesis	Tfu_2345	Tfu_2345 heme oxygenase (decyclizing)						
METACYC	PWY-6080	4-ethylphenol degradation (anaerobic)	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6080	4-ethylphenol degradation (anaerobic)	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-3161	IAA biosynthesis VI (via indole-3-acetamide)	Tfu_2207	Tfu_2207 amidase					14.6	
METACYC	PWY-5876	magnoflorine biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5876	magnoflorine biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	CITRULBIO-PWY	citrulline biosynthesis	Tfu_0434	Tfu_0434 proline dehydrogenase	18.28	18.4	17.73	16.85	22.15	1.304
METACYC	CITRULBIO-PWY	citrulline biosynthesis	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
METACYC	CITRULBIO-PWY	citrulline biosynthesis	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
METACYC	CITRULBIO-PWY	citrulline biosynthesis	Tfu_2175	Tfu_2175 gamma-glutamyl phosphate reductase GPR	16.65	16.53	17.82	17.26	21.71	
METACYC	CITRULBIO-PWY	citrulline biosynthesis	Tfu_2179	Tfu_2179 gamma-glutamyl kinase					17.69	
METACYC	CITRULBIO-PWY	citrulline biosynthesis	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
METACYC	PWY-5122	geranyl diphosphate biosynthesis	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
METACYC	PWY1-2	alanine degradation IV	Tfu_0961	Tfu_0961 alanine dehydrogenase and pyridine nucleotide transhydrogena			19.5	19.59	23.05	1.544
METACYC	PWY0-1319	CDP-diacylglycerol biosynthesis II	Tfu_0271	Tfu_0271 Fatty acid synthesis plsX protein		15.01			17.65	
METACYC	PWY0-1319	CDP-diacylglycerol biosynthesis II	Tfu_0631	Tfu_0631 glycerol-3-phosphate dehydrogenase (NAD(P)-	14.3	15.55	14.47		20.42	
METACYC	PWY0-1319	CDP-diacylglycerol biosynthesis II	Tfu_0680	Tfu_0680 phosphatidate cytidylyltransferase	15.69	15.29	15.87	15.37	19.59	
METACYC	PWY0-1319	CDP-diacylglycerol biosynthesis II	Tfu_1036	Tfu_1036 phospholipid/glycerol acyltransferase	18.2	17.54	17.83	17.5	21.56	
METACYC	PWY0-1319	CDP-diacylglycerol biosynthesis II	Tfu_1417	Tfu_1417 phospholipid/glycerol acyltransferase	13.91	13.6		12.45	17.58	
METACYC	PWY-6704	L-ascorbate degradation IV	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6704	L-ascorbate degradation IV	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6131	glycerol degradation II	Tfu_1716	Tfu_1716 glycerone kinase	16	15.49	13.71		18.65	

METACYC	PWY-6131	glycerol degradation II	Tfu_2801	Tfu_2801 glycerol dehydrogenase					18.62	
METACYC	PWY-6963	ammonia assimilation cycle I	Tfu_0982	Tfu_0982 glutamine synthetase type I	16.36	15.34	14.3	15.33	20.84	1.147
METACYC	PWY-6963	ammonia assimilation cycle I	Tfu_0988	Tfu_0988 glutamine synthetase type I		16.24	19.93	19.87	23.49	1.247
METACYC	PWY-6963	ammonia assimilation cycle I	Tfu_1173	Tfu_1173 glutamate synthase (ferredoxin)					19.09	
METACYC	PWY-6963	ammonia assimilation cycle I	Tfu_1174	Tfu_1174 glutamate synthase, NADH/NADPH, small subunit 1						
METACYC	PWY-5189	tetrapyrrole biosynthesis II	Tfu_2730	Tfu_2730 porphobilinogen synthase					18.56	
METACYC	PWY-5189	tetrapyrrole biosynthesis II	Tfu_2731	Tfu_2731 putative uroporphyrin-III C-methyltransferase	19.75	19.58	19.91	19.51	24.15	1.231
METACYC	PWY-5189	tetrapyrrole biosynthesis II	Tfu_2732	Tfu_2732 porphobilinogen deaminase	13.44				19.8	
METACYC	PWY-101	photosynthesis light reactions	Tfu_1915	Tfu_1915 ferredoxin/ferredoxin--NADP reductase, putative		13.93			20	
METACYC	PWY-31	canavanine degradation	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
METACYC	PWY-6316	aromatic polyketides biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6316	aromatic polyketides biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6316	aromatic polyketides biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6316	aromatic polyketides biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6952	glycerophosphodiester degradation	Tfu_0245	Tfu_0245 glycerophosphoryl diester phosphodiesterase	13.34	13.18		14.83	20.82	
METACYC	PWY-6952	glycerophosphodiester degradation	Tfu_1757	Tfu_1757 putative glycerophosphoryl diester phosphodiesterase						
METACYC	PWY-6952	glycerophosphodiester degradation	Tfu_2540	Tfu_2540 glycerophosphoryl diester phosphodiesterase, putative					18.74	
METACYC	PWY-6952	glycerophosphodiester degradation	Tfu_2593	Tfu_2593 glycerol-3-phosphate dehydrogenase	19.6	19.46	17.83	17.65	23.22	0.765
METACYC	GLUTAMATE-DEG1-PWY	glutamate degradation I	Tfu_2481	Tfu_2481 putative NAD-glutamate dehydrogenase	20.96	20.83	21.88	21.73	25.49	1.153
METACYC	PWY-6185	4-methylcatechol degradation (ortho cleavag	Tfu_0162	Tfu_0162 b-ketoadipate enol-lactone hydrolase				14.37	20.07	
METACYC	PWY-6185	4-methylcatechol degradation (ortho cleavag	Tfu_0874	Tfu_0874 Alpha/beta hydrolase	16.84	15.52	17.31	18.48	22.22	0.937
METACYC	PWY-6424	sitosterol biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6424	sitosterol biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5794	malonate degradation I (biotin-independent)	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5794	malonate degradation I (biotin-independent)	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5794	malonate degradation I (biotin-independent)	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5794	malonate degradation I (biotin-independent)	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5353	arachidonate biosynthesis	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-5353	arachidonate biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-5353	arachidonate biosynthesis	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWY-5353	arachidonate biosynthesis	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-5353	arachidonate biosynthesis	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWY-5353	arachidonate biosynthesis	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWY-5353	arachidonate biosynthesis	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-5353	arachidonate biosynthesis	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-5353	arachidonate biosynthesis	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	PWY-7048	malate-oxaloacetate shuttle II	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	ARGININE-SYN4-PWY	arginine biosynthesis IV	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
METACYC	ARGININE-SYN4-PWY	arginine biosynthesis IV	Tfu_2051	Tfu_2051 argininosuccinate lyase	15.68	16.51	18.68	18.9	22.79	
METACYC	ARGININE-SYN4-PWY	arginine biosynthesis IV	Tfu_2052	Tfu_2052 argininosuccinate synthase	13.3		18.49	17.16	22.53	
METACYC	ARGININE-SYN4-PWY	arginine biosynthesis IV	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
METACYC	PWY-321	cutin biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-321	cutin biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	DARABITOLUTIL-PWY	D-arabitol degradation	Tfu_1575	Tfu_1575 putative sugar kinase protein						
METACYC	DARABITOLUTIL-PWY	D-arabitol degradation	Tfu_1604	Tfu_1604 xylulokinase	16.69	16.85	17.01	17.12	22.06	
METACYC	PANTO-PWY	phosphopantothenate biosynthesis I	Tfu_0981	Tfu_0981 3-methyl-2-oxobutanoate hydroxymethyltrans	18.23	17.36	19.12	19.31	23.68	0.787
METACYC	PANTO-PWY	phosphopantothenate biosynthesis I	Tfu_2610	Tfu_2610 pantothenate kinase			14.28		19	
METACYC	PANTO-PWY	phosphopantothenate biosynthesis I	Tfu_2882	Tfu_2882 Bvg accessory factor	15.79	15.26	16.09	15.65	20.23	
METACYC	PANTO-PWY	phosphopantothenate biosynthesis I	Tfu_2884	Tfu_2884 pantoate-beta-alanine ligase	18.94	18.13	19.39	18.92	22.68	1.137
METACYC	PWY-5890	menaquinol-10 biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	

METACYC	PWY-5890	menaquinol-10 biosynthesis	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY0-1415	superpathway of heme biosynthesis from uroporphy	Tfu_1897	Tfu_1897 protoporphyrinogen oxidase			14.61		20.74	1.244
METACYC	PWY0-1415	superpathway of heme biosynthesis from uroporphy	Tfu_1899	Tfu_1899 uroporphyrinogen decarboxylase HemE		14.37	15.41	15.99	20.69	0.856
METACYC	PWY0-1415	superpathway of heme biosynthesis from uroporphy	Tfu_1945	Tfu_1945 ferrochelatase		13.87	18.69	18.79	22.82	1.023
METACYC	PWY-6518	glycocholate metabolism (bacteria)	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6518	glycocholate metabolism (bacteria)	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5129	sphingolipid biosynthesis (plants)	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5129	sphingolipid biosynthesis (plants)	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5129	sphingolipid biosynthesis (plants)	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5129	sphingolipid biosynthesis (plants)	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5129	sphingolipid biosynthesis (plants)	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5129	sphingolipid biosynthesis (plants)	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5129	sphingolipid biosynthesis (plants)	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2682	Tfu_2682 NADH dehydrogenase subunit N	15.55	15.11	17.89	15.78	21.55	1.549
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2683	Tfu_2683 NADH dehydrogenase subunit M	15.96	15.61	18.67	18.21	22.04	1.217
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2684	Tfu_2684 NADH dehydrogenase subunit L	16.72	16.18	19.09	19.32	22.49	1.313
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2685	Tfu_2685 NADH dehydrogenase kappa subunit	15.96	16.12	17.42	17.06	21.01	1.226
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2686	Tfu_2686 NADH dehydrogenase subunit J	14.57		19.26	18.19	22.25	
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2687	Tfu_2687 NADH-quinone oxidoreductase, chain I	17.42	17.05	19.49	19.25	23.17	1.344
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2688	Tfu_2688 NADH dehydrogenase subunit H	16.85	15.81	18.1	18.62	22.74	1.366
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2689	Tfu_2689 NADH dehydrogenase gamma subunit	19.85	19.4	22.2	22.17	25.89	1.474
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2690	Tfu_2690 NADH-quinone oxidoreductase, F subunit	18.4	18.59	21.04	20.94	24.09	1.696
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2691	Tfu_2691 ATP synthase subunit E	18.11	17.48	19.19	19.38	23.19	
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2692	Tfu_2692 NADH dehydrogenase delta subunit	17.85	17.37	21.19	20.56	24.79	1.513
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2693	Tfu_2693 NADH dehydrogenase subunit C	17.89	18.01	20.34	20.17	23.82	1.361
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2694	Tfu_2694 NADH dehydrogenase beta subunit	17.52	17.43	19.51	19.02	23.25	1.847
METACYC	PWY-4302	aerobic respiration (alternative oxidase pathway)	Tfu_2695	Tfu_2695 NADH dehydrogenase alpha subunit	15.61	15.66	16.21	16.57	20.39	
METACYC	PWY-2901	cytokinins 9-N-glucoside biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-2901	cytokinins 9-N-glucoside biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-2901	cytokinins 9-N-glucoside biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6154	autoinducer AI-2 biosynthesis II (Vibrio)	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6154	autoinducer AI-2 biosynthesis II (Vibrio)	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	XYLCAT-PWY	xylose degradation I	Tfu_1575	Tfu_1575 putative sugar kinase protein						
METACYC	XYLCAT-PWY	xylose degradation I	Tfu_1603	Tfu_1603 xylose isomerase	19.44	19.38	19.81	20.12	23.3	1.128
METACYC	XYLCAT-PWY	xylose degradation I	Tfu_1604	Tfu_1604 xylulokinase	16.69	16.85	17.01	17.12	22.06	
METACYC	PWY-5329	L-cysteine degradation III	Tfu_0354	Tfu_0354 3-mercaptopyruvate sulfurtransferase					18.69	
METACYC	PWY-5329	L-cysteine degradation III	Tfu_2719	Tfu_2719 thiosulfate sulfurtransferase	22.47	22.41	22.74	22.62	25.34	0.79
METACYC	PWY-5254	methanofuran biosynthesis	Tfu_1156	Tfu_1156 histidine biosynthesis protein HisF	14.6	14.45	14.77	14.57	20.69	
METACYC	SALVPURINE2-PWY	xanthine and xanthosine salvage	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY-7016	neomycin biosynthesis	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-7016	neomycin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-7016	neomycin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-7016	neomycin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-7016	neomycin biosynthesis	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY0-163	salvage pathways of pyrimidine ribonucleotides	Tfu_0027	Tfu_0027 putative deaminase					17.96	0.99
METACYC	PWY0-163	salvage pathways of pyrimidine ribonucleotides	Tfu_1053	Tfu_1053 pyrimidine regulatory protein PyrR	17.14	17.38	18.18	18.29	22.2	0.824
METACYC	PWY0-163	salvage pathways of pyrimidine ribonucleotides	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
METACYC	PWY0-1353	succinate to cytochrome bd oxidase electron	Tfu_0637	Tfu_0637 cytochrome bd ubiquinol oxidase, subunit II			18.7	17.36	23.03	2.71
METACYC	PWY0-1353	succinate to cytochrome bd oxidase electron	Tfu_0638	Tfu_0638 putative cytochrome oxidase subunit I			19.89	19.95	23.08	
METACYC	PWY0-1353	succinate to cytochrome bd oxidase electron	Tfu_0766	Tfu_0766 highly similar to cytochrome D ubiquinol oxidase subunit I						

METACYC	PWY-5398	crocetin esters biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5398	crocetin esters biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5398	crocetin esters biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY66-21	ethanol degradation II	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY66-21	ethanol degradation II	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY66-21	ethanol degradation II	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY66-21	ethanol degradation II	Tfu_1546	Tfu_1546 putative acyl-CoA synthetase					20.01	
METACYC	PWY66-21	ethanol degradation II	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY66-21	ethanol degradation II	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY66-21	ethanol degradation II	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY66-21	ethanol degradation II	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY66-21	ethanol degradation II	Tfu_2808	Tfu_2808 putative acetyl-coenzyme A synthetase			16.12	15.88	21.7	
METACYC	PWY66-21	ethanol degradation II	Tfu_2856	Tfu_2856 acetyl-coenzyme A synthetase	24.08	23.76	23.99	23.94	27	1.638
METACYC	GLUAMCAT-PWY	N-acetylglucosamine degradation I	Tfu_2473	Tfu_2473 n-acetylglucosamine-6-phosphate deacetylase	14.21				17.55	
METACYC	PWY-7044	5-nitroanthranilate degradation	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY-6168	flavin biosynthesis III (fungi)	Tfu_0782	Tfu_0782 Cytidyltransferase-related		13.35	14.92	14.18	20.03	
METACYC	PWY-6168	flavin biosynthesis III (fungi)	Tfu_1078	Tfu_1078 Lumazine-binding protein		13.92	16.4	17.05	20.31	
METACYC	PWY-6168	flavin biosynthesis III (fungi)	Tfu_1080	Tfu_1080 bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein						
METACYC	PWY-6168	flavin biosynthesis III (fungi)	Tfu_1081	Tfu_1081 6,7-dimethyl-8-ribityllumazine synthase	15.97	15.69	16.33	16.62	21.62	
METACYC	PWY1G-0	mycothiol biosynthesis	Tfu_0486	Tfu_0486 hypothetical protein	15.4	16.4	16.51	15.88	21.61	0.747
METACYC	PWY1G-0	mycothiol biosynthesis	Tfu_1832	Tfu_1832 cysteinyl-tRNA synthetase	15.91	16.04	18.24	17.09	22.24	1.186
METACYC	PWY1G-0	mycothiol biosynthesis	Tfu_2739	Tfu_2739 putative acetyltransferase	18.06	18.1	17.74	17.44	21.61	
METACYC	PWY1G-0	mycothiol biosynthesis	Tfu_2913	Tfu_2913 putative glycosyltransferase						
METACYC	PWY1G-0	mycothiol biosynthesis	Tfu_3099	Tfu_3099 myo-inositol-1-phosphate synthase	16.21	15.62	18.24	18.23	23.01	0.924
METACYC	PWY-1422	vitamin E biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-1422	vitamin E biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	BETSYN-PWY	glycine betaine biosynthesis I (Gram-negative bacter	Tfu_0279	Tfu_0279 betaine-aldehyde dehydrogenase	21.7	21.51	19.8	20.02	23.9	0.958
METACYC	BETSYN-PWY	glycine betaine biosynthesis I (Gram-negative bacter	Tfu_1287	Tfu_1287 betaine-aldehyde dehydrogenase					18.53	
METACYC	BETSYN-PWY	glycine betaine biosynthesis I (Gram-negative bacter	Tfu_1471	Tfu_1471 betaine-aldehyde dehydrogenase					16.26	
METACYC	BETSYN-PWY	glycine betaine biosynthesis I (Gram-negative bacter	Tfu_1776	Tfu_1776 betaine-aldehyde dehydrogenase	16	15.03			18.4	
METACYC	PWY-6683	sulfate reduction III (assimilatory)	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
METACYC	PWY-6683	sulfate reduction III (assimilatory)	Tfu_0420	Tfu_0420 Small GTP-binding protein domain:Sulfate adenylyltransferase, l			14.13		18.76	0.81
METACYC	PWY-6683	sulfate reduction III (assimilatory)	Tfu_0425	Tfu_0425 adenylylsulfate kinase					17.66	
METACYC	PWY-5059	pinobanksin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5059	pinobanksin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5059	pinobanksin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5059	pinobanksin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	ENTNER-DOUDOROFF-PWY	Entner-Doudoroff pathway I	Tfu_0188	Tfu_0188 2-dehydro-3-deoxyphosphogluconate aldolase	14.36				15.14	
METACYC	PWY-7019	butirosin biosynthesis	Tfu_1234	Tfu_1234 putative hydrolase			13.82	13	20.38	
METACYC	PWY-7019	butirosin biosynthesis	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-7019	butirosin biosynthesis	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_0174	Tfu_0174 ATP phosphoribosyltransferase	19.33	18.84	19.91	18.99	23.24	1.037
METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_0175	Tfu_0175 phosphoribosyl-ATP pyrophosphatase	17.66	17.21	14.18	15.95	21.68	0.868
METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_0542	Tfu_0542 histidinol-phosphate phosphatase, putative, inc	18.79	18.37	16.97	17.19	21.21	
METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_1150	Tfu_1150 histidinol dehydrogenase	19.66	19.37	19.47	19.89	23.27	0.966
METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_1151	Tfu_1151 histidinol-phosphate aminotransferase					19.66	1.354
METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_1152	Tfu_1152 imidazoleglycerol-phosphate dehydratase					17.24	
METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_1155	Tfu_1155 1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylidene			15.7	16.67	21.72	
METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_1159	Tfu_1159 phosphoribosyl-AMP cyclohydrolase					16.88	

METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_2223	Tfu_2223 putative aminotransferase					16.25	
METACYC	HISTSYN-PWY	histidine biosynthesis	Tfu_3018	Tfu_3018 putative aminotransferase					19.29	1.473
METACYC	P181-PWY	nicotine degradation I	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
METACYC	P181-PWY	nicotine degradation I	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	P181-PWY	nicotine degradation I	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	P181-PWY	nicotine degradation I	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	P181-PWY	nicotine degradation I	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6737	starch degradation V	Tfu_0586	Tfu_0586 alpha-glucan phosphorylase					15.86	
METACYC	PWY-6737	starch degradation V	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6737	starch degradation V	Tfu_2205	Tfu_2205 glycoside hydrolase, family 77					15.25	
METACYC	PWY-6737	starch degradation V	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	GLYCLEAV-PWY	glycine cleavage complex	Tfu_0994	Tfu_0994 dihydrolipoamide dehydrogenase	23.87	23.67	23.96	23.71	27.03	1.154
METACYC	GLYCLEAV-PWY	glycine cleavage complex	Tfu_1398	Tfu_1398 glycine dehydrogenase	19.26	19.25	19.62	19.33	23.73	1.358
METACYC	GLYCLEAV-PWY	glycine cleavage complex	Tfu_2351	Tfu_2351 aminomethyltransferase	17.24	17.22	16.2	16.08	20.82	0.867
METACYC	GLYCLEAV-PWY	glycine cleavage complex	Tfu_2559	Tfu_2559 dihydrolipoamide dehydrogenase	17.62	17.97	18.6	18.7	23.28	1.063
METACYC	GALACTCAT-PWY	D-galactonate degradation	Tfu_1786	Tfu_1786 mandelate racemase/muconate lactonizing enz	16.66	16.7	15.07	15.62	20.33	1.311
METACYC	GLYOXYLATE-BYPASS	glyoxylate cycle	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	GLYOXYLATE-BYPASS	glyoxylate cycle	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	GLYOXYLATE-BYPASS	glyoxylate cycle	Tfu_0819	Tfu_0819 malate synthase	20.71	20.65	20.77	20.84	24.52	0.986
METACYC	GLYOXYLATE-BYPASS	glyoxylate cycle	Tfu_1377	Tfu_1377 isocitrate lyase	17.24	15.99	17.23	17.21	21.54	
METACYC	GLYOXYLATE-BYPASS	glyoxylate cycle	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	PWY-5476	cornusiin E biosynthesis	Tfu_0637	Tfu_0637 cytochrome bd ubiquinol oxidase, subunit II			18.7	17.36	23.03	2.71
METACYC	PWY-5476	cornusiin E biosynthesis	Tfu_0638	Tfu_0638 putative cytochrome oxidase subunit I			19.89	19.95	23.08	
METACYC	PWY-5476	cornusiin E biosynthesis	Tfu_0766	Tfu_0766 highly similar to cytochrome D ubiquinol oxidase subunit I						
METACYC	PWY-6892	thiazole biosynthesis I (E. coli)	Tfu_0595	Tfu_0595 putative pyridoxal-phosphate-dependent aminotransferase					16.06	
METACYC	PWY-6892	thiazole biosynthesis I (E. coli)	Tfu_1917	Tfu_1917 1-deoxy-D-xylulose-5-phosphate synthase					16.98	
METACYC	PWY-6892	thiazole biosynthesis I (E. coli)	Tfu_1983	Tfu_1983 cysteine desulphurases, SufS	14.11			13.91	18.52	0.647
METACYC	PWY0-662	PRPP biosynthesis I	Tfu_0415	Tfu_0415 ribose-phosphate pyrophosphokinase	18.35	17.7	20.22	20.21	23.7	1.099
METACYC	NONMEVIPP-PWY	methylerythritol phosphate pathway	Tfu_0407	Tfu_0407 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase					17.64	
METACYC	NONMEVIPP-PWY	methylerythritol phosphate pathway	Tfu_0471	Tfu_0471 4-hydroxy-3-methylbut-2-enyl diphosphate reductase					19.27	
METACYC	NONMEVIPP-PWY	methylerythritol phosphate pathway	Tfu_0747	Tfu_0747 1-deoxy-D-xylulose 5-phosphate reductoisomerase						
METACYC	NONMEVIPP-PWY	methylerythritol phosphate pathway	Tfu_0749	Tfu_0749 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase					16.63	
METACYC	NONMEVIPP-PWY	methylerythritol phosphate pathway	Tfu_1917	Tfu_1917 1-deoxy-D-xylulose-5-phosphate synthase					16.98	
METACYC	NONMEVIPP-PWY	methylerythritol phosphate pathway	Tfu_2906	Tfu_2906 MECDP-synthase	14.67		15.37		18.41	0.633
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_0562	Tfu_0562 malate dehydrogenase (oxaloacetate decarboxylating)						
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_2390	Tfu_2390 malate dehydrogenase (oxaloacetate decarboxy	15.54	15.17	14.98	15.9	20.7	0.661
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	GLUCONEO-PWY	gluconeogenesis I	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY4FS-17	abscisic acid biosynthesis shunt	Tfu_1221	Tfu_1221 hypothetical protein						

METACYC	PWY4FS-17	abscisic acid biosynthesis shunt	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY0-862	cis-dodecenoyl biosynthesis	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWY0-862	cis-dodecenoyl biosynthesis	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWY0-862	cis-dodecenoyl biosynthesis	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWY0-862	cis-dodecenoyl biosynthesis	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	CHOLINE-BETAINE-ANA-PWY	choline degradation I	Tfu_0279	Tfu_0279 betaine-aldehyde dehydrogenase	21.7	21.51	19.8	20.02	23.9	0.958
METACYC	CHOLINE-BETAINE-ANA-PWY	choline degradation I	Tfu_1287	Tfu_1287 betaine-aldehyde dehydrogenase					18.53	
METACYC	CHOLINE-BETAINE-ANA-PWY	choline degradation I	Tfu_1471	Tfu_1471 betaine-aldehyde dehydrogenase					16.26	
METACYC	CHOLINE-BETAINE-ANA-PWY	choline degradation I	Tfu_1776	Tfu_1776 betaine-aldehyde dehydrogenase	16	15.03			18.4	
METACYC	PWY0-901	selenocysteine biosynthesis I (bacteria)	Tfu_0031	Tfu_0031 seryl-tRNA synthetase	19.71	19.5	20.47	20.38	23.8	0.939
METACYC	PWY-2161	folate polyglutamylation	Tfu_2190	Tfu_2190 folylpolyglutamate synthetase					19.35	
METACYC	PWY-2161	folate polyglutamylation	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
METACYC	GLYCOLYSIS-E-D	superpathway of glycolysis and Entner-Doudoroff	Tfu_2005	Tfu_2005 glucose-6-phosphate 1-dehydrogenase	16.6	15.74	16.81	16.27	21.46	
METACYC	GLYCOLYSIS-E-D	superpathway of glycolysis and Entner-Doudoroff	Tfu_2007	Tfu_2007 6-phosphogluconolactonase	18.7	19.13	18.21	17.98	22.37	0.913
METACYC	PWY-6611	adenine and adenosine salvage V	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY-6611	adenine and adenosine salvage V	Tfu_2563	Tfu_2563 adenosine deaminase					16.67	
METACYC	PWY-6611	adenine and adenosine salvage V	Tfu_2662	Tfu_2662 adenosine deaminase				13.97	19.93	1.018
METACYC	PWY-862	fructan degradation	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6790	L-arabinan degradation	Tfu_1616	Tfu_1616 alpha-L-arabinofuranosidase	18.6	18.38			20.92	1.664
METACYC	PWY-5381	pyridine nucleotide cycling (plants)	Tfu_0527	Tfu_0527 hypothetical protein					16.28	
METACYC	PWY-5381	pyridine nucleotide cycling (plants)	Tfu_0694	Tfu_0694 putative DNA repair hydrolase						
METACYC	PWY-5381	pyridine nucleotide cycling (plants)	Tfu_0983	Tfu_0983 NAD+ synthase	16.91	16.85	17.72	17.22	22.21	0.82
METACYC	PWY-5381	pyridine nucleotide cycling (plants)	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
METACYC	PWY-5381	pyridine nucleotide cycling (plants)	Tfu_1918	Tfu_1918 putative DNA glycosylase						
METACYC	PWY-5381	pyridine nucleotide cycling (plants)	Tfu_2171	Tfu_2171 nicotinic acid mononucleotide adenyltransferase					18.95	
METACYC	PWY-5381	pyridine nucleotide cycling (plants)	Tfu_2373	Tfu_2373 nicotinate phosphoribosyltransferase	14.96		15.9	12.14	20.35	
METACYC	PWY-5381	pyridine nucleotide cycling (plants)	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-5381	pyridine nucleotide cycling (plants)	Tfu_2875	Tfu_2875 HhH-GPD:Iron-sulfur cluster loop						
METACYC	PWY-6147	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_0543	Tfu_0543 hypothetical protein			13.59	14.81	19.36	
METACYC	PWY-6147	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_0576	Tfu_0576 hypothetical protein					17.31	
METACYC	PWY-6147	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_2457	Tfu_2457 putative mutT-like protein						
METACYC	PWY-6147	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_2890	Tfu_2890 7, 8-Dihydro-6-hydroxymethylpterin-pyrophosphokinase, HPPK					15.52	
METACYC	PWY-6147	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_2891	Tfu_2891 dihydroneopterin aldolase family:Dihydroneop	14.95	14.62	16	15.74	20.08	
METACYC	PWY-6147	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_2894	Tfu_2894 GTP cyclohydrolase I		15.85	17.62	17.38	21.27	0.628
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2003	Tfu_2003 transaldolase	20.04	20.08	21.54	21.1	24.47	1.211
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078

METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2970	Tfu_2970 putative phosphoketolase						
METACYC	P124-PWY	Bifidobacterium shunt	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	PWY-361	phenylpropanoid biosynthesis	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-361	phenylpropanoid biosynthesis	Tfu_0966	Tfu_0966 caffeoyl-CoA O-methyltransferase		13.62			16.15	
METACYC	PWY-361	phenylpropanoid biosynthesis	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-361	phenylpropanoid biosynthesis	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PROSYN-PWY	proline biosynthesis I	Tfu_2175	Tfu_2175 gamma-glutamyl phosphate reductase GPR	16.65	16.53	17.82	17.26	21.71	
METACYC	PROSYN-PWY	proline biosynthesis I	Tfu_2179	Tfu_2179 gamma-glutamyl kinase					17.69	
METACYC	PROSYN-PWY	proline biosynthesis I	Tfu_2708	Tfu_2708 delta 1-pyrroline-5-carboxylate reductase	17.73	17.16	18.03	17.57	21.11	
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	FERMENTATION-PWY	mixed acid fermentation	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	PWY-6163	chorismate biosynthesis from 3-dehydroquinate	Tfu_0544	Tfu_0544 3-phosphoshikimate 1-carboxyvinyltransferase						
METACYC	PWY-6163	chorismate biosynthesis from 3-dehydroquinate	Tfu_1090	Tfu_1090 chorismate synthase	19.19	18.56	19.76	19.46	23.47	
METACYC	PWY-6163	chorismate biosynthesis from 3-dehydroquinate	Tfu_1091	Tfu_1091 shikimate kinase					19.23	
METACYC	PWY-6163	chorismate biosynthesis from 3-dehydroquinate	Tfu_1635	Tfu_1635 dehydroquinase, class II					16.28	
METACYC	PWY-6163	chorismate biosynthesis from 3-dehydroquinate	Tfu_2067	Tfu_2067 shikimate 5-dehydrogenase					17.29	
METACYC	ARGASEDEG-PWY	arginine degradation I (arginase pathway)	Tfu_0433	Tfu_0433 delta-1-pyrroline-5-carboxylate dehydrogenas	20.87	20.52	20.5	20.22	24.05	1.051
METACYC	ARGASEDEG-PWY	arginine degradation I (arginase pathway)	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
METACYC	ARGASEDEG-PWY	arginine degradation I (arginase pathway)	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
METACYC	P601-PWY	(+)-camphor degradation	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	P601-PWY	(+)-camphor degradation	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	P601-PWY	(+)-camphor degradation	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	P601-PWY	(+)-camphor degradation	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY6666-2	dopamine degradation	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY6666-2	dopamine degradation	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY6666-2	dopamine degradation	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-5893	tridecaprenyl diphosphate biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5893	tridecaprenyl diphosphate biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5893	tridecaprenyl diphosphate biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6964	ammonia assimilation cycle II	Tfu_0982	Tfu_0982 glutamine synthetase type I	16.36	15.34	14.3	15.33	20.84	1.147
METACYC	PWY-6964	ammonia assimilation cycle II	Tfu_0988	Tfu_0988 glutamine synthetase type I		16.24	19.93	19.87	23.49	1.247
METACYC	SALVADEHYPOX-PWY	adenosine nucleotides degradation II	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	SALVADEHYPOX-PWY	adenosine nucleotides degradation II	Tfu_2563	Tfu_2563 adenosine deaminase					16.67	
METACYC	SALVADEHYPOX-PWY	adenosine nucleotides degradation II	Tfu_2662	Tfu_2662 adenosine deaminase				13.97	19.93	1.018
METACYC	CYANCAT-PWY	cyanate degradation	Tfu_2132	Tfu_2132 carbonic anhydrase, putative					20.01	
METACYC	PWY-5667	CDP-diacylglycerol biosynthesis I	Tfu_0271	Tfu_0271 Fatty acid synthesis plsX protein		15.01			17.65	
METACYC	PWY-5667	CDP-diacylglycerol biosynthesis I	Tfu_0631	Tfu_0631 glycerol-3-phosphate dehydrogenase (NAD(P)-	14.3	15.55	14.47		20.42	
METACYC	PWY-5667	CDP-diacylglycerol biosynthesis I	Tfu_0680	Tfu_0680 phosphatidate cytidylyltransferase	15.69	15.29	15.87	15.37	19.59	
METACYC	PWY-5667	CDP-diacylglycerol biosynthesis I	Tfu_1036	Tfu_1036 phospholipid/glycerol acyltransferase	18.2	17.54	17.83	17.5	21.56	
METACYC	PWY-5667	CDP-diacylglycerol biosynthesis I	Tfu_1417	Tfu_1417 phospholipid/glycerol acyltransferase	13.91	13.6		12.45	17.58	

METACYC	PWY-5344	homocysteine biosynthesis	Tfu_2822	Tfu_2822 homoserine O-acetyltransferase	15.5	15.63		15.19	19.08	
METACYC	PWY-5344	homocysteine biosynthesis	Tfu_2823	Tfu_2823 O-acetylhomoserine sulfhydrylase	22.33	21.67	21.43	21.62	25.14	0.779
METACYC	PWY-5437	threonine degradation I	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5437	threonine degradation I	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5437	threonine degradation I	Tfu_1741	Tfu_1741 threonine dehydratase					16.86	
METACYC	PWY-5437	threonine degradation I	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5437	threonine degradation I	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6313	serotonin degradation	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-6313	serotonin degradation	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-6313	serotonin degradation	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-6313	serotonin degradation	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-6313	serotonin degradation	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-6313	serotonin degradation	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-6313	serotonin degradation	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-6367	D-myo-inositol-5-phosphate metabolism	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-5367	petroselinate biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-5367	petroselinate biosynthesis	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWY-5367	petroselinate biosynthesis	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWY-5367	petroselinate biosynthesis	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWY-5367	petroselinate biosynthesis	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_0637	Tfu_0637 cytochrome bd ubiquinol oxidase, subunit II			18.7	17.36	23.03	2.71
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_0638	Tfu_0638 putative cytochrome oxidase subunit I			19.89	19.95	23.08	
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_0766	Tfu_0766 highly similar to cytochrome D ubiquinol oxidase subunit I						
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2682	Tfu_2682 NADH dehydrogenase subunit N	15.55	15.11	17.89	15.78	21.55	1.549
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2683	Tfu_2683 NADH dehydrogenase subunit M	15.96	15.61	18.67	18.21	22.04	1.217
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2684	Tfu_2684 NADH dehydrogenase subunit L	16.72	16.18	19.09	19.32	22.49	1.313
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2685	Tfu_2685 NADH dehydrogenase kappa subunit	15.96	16.12	17.42	17.06	21.01	1.226
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2686	Tfu_2686 NADH dehydrogenase subunit J	14.57		19.26	18.19	22.25	
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2687	Tfu_2687 NADH-quinone oxidoreductase, chain I	17.42	17.05	19.49	19.25	23.17	1.344
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2688	Tfu_2688 NADH dehydrogenase subunit H	16.85	15.81	18.1	18.62	22.74	1.366
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2689	Tfu_2689 NADH dehydrogenase gamma subunit	19.85	19.4	22.2	22.17	25.89	1.474
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2690	Tfu_2690 NADH-quinone oxidoreductase, F subunit	18.4	18.59	21.04	20.94	24.09	1.696
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2691	Tfu_2691 ATP synthase subunit E	18.11	17.48	19.19	19.38	23.19	
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2692	Tfu_2692 NADH dehydrogenase delta subunit	17.85	17.37	21.19	20.56	24.79	1.513
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2693	Tfu_2693 NADH dehydrogenase subunit C	17.89	18.01	20.34	20.17	23.82	1.361
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2694	Tfu_2694 NADH dehydrogenase beta subunit	17.52	17.43	19.51	19.02	23.25	1.847
METACYC	PWY0-1334	NADH to cytochrome bd oxidase electron tra	Tfu_2695	Tfu_2695 NADH dehydrogenase alpha subunit	15.61	15.66	16.21	16.57	20.39	
METACYC	PWY-6792	scopoletin biosynthesis	Tfu_0966	Tfu_0966 caffeoyl-CoA O-methyltransferase		13.62			16.15	
METACYC	PWY-6792	scopoletin biosynthesis	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-6848	rutin degradation	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6848	rutin degradation	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY0-1312	acetate formation from acetyl-CoA I	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_1278	Tfu_1278 thiolase						

METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-5136	fatty acid β-oxidation II (plants)	Tfu_2239	Tfu_2239 hypothetical protein	17.58	17.57	18.21	17.62	22.75	0.874
METACYC	PWY-5751	phenylethanol biosynthesis	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-5751	phenylethanol biosynthesis	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-5751	phenylethanol biosynthesis	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-5751	phenylethanol biosynthesis	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-5686	uridine-5'-phosphate biosynthesis	Tfu_0962	Tfu_0962 allantoinase						
METACYC	PWY-5686	uridine-5'-phosphate biosynthesis	Tfu_1054	Tfu_1054 aspartate carbamoyltransferase catalytic subunit					19.72	1.183
METACYC	PWY-5686	uridine-5'-phosphate biosynthesis	Tfu_1055	Tfu_1055 dihydroorotase	13.79		18.6	18.17	22.62	
METACYC	PWY-5686	uridine-5'-phosphate biosynthesis	Tfu_1056	Tfu_1056 carbamoyl-phosphate synthase, small subunit		15.52	17.25	17.26	22.56	0.884
METACYC	PWY-5686	uridine-5'-phosphate biosynthesis	Tfu_1057	Tfu_1057 carbamoyl-phosphate synthase, large subunit,	16.53	16.24	19.8	19.69	24.13	0.99
METACYC	PWY-5686	uridine-5'-phosphate biosynthesis	Tfu_1060	Tfu_1060 orotidine 5'-phosphate decarboxylase	17.31	17.43	16.58	16.96	22.37	0.988
METACYC	PWY-5686	uridine-5'-phosphate biosynthesis	Tfu_3008	Tfu_3008 orotate phosphoribosyltransferase	17.41	17.4	17.96	17.05	22.2	0.852
METACYC	PWY-6834	spermidine biosynthesis III	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-6834	spermidine biosynthesis III	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-6834	spermidine biosynthesis III	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6073	alginate biosynthesis I	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / pl	19.06	18.82	21.97	21.81	25.49	1.131
METACYC	PWY-6342	noradrenaline and adrenaline degradation	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-6342	noradrenaline and adrenaline degradation	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-6342	noradrenaline and adrenaline degradation	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-6342	noradrenaline and adrenaline degradation	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-6342	noradrenaline and adrenaline degradation	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-6342	noradrenaline and adrenaline degradation	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-6342	noradrenaline and adrenaline degradation	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-2541	plant sterol biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-2541	plant sterol biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6281	selenocysteine biosynthesis II (archaea and eukaryot	Tfu_0031	Tfu_0031 seryl-tRNA synthetase	19.71	19.5	20.47	20.38	23.8	0.939
METACYC	PWY-5651	tryptophan degradation to 2-amino-3-carboxymucor	Tfu_0921	Tfu_0921 putative tryptophan 2,3-dioxygenase	13.54	14.16			17.35	
METACYC	PWY-5651	tryptophan degradation to 2-amino-3-carboxymucor	Tfu_0922	Tfu_0922 kynureninase	16.91	15.34	13.9	14.63	19.53	1.172
METACYC	PWY-5651	tryptophan degradation to 2-amino-3-carboxymucor	Tfu_1418	Tfu_1418 hypothetical protein	18.89	18.42	20.57	20.44	23.75	0.572
METACYC	PWY-5651	tryptophan degradation to 2-amino-3-carboxymucor	Tfu_1722	Tfu_1722 hypothetical protein					14.24	
METACYC	PWY-6502	oxidized GTP and dGTP detoxification	Tfu_0543	Tfu_0543 hypothetical protein			13.59	14.81	19.36	
METACYC	PWY-6502	oxidized GTP and dGTP detoxification	Tfu_0576	Tfu_0576 hypothetical protein					17.31	
METACYC	PWY-6502	oxidized GTP and dGTP detoxification	Tfu_2457	Tfu_2457 putative mutT-like protein						
METACYC	PWY-5973	cis-vaccenate biosynthesis	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWY-5973	cis-vaccenate biosynthesis	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWY-5973	cis-vaccenate biosynthesis	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWY-5973	cis-vaccenate biosynthesis	Tfu_1976	Tfu_1976 putative 3-oxoacyl-ACP synthase II	18.39	18.02	19.63	19.4	22.79	0.718
METACYC	PWY-5973	cis-vaccenate biosynthesis	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	PWY66-373	sucrose degradation V (mammalian)	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
METACYC	PWY66-373	sucrose degradation V (mammalian)	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-6535	4-aminobutyrate degradation I	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
METACYC	KDO-NAGLIPASYN-PWY	superpathway of (KDO)₂-lipid A biosy	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	KDO-NAGLIPASYN-PWY	superpathway of (KDO)₂-lipid A biosy	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	KDO-NAGLIPASYN-PWY	superpathway of (KDO)₂-lipid A biosy	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						

METACYC	KDO-NAGLIPASYN-PWY	superpathway of (KDO)₂-lipid A biosy	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6807	xyloglucan degradation II (exoglucanase)	Tfu_1615	Tfu_1615 beta-galactosidase					16.26	
METACYC	PWY-5101	isoleucine biosynthesis II	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
METACYC	PWY-5101	isoleucine biosynthesis II	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	
METACYC	PWY-5101	isoleucine biosynthesis II	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
METACYC	PWY-5101	isoleucine biosynthesis II	Tfu_0613	Tfu_0613 ketol-acid reductoisomerase	19.9	19.77	19.96	19.71	23.42	0.799
METACYC	PWY-5101	isoleucine biosynthesis II	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	PWY-5101	isoleucine biosynthesis II	Tfu_0626	Tfu_0626 isopropylmalate isomerase large subunit			15.08	14.46	19.36	
METACYC	PWY-5101	isoleucine biosynthesis II	Tfu_0627	Tfu_0627 isopropylmalate isomerase small subunit	13.33				18.83	
METACYC	PWY-5101	isoleucine biosynthesis II	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	PWY-5101	isoleucine biosynthesis II	Tfu_2209	Tfu_2209 dihydroxy-acid dehydratase	14.66	14.56	15.67	16.08	21.64	
METACYC	PWY-5084	2-ketoglutarate dehydrogenase complex	Tfu_0566	Tfu_0566 alpha-ketoglutarate decarboxylase	22.63	22.08	23.34	23.51	26.75	1.555
METACYC	PWY-5084	2-ketoglutarate dehydrogenase complex	Tfu_0993	Tfu_0993 dihydrolipoamide S-succinyltransferase	21.69	21.57	21.99	21.46	25.01	1.46
METACYC	PWY-5084	2-ketoglutarate dehydrogenase complex	Tfu_0994	Tfu_0994 dihydrolipoamide dehydrogenase	23.87	23.67	23.96	23.71	27.03	1.154
METACYC	PWY-5084	2-ketoglutarate dehydrogenase complex	Tfu_2559	Tfu_2559 dihydrolipoamide dehydrogenase	17.62	17.97	18.6	18.7	23.28	1.063
METACYC	PWY-4202	arsenate detoxification I (glutaredoxin)	Tfu_1521	Tfu_1521 similar to Arsenate reductase and related proteins glutaredoxin family					17.85	
METACYC	PWY-4202	arsenate detoxification I (glutaredoxin)	Tfu_1554	Tfu_1554 Low molecular weight phosphotyrosine protei	12.56	12.64	14.42	12.86	16.39	
METACYC	PWY-4202	arsenate detoxification I (glutaredoxin)	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY-6973	dTDP-D-olivose, dTDP-D-oliose and dTDP-D-mycaro	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6973	dTDP-D-olivose, dTDP-D-oliose and dTDP-D-mycaro	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6973	dTDP-D-olivose, dTDP-D-oliose and dTDP-D-mycaro	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6973	dTDP-D-olivose, dTDP-D-oliose and dTDP-D-mycaro	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6973	dTDP-D-olivose, dTDP-D-oliose and dTDP-D-mycaro	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5047	gibberellin biosynthesis IV (Gibberella fujikuroi</	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-5523	5,6-dimethylbenzimidazole biosynthesis	Tfu_0782	Tfu_0782 Cytidyltransferase-related		13.35	14.92	14.18	20.03	
METACYC	PWY-6386	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_0633	Tfu_0633 D-alanylalanine synthetase	15.85	14.68	13.91		19.95	0.685
METACYC	PWY-6386	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_1106	Tfu_1106 UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diamino		13.98	15.35	14.44	21.31	0.824
METACYC	PWY-6386	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_1108	Tfu_1108 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase					18.55	
METACYC	PWY-6386	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_1111	Tfu_1111 UDP-N-acetylmuramate--alanine ligase			14.68	15.53	20.38	1.128
METACYC	PWY-6386	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_1640	Tfu_1640 D-alanine--D-alanine ligase					15.9	
METACYC	PWY-6386	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_2162	Tfu_2162 glutamate racemase						
METACYC	PWY-6386	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_2664	Tfu_2664 UDP-N-acetylenolpyruvoylglucosamine reduct	13.88				20.85	
METACYC	PWY-6386	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_3016	Tfu_3016 UDP-N-acetylglucosamine 1-carboxyvinyltransferase		14.48	17.9	17.73	22.19	1.204
METACYC	PWY-5531	chlorophyllide a biosynthesis II	Tfu_0313	Tfu_0313 Mg-chelatase subunit ChlI	16.96	16.73	17.38	16.55	20.43	
METACYC	PWY-5531	chlorophyllide a biosynthesis II	Tfu_0443	Tfu_0443 magnesium chelatase subunit ChlI					17.16	
METACYC	PWY-5531	chlorophyllide a biosynthesis II	Tfu_1897	Tfu_1897 protoporphyrinogen oxidase			14.61		20.74	1.244
METACYC	PWY-5531	chlorophyllide a biosynthesis II	Tfu_1899	Tfu_1899 uroporphyrinogen decarboxylase HemE		14.37	15.41	15.99	20.69	0.856
METACYC	PWY-6713	L-rhamnose degradation II	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6713	L-rhamnose degradation II	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6919	neopentalenoketolactone and pentalenate biosynthe	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-5507	adenosylcobalamin biosynthesis I (early cobalt inser	Tfu_0311	Tfu_0311 cobyrinic acid a,c-diamide synthase CbiA					16.36	
METACYC	PWY-5507	adenosylcobalamin biosynthesis I (early cobalt inser	Tfu_0315	Tfu_0315 precorrin-4 C11-methyltransferase region					19.46	0.814
METACYC	PWY-5507	adenosylcobalamin biosynthesis I (early cobalt inser	Tfu_0316	Tfu_0316 precorrin-3B C17-methyltransferase region:Precorrin-2 C20-methyltransferase						
METACYC	PWY-5507	adenosylcobalamin biosynthesis I (early cobalt inser	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5507	adenosylcobalamin biosynthesis I (early cobalt inser	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5194	siroheme biosynthesis	Tfu_2221	Tfu_2221 uroporphyrin-III C-methyltransferase, C-termi	17.11	16.52	17.24	16.23	21.37	0.99
METACYC	PWY-5882	epoxypseudoisoeugenol-2-methylbutyrate biosynthe	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5882	epoxypseudoisoeugenol-2-methylbutyrate biosynthe	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6269	adenosylcobalamin salvage from cobinamide II	Tfu_0312	Tfu_0312 cob(I)yrinic acid a,c-diamide adenosyltransferase					16.96	
METACYC	PWY-6269	adenosylcobalamin salvage from cobinamide II	Tfu_0996	Tfu_0996 putative cobalamin (5'-phosphate) synthase : adenosylcobinamide-GDP ribazoletransferase						

METACYC	PWY-6269	adenosylcobalamin salvage from cobinamide II	Tfu_0997	Tfu_0997 adenosylcobinamide kinase / adenosylcobinamide-phos	15.35		15.47	20.21		
METACYC	PWY-6269	adenosylcobalamin salvage from cobinamide II	Tfu_2222	Tfu_2222 nicotinate-nucleotide-dimethylbenzimidazole p	15.06		15.97	15.99	20.79	0.7
METACYC	PWY-6269	adenosylcobalamin salvage from cobinamide II	Tfu_2224	Tfu_2224 cobalamin biosynthesis protein						
METACYC	PWY-6432	curcuminoid biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6432	curcuminoid biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6432	curcuminoid biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6432	curcuminoid biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PHOSLIPSYN2-PWY	phospholipid biosynthesis II	Tfu_1895	Tfu_1895 putative phosphatidylserine synthase						
METACYC	PWY-6573	chondroitin sulfate degradation (metazoa)	Tfu_2486	Tfu_2486 hypothetical protein	16.26	16.75		15.08	20.28	
METACYC	PWY-761	rhizobactin 1021 biosynthesis	Tfu_0301	Tfu_0301 diaminobutyrate--2-oxoglutarate aminotransferase						
METACYC	PWY-6824	justicidin B biosynthesis	Tfu_0637	Tfu_0637 cytochrome bd ubiquinol oxidase, subunit II			18.7	17.36	23.03	2.71
METACYC	PWY-6824	justicidin B biosynthesis	Tfu_0638	Tfu_0638 putative cytochrome oxidase subunit I			19.89	19.95	23.08	
METACYC	PWY-6824	justicidin B biosynthesis	Tfu_0766	Tfu_0766 highly similar to cytochrome D ubiquinol oxidase subunit I						
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY-7007	methyl ketone biosynthesis	Tfu_2239	Tfu_2239 hypothetical protein	17.58	17.57	18.21	17.62	22.75	0.874
METACYC	PWY-5662	glucosylglycerate biosynthesis I	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5662	glucosylglycerate biosynthesis I	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5662	glucosylglycerate biosynthesis I	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5022	4-aminobutyrate degradation V	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
METACYC	PWY-5022	4-aminobutyrate degradation V	Tfu_0946	Tfu_0946 putative acyl-CoA dehydrogenase	20.62	20.44	21.21	21.21	24.67	0.91
METACYC	PWY-5022	4-aminobutyrate degradation V	Tfu_1281	Tfu_1281 butyryl-CoA dehydrogenase						
METACYC	PWY-5022	4-aminobutyrate degradation V	Tfu_2481	Tfu_2481 putative NAD-glutamate dehydrogenase	20.96	20.83	21.88	21.73	25.49	1.153
METACYC	PWY-5143	fatty acid activation	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-5143	fatty acid activation	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-5143	fatty acid activation	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-5143	fatty acid activation	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-5665	vanilla biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5665	vanilla biosynthesis	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-5665	vanilla biosynthesis	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-5665	vanilla biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6681	neurosporaxanthin biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-6681	neurosporaxanthin biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-6681	neurosporaxanthin biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6681	neurosporaxanthin biosynthesis	Tfu_3076	Tfu_3076 putative phytoene synthase						
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057

METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_1278	Tfu_1278 thiolase						
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	FAO-PWY	fatty acid β-oxidation I	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	KDO-LIPASYN-PWY	(KDO)₂-lipid A biosynthesis I	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	KDO-LIPASYN-PWY	(KDO)₂-lipid A biosynthesis I	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	KDO-LIPASYN-PWY	(KDO)₂-lipid A biosynthesis I	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	KDO-LIPASYN-PWY	(KDO)₂-lipid A biosynthesis I	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6933	seleno-amino acid detoxification and volatilization II	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6933	seleno-amino acid detoxification and volatilization II	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	COBALSYN-PWY	adenosylcobalamin salvage from cobinamide I	Tfu_0312	Tfu_0312 cob(I)yrinic acid a,c-diamide adenosyltransferase					16.96	
METACYC	COBALSYN-PWY	adenosylcobalamin salvage from cobinamide I	Tfu_0996	Tfu_0996 putative cobalamin (5'-phosphate) synthase : adenosylcobinamide-GDP ribazoletransferase						
METACYC	COBALSYN-PWY	adenosylcobalamin salvage from cobinamide I	Tfu_0997	Tfu_0997 adenosylcobinamide kinase / adenosylcobinamide-phos		15.35		15.47	20.21	
METACYC	COBALSYN-PWY	adenosylcobalamin salvage from cobinamide I	Tfu_2222	Tfu_2222 nicotinate-nucleotide-dimethylbenzimidazole p	15.06		15.97	15.99	20.79	0.7
METACYC	PWY-5041	S-adenosyl-L-methionine cycle II	Tfu_1065	Tfu_1065 S-adenosylmethionine synthetase	15.28	15.32	15.74	16.4	20.99	0.962
METACYC	PWY-5041	S-adenosyl-L-methionine cycle II	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5041	S-adenosyl-L-methionine cycle II	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5041	S-adenosyl-L-methionine cycle II	Tfu_2505	Tfu_2505 S-adenosyl-L-homocysteine hydrolase	18.66	19.01	19.8	19.23	23.56	1.126
METACYC	PWY-5975	furaneol biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5975	furaneol biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	P302-PWY	L-sorbose degradation	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	P302-PWY	L-sorbose degradation	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6802	salidroside biosynthesis	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-6802	salidroside biosynthesis	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-6802	salidroside biosynthesis	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-6802	salidroside biosynthesis	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-5305	bixin biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5305	bixin biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	HISDEG-PWY	histidine degradation I	Tfu_0821	Tfu_0821 imidazolonepropionase					17.2	
METACYC	PWY-6004	glycine betaine biosynthesis V (from glycine)	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6004	glycine betaine biosynthesis V (from glycine)	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	GLUTORN-PWY	ornithine biosynthesis	Tfu_2054	Tfu_2054 acetylornithine and succinylornithine aminotra	16.33	18.16	18.68	18.83	22.2	1.056
METACYC	GLUTORN-PWY	ornithine biosynthesis	Tfu_2055	Tfu_2055 acetylglutamate kinase		13.89	16.85	16.6	21.88	1.485
METACYC	GLUTORN-PWY	ornithine biosynthesis	Tfu_2056	Tfu_2056 bifunctional ornithine acetyltransferase/N-acet	17.05	16.43	18.49	17.65	22.7	
METACYC	GLUTORN-PWY	ornithine biosynthesis	Tfu_2057	Tfu_2057 N-acetyl-gamma-glutamyl-phosphate reductase					20.33	
METACYC	GLUTORN-PWY	ornithine biosynthesis	Tfu_2879	Tfu_2879 hypothetical protein	13.85	13.58			19.82	
METACYC	P341-PWY	glycolysis V (Pyrococcus)	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	P341-PWY	glycolysis V (Pyrococcus)	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	P341-PWY	glycolysis V (Pyrococcus)	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	P341-PWY	glycolysis V (Pyrococcus)	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	P341-PWY	glycolysis V (Pyrococcus)	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	P341-PWY	glycolysis V (Pyrococcus)	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
METACYC	P341-PWY	glycolysis V (Pyrococcus)	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	P341-PWY	glycolysis V (Pyrococcus)	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	P341-PWY	glycolysis V (Pyrococcus)	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	P341-PWY	glycolysis V (Pyrococcus)	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-6501	D-glucuronate degradation II	Tfu_1221	Tfu_1221 hypothetical protein						

METACYC	PWY-6501	D-glucuronate degradation II	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5321	quercetin glucoside biosynthesis (Arabidopsis)	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5321	quercetin glucoside biosynthesis (Arabidopsis)	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5321	quercetin glucoside biosynthesis (Arabidopsis)	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	GLUCARDEG-PWY	D-glucarate degradation I	Tfu_1265	Tfu_1265 2-hydroxy-3-oxopropionate reductase			15.84	13.26	19.37	
METACYC	PWY-5849	menaquinol-6 biosynthesis	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PYRIDNUCSAL-PWY	NAD salvage pathway I	Tfu_0527	Tfu_0527 hypothetical protein					16.28	
METACYC	PYRIDNUCSAL-PWY	NAD salvage pathway I	Tfu_0983	Tfu_0983 NAD+ synthase	16.91	16.85	17.72	17.22	22.21	0.82
METACYC	PYRIDNUCSAL-PWY	NAD salvage pathway I	Tfu_2171	Tfu_2171 nicotinic acid mononucleotide adenyltransferase					18.95	
METACYC	PYRIDNUCSAL-PWY	NAD salvage pathway I	Tfu_2373	Tfu_2373 nicotinate phosphoribosyltransferase	14.96		15.9	12.14	20.35	
METACYC	PYRIDNUCSAL-PWY	NAD salvage pathway I	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-6415	ascorbate biosynthesis VII	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
METACYC	HSERMETANA-PWY	methionine biosynthesis III	Tfu_1825	Tfu_1825 5-methyltetrahydrofolate--homocysteine methyltransferase					15.39	
METACYC	PWY-5384	sucrose degradation IV	Tfu_0928	Tfu_0928 fructokinase	18.37	17.96	18.63	18.42	22.16	0.898
METACYC	PWY-5384	sucrose degradation IV	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	PWY-5384	sucrose degradation IV	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-5384	sucrose degradation IV	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PWY-5080	very long chain fatty acid biosynthesis I	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5080	very long chain fatty acid biosynthesis I	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5080	very long chain fatty acid biosynthesis I	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5080	very long chain fatty acid biosynthesis I	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-5080	very long chain fatty acid biosynthesis I	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5080	very long chain fatty acid biosynthesis I	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5080	very long chain fatty acid biosynthesis I	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6373	acrylate degradation	Tfu_0687	Tfu_0687 methylmalonate-semialdehyde dehydrogenase	18.43	17.24	18.03	18.14	22.37	1.017
METACYC	PWY-6786	detoxification of reactive carbonyls in chloroplasts	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6786	detoxification of reactive carbonyls in chloroplasts	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5852	demethylmenaquinol-8 biosynthesis I	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-81	toluene degradation to benzoyl-CoA (anaerobic)	Tfu_1480	Tfu_1480 subunit of CoA-transferase of family III						
METACYC	PWY-6620	guanine and guanosine salvage I	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY-6620	guanine and guanosine salvage I	Tfu_2896	Tfu_2896 hypoxanthine phosphoribosyl transferase		16.7	16.94	16.58	21.76	0.668
METACYC	P541-PWY	glycine betaine biosynthesis IV (from glycine)	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	P541-PWY	glycine betaine biosynthesis IV (from glycine)	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5875	staphyloxanthin biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5875	staphyloxanthin biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5875	staphyloxanthin biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5875	staphyloxanthin biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-5875	staphyloxanthin biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5103	isoleucine biosynthesis III	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
METACYC	PWY-5103	isoleucine biosynthesis III	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	
METACYC	PWY-5103	isoleucine biosynthesis III	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
METACYC	PWY-5103	isoleucine biosynthesis III	Tfu_0613	Tfu_0613 ketol-acid reductoisomerase	19.9	19.77	19.96	19.71	23.42	0.799
METACYC	PWY-5103	isoleucine biosynthesis III	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	PWY-5103	isoleucine biosynthesis III	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	PWY-5103	isoleucine biosynthesis III	Tfu_2209	Tfu_2209 dihydroxy-acid dehydratase	14.66	14.56	15.67	16.08	21.64	
METACYC	PWY-6638	sulfolactate degradation III	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6638	sulfolactate degradation III	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6268	adenosylcobalamin salvage from cobalamin	Tfu_0312	Tfu_0312 cob(I)yrinic acid a,c-diamide adenosyltransferase					16.96	
METACYC	PWY-6975	erythromycin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6975	erythromycin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						

METACYC	PWY-6975	erythromycin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6438	phenylphenalenone biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6438	phenylphenalenone biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6438	phenylphenalenone biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6438	phenylphenalenone biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6670	citronellol degradation	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-6670	citronellol degradation	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	ALANINE-VALINESYN-PWY	alanine biosynthesis I	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	ALANINE-VALINESYN-PWY	alanine biosynthesis I	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	ALANINE-VALINESYN-PWY	alanine biosynthesis I	Tfu_2606	Tfu_2606 alanine racemase region	16.31	14.93	16.54	16.55	20.86	
METACYC	PWY-721	3-methylquinoline degradation	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PYRIDNUCSYN-PWY	NAD biosynthesis I (from aspartate)	Tfu_0575	Tfu_0575 quinolinate synthetase						
METACYC	PYRIDNUCSYN-PWY	NAD biosynthesis I (from aspartate)	Tfu_0983	Tfu_0983 NAD+ synthase	16.91	16.85	17.72	17.22	22.21	0.82
METACYC	PYRIDNUCSYN-PWY	NAD biosynthesis I (from aspartate)	Tfu_2171	Tfu_2171 nicotinic acid mononucleotide adenyltransferase					18.95	
METACYC	PYRIDNUCSYN-PWY	NAD biosynthesis I (from aspartate)	Tfu_2883	Tfu_2883 L-aspartate oxidase			15.62	16.95	20.84	
METACYC	PWY-6863	pyruvate fermentation to hexanol	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-6863	pyruvate fermentation to hexanol	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-6863	pyruvate fermentation to hexanol	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
METACYC	PWY-6863	pyruvate fermentation to hexanol	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6863	pyruvate fermentation to hexanol	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6863	pyruvate fermentation to hexanol	Tfu_1278	Tfu_1278 thiolase						
METACYC	PWY-6863	pyruvate fermentation to hexanol	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-6863	pyruvate fermentation to hexanol	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
METACYC	PWY-6863	pyruvate fermentation to hexanol	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-6863	pyruvate fermentation to hexanol	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5410	traumatin and (Z)-3-hexen-1-yl acetate biosy	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5410	traumatin and (Z)-3-hexen-1-yl acetate biosy	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5808	hyperforin biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5808	hyperforin biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5808	hyperforin biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	MALATE-ASPARTATE-SHUTTLE-PWY	aspartate degradation II	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	PWY0-1275	lipoate biosynthesis and incorporation II	Tfu_0991	Tfu_0991 lipoyl synthase					17.9	1.46
METACYC	LACTOSEUTIL-PWY	lactose degradation II	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	LACTOSEUTIL-PWY	lactose degradation II	Tfu_1615	Tfu_1615 beta-galactosidase					16.26	
METACYC	LACTOSEUTIL-PWY	lactose degradation II	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY0-1182	trehalose degradation II (trehalase)	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	PWY0-1182	trehalose degradation II (trehalase)	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	ARGDEGRAD-PWY	arginine degradation V (arginine deiminase pathway	Tfu_1993	Tfu_1993 arginine deiminase	17.46	16.86	15.61	15.61	20.88	1.353
METACYC	PWY-6626	CDP-2-glycerol biosynthesis	Tfu_0866	Tfu_0866 DNA primase					16.49	
METACYC	PWY-6626	CDP-2-glycerol biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6626	CDP-2-glycerol biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	COA-PWY	coenzyme A biosynthesis	Tfu_0648	Tfu_0648 coenzyme A biosynthesis protein:Cytidyltransf	18.01	16.72	17.97	17.55	22.5	1.132
METACYC	COA-PWY	coenzyme A biosynthesis	Tfu_1064	Tfu_1064 phosphopantothenoylcysteine synthase/decarl	18.49	18.47	18.49	18.95	22.74	1.103
METACYC	COA-PWY	coenzyme A biosynthesis	Tfu_1192	Tfu_1192 dephospho-CoA kinase	17.51	17.36	16.73	16.92	20.12	
METACYC	VALSYN-PWY	valine biosynthesis	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
METACYC	VALSYN-PWY	valine biosynthesis	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	
METACYC	VALSYN-PWY	valine biosynthesis	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
METACYC	VALSYN-PWY	valine biosynthesis	Tfu_0613	Tfu_0613 ketol-acid reductoisomerase	19.9	19.77	19.96	19.71	23.42	0.799
METACYC	VALSYN-PWY	valine biosynthesis	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	VALSYN-PWY	valine biosynthesis	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849

METACYC	VALSYN-PWY	valine biosynthesis	Tfu_2209	Tfu_2209 dihydroxy-acid dehydratase	14.66	14.56	15.67	16.08	21.64	
METACYC	PWY-6435	4-hydroxybenzoate biosynthesis V	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	PWY-6435	4-hydroxybenzoate biosynthesis V	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	PWY-6435	4-hydroxybenzoate biosynthesis V	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
METACYC	PWY-6435	4-hydroxybenzoate biosynthesis V	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	PWY-6435	4-hydroxybenzoate biosynthesis V	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
METACYC	PWY-6435	4-hydroxybenzoate biosynthesis V	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
METACYC	PWY-6435	4-hydroxybenzoate biosynthesis V	Tfu_1278	Tfu_1278 thiolase						
METACYC	PWY-6435	4-hydroxybenzoate biosynthesis V	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	PWY-6435	4-hydroxybenzoate biosynthesis V	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	PWY-6435	4-hydroxybenzoate biosynthesis V	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
METACYC	PWY-5895	menaquinol-13 biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5895	menaquinol-13 biosynthesis	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-5076	leucine degradation III	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	PWY-5076	leucine degradation III	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-5076	leucine degradation III	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-5076	leucine degradation III	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-5076	leucine degradation III	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	PWY-5076	leucine degradation III	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-7014	paromamine biosynthesis I	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-7014	paromamine biosynthesis I	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-7014	paromamine biosynthesis I	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-7014	paromamine biosynthesis I	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-7014	paromamine biosynthesis I	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-7014	paromamine biosynthesis I	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-7014	paromamine biosynthesis I	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5669	phosphatidylethanolamine biosynthesis I	Tfu_1894	Tfu_1894 phosphatidylserine decarboxylase	16.99	15.03	17.14	16.9	21.01	1.091
METACYC	PWY-5669	phosphatidylethanolamine biosynthesis I	Tfu_1895	Tfu_1895 putative phosphatidylserine synthase						
METACYC	PWY-822	fructan biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-822	fructan biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-822	fructan biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5729	vestitol and sativan biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5729	vestitol and sativan biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6981	chitin biosynthesis	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase,	16.85	15	17.24	17.46	22.15	
METACYC	PWY-6981	chitin biosynthesis	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	PWY-6981	chitin biosynthesis	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-6944	androstenedione degradation	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-6944	androstenedione degradation	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-6944	androstenedione degradation	Tfu_1156	Tfu_1156 histidine biosynthesis protein HisF	14.6	14.45	14.77	14.57	20.69	
METACYC	PWY-6944	androstenedione degradation	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6944	androstenedione degradation	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-6944	androstenedione degradation	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-6944	androstenedione degradation	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6944	androstenedione degradation	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-6944	androstenedione degradation	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY-5661	GDP-glucose biosynthesis	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	PWY-5661	GDP-glucose biosynthesis	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	PWY-5661	GDP-glucose biosynthesis	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PWY-5486	pyruvate fermentation to ethanol II	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-5486	pyruvate fermentation to ethanol II	Tfu_1489	Tfu_1489 oxidoreductase						

METACYC	PWY-5486	pyruvate fermentation to ethanol II	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-5486	pyruvate fermentation to ethanol II	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-5439	betacyanin biosynthesis (via dopamine)	Tfu_0637	Tfu_0637 cytochrome bd ubiquinol oxidase, subunit II			18.7	17.36	23.03	2.71
METACYC	PWY-5439	betacyanin biosynthesis (via dopamine)	Tfu_0638	Tfu_0638 putative cytochrome oxidase subunit I			19.89	19.95	23.08	
METACYC	PWY-5439	betacyanin biosynthesis (via dopamine)	Tfu_0766	Tfu_0766 highly similar to cytochrome D ubiquinol oxidase subunit I						
METACYC	PWY-6546	brassinosteroids inactivation	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6546	brassinosteroids inactivation	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6546	brassinosteroids inactivation	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-1822	IAA biosynthesis II	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-1822	IAA biosynthesis II	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-5995	linoleate biosynthesis I (plants)	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-5995	linoleate biosynthesis I (plants)	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-5995	linoleate biosynthesis I (plants)	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-5995	linoleate biosynthesis I (plants)	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-6277	superpathway of 5-aminoimidazole ribonucleotide b	Tfu_0156	Tfu_0156 phosphoribosylformylglycinamidine synthase I			15.57	15.14	21.14	0.902
METACYC	PWY-6277	superpathway of 5-aminoimidazole ribonucleotide b	Tfu_0158	Tfu_0158 phosphoribosylformylglycinamidine synthase s	13.89	15.06	17.93	18.1	22.88	0.924
METACYC	PWY-6277	superpathway of 5-aminoimidazole ribonucleotide b	Tfu_0178	Tfu_0178 phosphoribosylformylglycinamidine synthase					17.74	
METACYC	PWY-6277	superpathway of 5-aminoimidazole ribonucleotide b	Tfu_2747	Tfu_2747 amidophosphoribosyltransferase						
METACYC	PWY-6277	superpathway of 5-aminoimidazole ribonucleotide b	Tfu_2748	Tfu_2748 phosphoribosylaminoimidazole synthetase	14.77		17.56	17.33	20.81	0.689
METACYC	PWY-6277	superpathway of 5-aminoimidazole ribonucleotide b	Tfu_3013	Tfu_3013 phosphoribosylglycinamide synthetase			17.63	17.26	21.77	
METACYC	PWY-2942	lysine biosynthesis III	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1	18.57	18.71	20.61	20.33	23.82	0.982
METACYC	PWY-2942	lysine biosynthesis III	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
METACYC	PWY-2942	lysine biosynthesis III	Tfu_0786	Tfu_0786 dihydrodipicolinate reductase	18.87	17.45	19.64	18.4	23.22	0.825
METACYC	PWY-2942	lysine biosynthesis III	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844
METACYC	PWY-2942	lysine biosynthesis III	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
METACYC	PWY-2942	lysine biosynthesis III	Tfu_2425	Tfu_2425 diaminopimelate decarboxylase					18.01	
METACYC	PWY-5397	crocetin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5397	crocetin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5397	crocetin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_2132	Tfu_2132 carbonic anhydrase, putative					20.01	
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	PWY-6142	gluconeogenesis II (Methanobacterium thermoau	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-5320	kaempferol glucoside biosynthesis (Arabidopsis)	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5320	kaempferol glucoside biosynthesis (Arabidopsis)	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5320	kaempferol glucoside biosynthesis (Arabidopsis)	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5365	linear furanocoumarin biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5365	linear furanocoumarin biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5365	linear furanocoumarin biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	ARGDEG-V-PWY	arginine degradation X (arginine monooxygenase pat	Tfu_2207	Tfu_2207 amidase					14.6	
METACYC	PWY-5867	t-anethole biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5867	t-anethole biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	

METACYC	HOMOSER-METSYN-PWY	methionine biosynthesis I	Tfu_0440	Tfu_0440 cystathionine gamma-synthase					17.4	
METACYC	HOMOSER-METSYN-PWY	methionine biosynthesis I	Tfu_0632	Tfu_0632 cystathionine gamma-synthase					15.55	0.471
METACYC	HOMOSER-METSYN-PWY	methionine biosynthesis I	Tfu_1825	Tfu_1825 5-methyltetrahydrofolate--homocysteine methyltransferase					15.39	
METACYC	PWY1A0-6325	actinorhodin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY1A0-6325	actinorhodin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY1A0-6325	actinorhodin biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY1A0-6325	actinorhodin biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY1A0-6325	actinorhodin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY1A0-6325	actinorhodin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY1A0-6325	actinorhodin biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-622	starch biosynthesis	Tfu_0582	Tfu_0582 1,4-alpha-glucan branching enzyme					16.55	
METACYC	PWY-622	starch biosynthesis	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	PWY-622	starch biosynthesis	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-622	starch biosynthesis	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PWY-5936	xyloglucan biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5936	xyloglucan biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5936	xyloglucan biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6780	hydrogen production VI	Tfu_2586	Tfu_2586 carbon monoxide dehydrogenase						
METACYC	PWY-6780	hydrogen production VI	Tfu_2587	Tfu_2587 molybdopterin dehydrogenase						
METACYC	CHLOROPHYLL-SYN	chlorophyllide a biosynthesis I	Tfu_0313	Tfu_0313 Mg-chelatase subunit ChlI	16.96	16.73	17.38	16.55	20.43	
METACYC	CHLOROPHYLL-SYN	chlorophyllide a biosynthesis I	Tfu_0443	Tfu_0443 magnesium chelatase subunit ChlI					17.16	
METACYC	CHLOROPHYLL-SYN	chlorophyllide a biosynthesis I	Tfu_1897	Tfu_1897 protoporphyrinogen oxidase			14.61		20.74	1.244
METACYC	CHLOROPHYLL-SYN	chlorophyllide a biosynthesis I	Tfu_1899	Tfu_1899 uroporphyrinogen decarboxylase HemE		14.37	15.41	15.99	20.69	0.856
METACYC	PWY-6619	adenine and adenosine salvage VI	Tfu_1012	Tfu_1012 putative carbohydrate kinase				14.19	20.45	
METACYC	LEU-DEG2-PWY	leucine degradation I	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	LEU-DEG2-PWY	leucine degradation I	Tfu_0948	Tfu_0948 propionyl-CoA carboxylase	20.47	20.23	20.41	20.19	24.8	
METACYC	LEU-DEG2-PWY	leucine degradation I	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	PWY3O-19	ubiquinol-6 biosynthesis (eukaryotic)	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-5477	gallotannin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5477	gallotannin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5477	gallotannin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5477	gallotannin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5138	fatty acid β-oxidation IV (unsaturated, even nun	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	PWY-5138	fatty acid β-oxidation IV (unsaturated, even nun	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	PWY-5138	fatty acid β-oxidation IV (unsaturated, even nun	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
METACYC	PWY-5138	fatty acid β-oxidation IV (unsaturated, even nun	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	PWY-5138	fatty acid β-oxidation IV (unsaturated, even nun	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
METACYC	PWY-5138	fatty acid β-oxidation IV (unsaturated, even nun	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	PWY-5138	fatty acid β-oxidation IV (unsaturated, even nun	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	PWY-5067	glycogen biosynthesis II (from UDP-D-Glucose)	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase,	16.85	15	17.24	17.46	22.15	
METACYC	PWY-5067	glycogen biosynthesis II (from UDP-D-Glucose)	Tfu_0582	Tfu_0582 1,4-alpha-glucan branching enzyme					16.55	
METACYC	PWY0-1479	tRNA processing pathway I	Tfu_1901	Tfu_1901 HRDC:3'-5' exonuclease	14.88		15.41	14.88	21.2	1.409
METACYC	PWY0-1479	tRNA processing pathway I	Tfu_2183	Tfu_2183 ribonuclease E and G	15.17	14.73	17.43	17.22	22.5	1.093
METACYC	PWY0-1479	tRNA processing pathway I	Tfu_2365	Tfu_2365 ribonuclease PH	18.55	18.11	18.5	18.13	22.43	
METACYC	PWY0-1479	tRNA processing pathway I	Tfu_3116	Tfu_3116 ribonuclease P protein	14.64	14.28	14.15	13.87	18.19	
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	

METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	ILEUDEG-PWY	isoleucine degradation I	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-6876	isopropanol biosynthesis	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-6876	isopropanol biosynthesis	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-6876	isopropanol biosynthesis	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-6876	isopropanol biosynthesis	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_2555	Tfu_2555 propionyl-CoA carboxylase complex B subunit	18.59	18.29	18.47	17.99	22.37	0.744
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
METACYC	PWY-5789	3-hydroxypropionate/4-hydroxybutyrate cycle	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
METACYC	PWY-6515	phloridzin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6515	phloridzin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6515	phloridzin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6515	phloridzin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6120	tyrosine biosynthesis III	Tfu_1207	Tfu_1207 chorismate mutase of the AroH class						
METACYC	PWY-6146	Methanobacterium thermoautotrophicum bio	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	PWY-5666	steroidal glycoalkaloid biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5666	steroidal glycoalkaloid biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5666	steroidal glycoalkaloid biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5097	lysine biosynthesis VI	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1	18.57	18.71	20.61	20.33	23.82	0.982
METACYC	PWY-5097	lysine biosynthesis VI	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
METACYC	PWY-5097	lysine biosynthesis VI	Tfu_0786	Tfu_0786 dihydrodipicolinate reductase	18.87	17.45	19.64	18.4	23.22	0.825
METACYC	PWY-5097	lysine biosynthesis VI	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844
METACYC	PWY-5097	lysine biosynthesis VI	Tfu_0816	Tfu_0816 diaminopimelate epimerase					18.06	
METACYC	PWY-5097	lysine biosynthesis VI	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
METACYC	PWY-5097	lysine biosynthesis VI	Tfu_2425	Tfu_2425 diaminopimelate decarboxylase					18.01	
METACYC	PWY-6894	thiamin diphosphate biosynthesis I (E. coli)	Tfu_0643	Tfu_0643 thiamine monophosphate kinase					14.5	
METACYC	PWY-6894	thiamin diphosphate biosynthesis I (E. coli)	Tfu_1046	Tfu_1046 thiamine-phosphate pyrophosphorylase		14.35			19.31	
METACYC	PWY-6295	olivetol biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6295	olivetol biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6295	olivetol biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6295	olivetol biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	P21-PWY	pentose phosphate pathway (partial)	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
METACYC	P21-PWY	pentose phosphate pathway (partial)	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081

METACYC	PWY-6151	S-adenosyl-L-methionine cycle I	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6151	S-adenosyl-L-methionine cycle I	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6871	3-methylbutanol biosynthesis	Tfu_0615	Tfu_0615 3-isopropylmalate dehydrogenase	19.78	19.7	19.64	19.42	23.35	1.025
METACYC	PWY-6871	3-methylbutanol biosynthesis	Tfu_0617	Tfu_0617 2-isopropylmalate synthase	16.51	16.22	15.8	13.84	20.9	
METACYC	PWY-6871	3-methylbutanol biosynthesis	Tfu_0626	Tfu_0626 isopropylmalate isomerase large subunit			15.08	14.46	19.36	
METACYC	PWY-6871	3-methylbutanol biosynthesis	Tfu_0627	Tfu_0627 isopropylmalate isomerase small subunit	13.33				18.83	
METACYC	PWY-6871	3-methylbutanol biosynthesis	Tfu_0850	Tfu_0850 2-isopropylmalate synthase	16.67	16.9	16.57	16.17	21.98	
METACYC	PWY-6871	3-methylbutanol biosynthesis	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-6871	3-methylbutanol biosynthesis	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-6871	3-methylbutanol biosynthesis	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-6871	3-methylbutanol biosynthesis	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	P303-PWY	ammonia oxidation II (anaerobic)	Tfu_2794	Tfu_2794 hypothetical protein						
METACYC	PWY-6679	jadomycin biosynthesis	Tfu_0866	Tfu_0866 DNA primase					16.49	
METACYC	PWY-6679	jadomycin biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6679	jadomycin biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6679	jadomycin biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5139	pelargonidin conjugates biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5139	pelargonidin conjugates biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5139	pelargonidin conjugates biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5139	pelargonidin conjugates biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5139	pelargonidin conjugates biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5139	pelargonidin conjugates biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5139	pelargonidin conjugates biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6907	thiamin diphosphate biosynthesis III (Staphylococcu	Tfu_1046	Tfu_1046 thiamine-phosphate pyrophosphorylase		14.35			19.31	
METACYC	HISHP-PWY	histidine degradation VI	Tfu_0821	Tfu_0821 imidazolonepropionase					17.2	
METACYC	PWY-1781	β-alanine degradation II	Tfu_0687	Tfu_0687 methylmalonate-semialdehyde dehydrogenase	18.43	17.24	18.03	18.14	22.37	1.017
METACYC	PWY-881	trehalose biosynthesis II	Tfu_0224	Tfu_0224 trehalose-phosphatase:HAD-superfamily hydr	14.64	15.78	17.3	17.76	22.74	0.78
METACYC	PWY-881	trehalose biosynthesis II	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-881	trehalose biosynthesis II	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-881	trehalose biosynthesis II	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-4984	urea cycle	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
METACYC	PWY-4984	urea cycle	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
METACYC	PWY-4984	urea cycle	Tfu_2051	Tfu_2051 argininosuccinate lyase	15.68	16.51	18.68	18.9	22.79	
METACYC	PWY-4984	urea cycle	Tfu_2052	Tfu_2052 argininosuccinate synthase	13.3		18.49	17.16	22.53	
METACYC	PWY-6471	peptidoglycan biosynthesis IV (Enterococcus faecium	Tfu_1104	Tfu_1104 peptidoglycan glycosyltransferase						
METACYC	PWY-6471	peptidoglycan biosynthesis IV (Enterococcus faecium	Tfu_1107	Tfu_1107 phospho-N-acetylmuramoyl-pentapeptide- transferase					17.98	
METACYC	PWY-6471	peptidoglycan biosynthesis IV (Enterococcus faecium	Tfu_1110	Tfu_1110 N-acetylglucosaminyl transferase	19.15	18.71	18.79	18.53	22.9	0.735
METACYC	PWY-6471	peptidoglycan biosynthesis IV (Enterococcus faecium	Tfu_2903	Tfu_2903 hypothetical protein					17.09	
METACYC	PWY-6471	peptidoglycan biosynthesis IV (Enterococcus faecium	Tfu_3064	Tfu_3064 hypothetical protein	17.05	16.02	15.7	15.59	20.75	
METACYC	PWY0-1355	formate to trimethylamine N-oxide electron transfer	Tfu_0340	Tfu_0340 trimethylamine-N-oxide reductase (cytochrom	16.72	15.79	15.16		21.33	
METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078

METACYC	PWY-5484	glycolysis II (from fructose-6P)	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-6599	guanine and guanosine salvage II	Tfu_2581	Tfu_2581 inosine-uridine preferring nucleoside hydrolas	16.93	16.72	16.96	15.37	21.32	
METACYC	PWY-6599	guanine and guanosine salvage II	Tfu_2896	Tfu_2896 hypoxanthine phosphoribosyl transferase		16.7	16.94	16.58	21.76	0.668
METACYC	PWY-7046	4-coumarate degradation (anaerobic)	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	PWY-7046	4-coumarate degradation (anaerobic)	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	PWY-7046	4-coumarate degradation (anaerobic)	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
METACYC	PWY-7046	4-coumarate degradation (anaerobic)	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	PWY-7046	4-coumarate degradation (anaerobic)	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
METACYC	PWY-7046	4-coumarate degradation (anaerobic)	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	PWY-7046	4-coumarate degradation (anaerobic)	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	PWY-5509	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_0309	Tfu_0309 cobyric acid synthase					19.41	
METACYC	PWY-5509	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_0312	Tfu_0312 cob(I)yrinic acid a,c-diamide adenosyltransferase					16.96	
METACYC	PWY-5509	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_0996	Tfu_0996 putative cobalamin (5'-phosphate) synthase : adenosylcobinamide-GDP ribazoletransferase						
METACYC	PWY-5509	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_0997	Tfu_0997 adenosylcobinamide kinase / adenosylcobinamide-phos		15.35		15.47	20.21	
METACYC	PWY-5509	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_2222	Tfu_2222 nicotinate-nucleotide-dimethylbenzimidazole p	15.06		15.97	15.99	20.79	0.7
METACYC	PWY-5509	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_2224	Tfu_2224 cobalamin biosynthesis protein						
METACYC	PWY-6038	citrate degradation	Tfu_0341	Tfu_0341 citryl-CoA lyase	17.85	17.79	17.74	17.05	21.43	
METACYC	PWY-6038	citrate degradation	Tfu_1285	Tfu_1285 citryl-CoA lyase						
METACYC	PWY-6038	citrate degradation	Tfu_1313	Tfu_1313 putative citrate lyase beta subunit	20.71	20.33	20.94	21.03	24.43	1.292
METACYC	PWY-5677	succinate fermentation to butyrate	Tfu_0946	Tfu_0946 putative acyl-CoA dehydrogenase	20.62	20.44	21.21	21.21	24.67	0.91
METACYC	PWY-5677	succinate fermentation to butyrate	Tfu_1281	Tfu_1281 butyryl-CoA dehydrogenase						
METACYC	PWY-6855	chitin degradation I (archaea)	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-6855	chitin degradation I (archaea)	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6855	chitin degradation I (archaea)	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-6052	dimethylsulfoniopropionate degradation III (demeth	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6052	dimethylsulfoniopropionate degradation III (demeth	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5350	thiosulfate disproportionation III (rhodanese)	Tfu_0354	Tfu_0354 3-mercaptopyruvate sulfurtransferase					18.69	
METACYC	PWY-5350	thiosulfate disproportionation III (rhodanese)	Tfu_2719	Tfu_2719 thiosulfate sulfurtransferase	22.47	22.41	22.74	22.62	25.34	0.79
METACYC	PWY4FS-4	phosphatidylcholine biosynthesis IV	Tfu_0735	Tfu_0735 ubiquinone/menaquinone biosynthesis methyltransferase						
METACYC	PWY4FS-4	phosphatidylcholine biosynthesis IV	Tfu_0866	Tfu_0866 DNA primase					16.49	
METACYC	PWY4FS-4	phosphatidylcholine biosynthesis IV	Tfu_1855	Tfu_1855 4'-phosphopantetheinyl transferase						
METACYC	PWY4FS-4	phosphatidylcholine biosynthesis IV	Tfu_2817	Tfu_2817 hypothetical protein					18.27	
METACYC	PWY-6113	superpathway of mycolate biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6113	superpathway of mycolate biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6113	superpathway of mycolate biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6113	superpathway of mycolate biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5530	sorbitol biosynthesis II	Tfu_2114	Tfu_2114 carbohydrate kinase, thermoresistant glucokin	15.34		15.45	14.87	18.89	
METACYC	PWYQT-4450	aliphatic glucosinolate biosynthesis, side chain elong	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWYQT-4450	aliphatic glucosinolate biosynthesis, side chain elong	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	HYDROXYPRODEG-PWY	4-hydroxyproline degradation I	Tfu_0188	Tfu_0188 2-dehydro-3-deoxyphosphogluconate aldolase	14.36				15.14	
METACYC	HYDROXYPRODEG-PWY	4-hydroxyproline degradation I	Tfu_0433	Tfu_0433 delta-1-pyrroline-5-carboxylate dehydrogenas	20.87	20.52	20.5	20.22	24.05	1.051
METACYC	PWY-6606	guanosine nucleotides degradation II	Tfu_2581	Tfu_2581 inosine-uridine preferring nucleoside hydrolas	16.93	16.72	16.96	15.37	21.32	
METACYC	ARGSYNBSUB-PWY	arginine biosynthesis II (acetyl cycle)	Tfu_1056	Tfu_1056 carbamoyl-phosphate synthase, small subunit		15.52	17.25	17.26	22.56	0.884
METACYC	ARGSYNBSUB-PWY	arginine biosynthesis II (acetyl cycle)	Tfu_1057	Tfu_1057 carbamoyl-phosphate synthase, large subunit,	16.53	16.24	19.8	19.69	24.13	0.99
METACYC	ARGSYNBSUB-PWY	arginine biosynthesis II (acetyl cycle)	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
METACYC	ARGSYNBSUB-PWY	arginine biosynthesis II (acetyl cycle)	Tfu_2051	Tfu_2051 argininosuccinate lyase	15.68	16.51	18.68	18.9	22.79	
METACYC	ARGSYNBSUB-PWY	arginine biosynthesis II (acetyl cycle)	Tfu_2052	Tfu_2052 argininosuccinate synthase	13.3		18.49	17.16	22.53	
METACYC	ARGSYNBSUB-PWY	arginine biosynthesis II (acetyl cycle)	Tfu_2054	Tfu_2054 acetylornithine and succinylornithine aminotra	16.33	18.16	18.68	18.83	22.2	1.056
METACYC	ARGSYNBSUB-PWY	arginine biosynthesis II (acetyl cycle)	Tfu_2055	Tfu_2055 acetylglutamate kinase		13.89	16.85	16.6	21.88	1.485
METACYC	ARGSYNBSUB-PWY	arginine biosynthesis II (acetyl cycle)	Tfu_2056	Tfu_2056 bifunctional ornithine acetyltransferase/N-ace	17.05	16.43	18.49	17.65	22.7	

METACYC	ARGSYNBSUB-PWY	arginine biosynthesis II (acetyl cycle)	Tfu_2057	Tfu_2057 N-acetyl-gamma-glutamyl-phosphate reductase					20.33	
METACYC	ARGSYNBSUB-PWY	arginine biosynthesis II (acetyl cycle)	Tfu_2879	Tfu_2879 hypothetical protein	13.85	13.58			19.82	
METACYC	PWY-6666	pyocyanin biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6666	pyocyanin biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-2501	fatty acid α-oxidation	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-2501	fatty acid α-oxidation	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-2501	fatty acid α-oxidation	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-5070	gibberellin biosynthesis I (non C-3, non C-13 hydroxy	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-6581	spirilloxanthin and 2,2'-diketo-spirilloxanthin biosyn	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6581	spirilloxanthin and 2,2'-diketo-spirilloxanthin biosyn	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5797	IAA degradation VI	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5797	IAA degradation VI	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5797	IAA degradation VI	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5105	hesperitin glycoside biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5105	hesperitin glycoside biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5105	hesperitin glycoside biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5393	raspberry ketone biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5393	raspberry ketone biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5393	raspberry ketone biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5393	raspberry ketone biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6983	tetrahydrobiopterin biosynthesis III	Tfu_2894	Tfu_2894 GTP cyclohydrolase I		15.85	17.62	17.38	21.27	0.628
METACYC	PWY-2722	trehalose degradation IV	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	PWY-2722	trehalose degradation IV	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	PWY-6660	2-heptyl-3-hydroxy-4(1H)-quinolone biosynt	Tfu_1386	Tfu_1386 glutamine amidotransferase of anthranilate syr	14.29	15.3	14.48	14.83	21.47	1.207
METACYC	PWY-6721	sangivamycin biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-5817	dodecaprenyl diphosphate biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5817	dodecaprenyl diphosphate biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5817	dodecaprenyl diphosphate biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-5286	anthocyanidin sophoroside metabolism	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5286	anthocyanidin sophoroside metabolism	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5286	anthocyanidin sophoroside metabolism	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	GLUCOSE1PMETAB-PWY	glucose and glucose-1-phosphate degradation	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	GLUCOSE1PMETAB-PWY	glucose and glucose-1-phosphate degradation	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	GLUCOSE1PMETAB-PWY	glucose and glucose-1-phosphate degradation	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PWY-5663	tetrahydrobiopterin biosynthesis I	Tfu_2894	Tfu_2894 GTP cyclohydrolase I		15.85	17.62	17.38	21.27	0.628
METACYC	PWY-3801	sucrose degradation VI (anaerobic)	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase,	16.85	15	17.24	17.46	22.15	
METACYC	PWY-3801	sucrose degradation VI (anaerobic)	Tfu_0928	Tfu_0928 fructokinase	18.37	17.96	18.63	18.42	22.16	0.898
METACYC	PWY-3801	sucrose degradation VI (anaerobic)	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	PWY-3801	sucrose degradation VI (anaerobic)	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-3801	sucrose degradation VI (anaerobic)	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PWY-5153	anthocyanin biosynthesis (delphinidin 3-O-glucoside	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-5690	TCA cycle II (eukaryotic)	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	PWY-5690	TCA cycle II (eukaryotic)	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	PWY-5690	TCA cycle II (eukaryotic)	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	PWY-5690	TCA cycle II (eukaryotic)	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	PWY-5690	TCA cycle II (eukaryotic)	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
METACYC	PWY-5690	TCA cycle II (eukaryotic)	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
METACYC	PWY-6457	trans-cinnamoyl-CoA biosynthesis	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-6457	trans-cinnamoyl-CoA biosynthesis	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-7028	UDP-N,N'-diacetylbacillosamine biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						

METACYC	PWY-7028	UDP-N,N'-diacetylbacillosamine biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-7028	UDP-N,N'-diacetylbacillosamine biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-7028	UDP-N,N'-diacetylbacillosamine biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6139	CMP-N-acetylneuraminate biosynthesis II (ba	Tfu_0009	Tfu_0009 putative transferase						
METACYC	PWY-6139	CMP-N-acetylneuraminate biosynthesis II (ba	Tfu_0010	Tfu_0010 n-acetylneuraminate synthase						
METACYC	P164-PWY	purine nucleotides degradation III (anaerobic)	Tfu_1737	Tfu_1737 oxidoreductase alpha (molybdopterin) subunit			14.39	13.79	19.93	
METACYC	P164-PWY	purine nucleotides degradation III (anaerobic)	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
METACYC	P164-PWY	purine nucleotides degradation III (anaerobic)	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	PWY-6672	cis-genanyl-CoA degradation	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6672	cis-genanyl-CoA degradation	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6672	cis-genanyl-CoA degradation	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6672	cis-genanyl-CoA degradation	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6672	cis-genanyl-CoA degradation	Tfu_1546	Tfu_1546 putative acyl-CoA synthetase					20.01	
METACYC	PWY-6672	cis-genanyl-CoA degradation	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6672	cis-genanyl-CoA degradation	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6672	cis-genanyl-CoA degradation	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6672	cis-genanyl-CoA degradation	Tfu_2808	Tfu_2808 putative acetyl-coenzyme A synthetase			16.12	15.88	21.7	
METACYC	PWY-6672	cis-genanyl-CoA degradation	Tfu_2856	Tfu_2856 acetyl-coenzyme A synthetase	24.08	23.76	23.99	23.94	27	1.638
METACYC	LIPAS-PWY	triacylglycerol degradation	Tfu_0155	Tfu_0155 esterase / lipase						
METACYC	LIPAS-PWY	triacylglycerol degradation	Tfu_0882	Tfu_0882 hypothetical protein						
METACYC	LIPAS-PWY	triacylglycerol degradation	Tfu_0883	Tfu_0883 hypothetical protein						
METACYC	LIPAS-PWY	triacylglycerol degradation	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY-6883	pyruvate fermentation to butanol II	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-6883	pyruvate fermentation to butanol II	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-6883	pyruvate fermentation to butanol II	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6883	pyruvate fermentation to butanol II	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6883	pyruvate fermentation to butanol II	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-6883	pyruvate fermentation to butanol II	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-6883	pyruvate fermentation to butanol II	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	GLYCOGENSYNTH-PWY	glycogen biosynthesis I (from ADP-D-Glucose)	Tfu_0582	Tfu_0582 1,4-alpha-glucan branching enzyme					16.55	
METACYC	PWY-6658	acetan biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6658	acetan biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6658	acetan biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-2902	cytokinins-O-glucoside biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-2902	cytokinins-O-glucoside biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-2902	cytokinins-O-glucoside biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5756	saponin biosynthesis II	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5756	saponin biosynthesis II	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5756	saponin biosynthesis II	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY3O-4108	tyrosine degradation III	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY3O-4108	tyrosine degradation III	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY3O-4108	tyrosine degradation III	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY3O-4108	tyrosine degradation III	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	P241-PWY	coenzyme B biosynthesis	Tfu_1156	Tfu_1156 histidine biosynthesis protein HisF	14.6	14.45	14.77	14.57	20.69	
METACYC	P241-PWY	coenzyme B biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	P241-PWY	coenzyme B biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5078	isoleucine degradation II	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	PWY-5078	isoleucine degradation II	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-5078	isoleucine degradation II	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-5078	isoleucine degradation II	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	

METACYC	PWY-5078	isoleucine degradation II	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	PWY-5078	isoleucine degradation II	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-1722	formaldehyde oxidation V (tetrahydrofolate pathway	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
METACYC	PWY-1881	formate oxidation to CO₂	Tfu_1737	Tfu_1737 oxidoreductase alpha (molybdopterin) subunit			14.39	13.79	19.93	
METACYC	PWY-6659	fusicoccins biosynthesis	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
METACYC	AEROBACTINSYN-PWY	aerobactin biosynthesis	Tfu_1788	Tfu_1788 hypothetical protein	19.06	18.7	19.67	19.63	23.68	1.295
METACYC	AEROBACTINSYN-PWY	aerobactin biosynthesis	Tfu_1796	Tfu_1796 putative proteasome component	14.51	14.96	17.7	16.83	22.14	
METACYC	PWY-4441	DIMBOA-glucoside activation	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	TREHALOSESYN-PWY	trehalose biosynthesis III	Tfu_0224	Tfu_0224 trehalose-phosphatase:HAD-superfamily hydr	14.64	15.78	17.3	17.76	22.74	0.78
METACYC	PWY-6262	demethylmenaquinol-8 biosynthesis II	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-6262	demethylmenaquinol-8 biosynthesis II	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-6262	demethylmenaquinol-8 biosynthesis II	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	ASPARAGINE-BIOSYNTHESIS	asparagine biosynthesis I	Tfu_1145	Tfu_1145 hypothetical protein						
METACYC	PWY-5873	ubiquinol-7 biosynthesis (eukaryotic)	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-6413	ginsenoside degradation III	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6413	ginsenoside degradation III	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6413	ginsenoside degradation III	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6413	ginsenoside degradation III	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6403	carrageenan biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-6403	carrageenan biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-6403	carrageenan biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6002	lotaustralin degradation	Tfu_0937	Tfu_0937 beta-glucosidase	16.92	16.79	21.22	20.91	23.7	2.426
METACYC	PWY-6002	lotaustralin degradation	Tfu_1607	Tfu_1607 beta-glucosidase						
METACYC	PWY-6002	lotaustralin degradation	Tfu_1629	Tfu_1629 beta-glucosidase	20.15	19.64	19.92	19.43	23.45	1.12
METACYC	TYRSYN	tyrosine biosynthesis I	Tfu_1207	Tfu_1207 chorismate mutase of the AroH class						
METACYC	TYRSYN	tyrosine biosynthesis I	Tfu_1208	Tfu_1208 prephenate dehydrogenase						
METACYC	PWY-6936	seleno-amino acid biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-6936	seleno-amino acid biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-6936	seleno-amino acid biosynthesis	Tfu_2368	Tfu_2368 cysteine synthase K/M		14.5	14.44		19.69	
METACYC	PWY-6936	seleno-amino acid biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-5466	matairesinol biosynthesis	Tfu_0637	Tfu_0637 cytochrome bd ubiquinol oxidase, subunit II			18.7	17.36	23.03	2.71
METACYC	PWY-5466	matairesinol biosynthesis	Tfu_0638	Tfu_0638 putative cytochrome oxidase subunit I			19.89	19.95	23.08	
METACYC	PWY-5466	matairesinol biosynthesis	Tfu_0766	Tfu_0766 highly similar to cytochrome D ubiquinol oxidase subunit I						
METACYC	PWY-5466	matairesinol biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5466	matairesinol biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-7037	undecaprenyl-diphosphate-linked di- and trisacchari	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-7037	undecaprenyl-diphosphate-linked di- and trisacchari	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-7037	undecaprenyl-diphosphate-linked di- and trisacchari	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-7037	undecaprenyl-diphosphate-linked di- and trisacchari	Tfu_1855	Tfu_1855 4'-phosphopantetheinyl transferase						
METACYC	PWY-7037	undecaprenyl-diphosphate-linked di- and trisacchari	Tfu_2817	Tfu_2817 hypothetical protein					18.27	
METACYC	PWY66-161	oxidative ethanol degradation III	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY66-161	oxidative ethanol degradation III	Tfu_1546	Tfu_1546 putative acyl-CoA synthetase					20.01	
METACYC	PWY66-161	oxidative ethanol degradation III	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY66-161	oxidative ethanol degradation III	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY66-161	oxidative ethanol degradation III	Tfu_2808	Tfu_2808 putative acetyl-coenzyme A synthetase			16.12	15.88	21.7	
METACYC	PWY66-161	oxidative ethanol degradation III	Tfu_2856	Tfu_2856 acetyl-coenzyme A synthetase	24.08	23.76	23.99	23.94	27	1.638
METACYC	PWY-6976	dTDP-L-mycarose biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6976	dTDP-L-mycarose biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6976	dTDP-L-mycarose biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6976	dTDP-L-mycarose biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						

METACYC	PWY-6976	dTDP-L-mycarose biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	GALACTARDEG-PWY	D-galactarate degradation I	Tfu_1265	Tfu_1265 2-hydroxy-3-oxopropionate reductase			15.84	13.26	19.37	
METACYC	IDNCAT-PWY	L-idonate degradation	Tfu_2114	Tfu_2114 carbohydrate kinase, thermoresistant glucokin	15.34		15.45	14.87	18.89	
METACYC	PWY66-367	ketogenesis	Tfu_0081	Tfu_0081 3-hydroxybutyrate dehydrogenase	21.11	21.46	19.94	20.31	23.95	1.187
METACYC	PWY66-367	ketogenesis	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY66-367	ketogenesis	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY66-367	ketogenesis	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY66-367	ketogenesis	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-5125	anthocyanin biosynthesis (pelargonidin 3-O-glucosid	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-6998	CDP-D-arabitol biosynthesis	Tfu_0866	Tfu_0866 DNA primase					16.49	
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_1278	Tfu_1278 thiolase						
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-6946	cholesterol degradation to androstenedione II (chole	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5938	(R)-acetoin biosynthesis I	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
METACYC	PWY-5938	(R)-acetoin biosynthesis I	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	
METACYC	PWY-5938	(R)-acetoin biosynthesis I	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
METACYC	PWY-4983	citrulline-nitric oxide cycle	Tfu_2051	Tfu_2051 argininosuccinate lyase	15.68	16.51	18.68	18.9	22.79	
METACYC	PWY-4983	citrulline-nitric oxide cycle	Tfu_2052	Tfu_2052 argininosuccinate synthase	13.3		18.49	17.16	22.53	
METACYC	PWY-6322	phosphinothricin tripeptide biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6322	phosphinothricin tripeptide biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6322	phosphinothricin tripeptide biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6322	phosphinothricin tripeptide biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6322	phosphinothricin tripeptide biosynthesis	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY-6991	(-)-camphor biosynthesis	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-3461	tyrosine biosynthesis II	Tfu_1207	Tfu_1207 chorismate mutase of the AroH class						
METACYC	PWY-6054	dimethylsulfoniopropionate biosynthesis I (Wollasto	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-6054	dimethylsulfoniopropionate biosynthesis I (Wollasto	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-6054	dimethylsulfoniopropionate biosynthesis I (Wollasto	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-6891	thiazole biosynthesis II (Bacillus)	Tfu_0595	Tfu_0595 putative pyridoxal-phosphate-dependent aminotransferase					16.06	
METACYC	PWY-6891	thiazole biosynthesis II (Bacillus)	Tfu_1044	Tfu_1044 thiamine biosynthesis oxidoreductase ThiO	14.05				17.56	0.833
METACYC	PWY-6891	thiazole biosynthesis II (Bacillus)	Tfu_1917	Tfu_1917 1-deoxy-D-xylulose-5-phosphate synthase					16.98	
METACYC	PWY-6891	thiazole biosynthesis II (Bacillus)	Tfu_1983	Tfu_1983 cysteine desulphurases, SufS	14.11			13.91	18.52	0.647
METACYC	SUCUTIL-PWY	sucrose degradation I	Tfu_0928	Tfu_0928 fructokinase	18.37	17.96	18.63	18.42	22.16	0.898
METACYC	PWY3DJ-35471	L-ascorbate biosynthesis VI	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase,	16.85	15	17.24	17.46	22.15	
METACYC	PWY3DJ-35471	L-ascorbate biosynthesis VI	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY3DJ-35471	L-ascorbate biosynthesis VI	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
METACYC	PWY-5870	ubiquinol-8 biosynthesis (eukaryotic)	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-5939	(R)-acetoin biosynthesis II	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
METACYC	PWY-5939	(R)-acetoin biosynthesis II	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	

METACYC	PWY-5939	(R)-acetoin biosynthesis II	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
METACYC	PWY-5028	histidine degradation II	Tfu_0821	Tfu_0821 imidazolonepropionase					17.2	
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-7003	glycerol degradation to butanol	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	P185-PWY	formaldehyde assimilation III (dihydroxyacetone cyc	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
METACYC	P185-PWY	formaldehyde assimilation III (dihydroxyacetone cyc	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
METACYC	P185-PWY	formaldehyde assimilation III (dihydroxyacetone cyc	Tfu_1716	Tfu_1716 glycerone kinase	16	15.49	13.71		18.65	
METACYC	P185-PWY	formaldehyde assimilation III (dihydroxyacetone cyc	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
METACYC	P185-PWY	formaldehyde assimilation III (dihydroxyacetone cyc	Tfu_2003	Tfu_2003 transaldolase	20.04	20.08	21.54	21.1	24.47	1.211
METACYC	P185-PWY	formaldehyde assimilation III (dihydroxyacetone cyc	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
METACYC	P185-PWY	formaldehyde assimilation III (dihydroxyacetone cyc	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	P185-PWY	formaldehyde assimilation III (dihydroxyacetone cyc	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	P185-PWY	formaldehyde assimilation III (dihydroxyacetone cyc	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
METACYC	P185-PWY	formaldehyde assimilation III (dihydroxyacetone cyc	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-5497	purine nucleotides degradation IV (anaerobic)	Tfu_1737	Tfu_1737 oxidoreductase alpha (molybdopterin) subunit			14.39	13.79	19.93	
METACYC	PWY-5497	purine nucleotides degradation IV (anaerobic)	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
METACYC	PWY-5497	purine nucleotides degradation IV (anaerobic)	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
METACYC	PWY-5497	purine nucleotides degradation IV (anaerobic)	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	PWY-5676	acetyl-CoA fermentation to butyrate II	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-5676	acetyl-CoA fermentation to butyrate II	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-5676	acetyl-CoA fermentation to butyrate II	Tfu_0946	Tfu_0946 putative acyl-CoA dehydrogenase	20.62	20.44	21.21	21.21	24.67	0.91
METACYC	PWY-5676	acetyl-CoA fermentation to butyrate II	Tfu_1281	Tfu_1281 butyryl-CoA dehydrogenase						
METACYC	PWY-5676	acetyl-CoA fermentation to butyrate II	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-5676	acetyl-CoA fermentation to butyrate II	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	OXIDATIVEPENT-PWY	pentose phosphate pathway (oxidative branch)	Tfu_0003	Tfu_0003 6-phosphogluconate dehydrogenase	20.18	20.31	19.92	19.72	23.9	0.655
METACYC	OXIDATIVEPENT-PWY	pentose phosphate pathway (oxidative branch)	Tfu_2005	Tfu_2005 glucose-6-phosphate 1-dehydrogenase	16.6	15.74	16.81	16.27	21.46	
METACYC	OXIDATIVEPENT-PWY	pentose phosphate pathway (oxidative branch)	Tfu_2007	Tfu_2007 6-phosphogluconolactonase	18.7	19.13	18.21	17.98	22.37	0.913
METACYC	PWY-6174	mevalonate pathway II (archaea)	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-6174	mevalonate pathway II (archaea)	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-6174	mevalonate pathway II (archaea)	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-6174	mevalonate pathway II (archaea)	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-6456	serinol biosynthesis	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_0881	Tfu_0881 cytochrome-c oxidase			17.98	18.28	22.45	
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_1015	Tfu_1015 hypothetical protein	20.5	19.96	19.7	20.09	23.2	1.256
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_1016	Tfu_1016 cytochrome-c oxidase					20.91	1.146
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_1022	Tfu_1022 cytochrome c oxidase subunit III						
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_1695	Tfu_1695 cytochrome-c oxidase						

METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2682	Tfu_2682 NADH dehydrogenase subunit N	15.55	15.11	17.89	15.78	21.55	1.549
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2683	Tfu_2683 NADH dehydrogenase subunit M	15.96	15.61	18.67	18.21	22.04	1.217
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2684	Tfu_2684 NADH dehydrogenase subunit L	16.72	16.18	19.09	19.32	22.49	1.313
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2685	Tfu_2685 NADH dehydrogenase kappa subunit	15.96	16.12	17.42	17.06	21.01	1.226
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2686	Tfu_2686 NADH dehydrogenase subunit J	14.57		19.26	18.19	22.25	
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2687	Tfu_2687 NADH-quinone oxidoreductase, chain I	17.42	17.05	19.49	19.25	23.17	1.344
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2688	Tfu_2688 NADH dehydrogenase subunit H	16.85	15.81	18.1	18.62	22.74	1.366
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2689	Tfu_2689 NADH dehydrogenase gamma subunit	19.85	19.4	22.2	22.17	25.89	1.474
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2690	Tfu_2690 NADH-quinone oxidoreductase, F subunit	18.4	18.59	21.04	20.94	24.09	1.696
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2691	Tfu_2691 ATP synthase subunit E	18.11	17.48	19.19	19.38	23.19	
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2692	Tfu_2692 NADH dehydrogenase delta subunit	17.85	17.37	21.19	20.56	24.79	1.513
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2693	Tfu_2693 NADH dehydrogenase subunit C	17.89	18.01	20.34	20.17	23.82	1.361
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2694	Tfu_2694 NADH dehydrogenase beta subunit	17.52	17.43	19.51	19.02	23.25	1.847
METACYC	PWY-3781	aerobic respiration (cytochrome c)	Tfu_2695	Tfu_2695 NADH dehydrogenase alpha subunit	15.61	15.66	16.21	16.57	20.39	
METACYC	PWY-6517	N-acetylglucosamine degradation II	Tfu_2473	Tfu_2473 n-acetylglucosamine-6-phosphate deacetylase	14.21				17.55	
METACYC	PWY-5133	cohumulone biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5133	cohumulone biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5133	cohumulone biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6735	starch degradation IV	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-83	monolignol glucosides biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-83	monolignol glucosides biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-83	monolignol glucosides biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-2021	IAA degradation IV	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-2021	IAA degradation IV	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-2021	IAA degradation IV	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5710	capsaicin biosynthesis	Tfu_0966	Tfu_0966 caffeoyl-CoA O-methyltransferase		13.62			16.15	
METACYC	P1-PWY	purine and pyrimidine metabolism	Tfu_0678	Tfu_0678 uridylate kinase	18.09	18.05	17.82	18.33	22.01	1.02
METACYC	P1-PWY	purine and pyrimidine metabolism	Tfu_1053	Tfu_1053 pyrimidine regulatory protein PyrR	17.14	17.38	18.18	18.29	22.2	0.824
METACYC	P1-PWY	purine and pyrimidine metabolism	Tfu_1062	Tfu_1062 guanylate kinase			14.95	15.22	19.61	
METACYC	P1-PWY	purine and pyrimidine metabolism	Tfu_2091	Tfu_2091 adenine phosphoribosyltransferase		14.26			19.51	0.761
METACYC	P1-PWY	purine and pyrimidine metabolism	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	P1-PWY	purine and pyrimidine metabolism	Tfu_2625	Tfu_2625 adenylate kinase, subfamily	19.36	20.27	22.16	21.48	24.95	0.736
METACYC	P1-PWY	purine and pyrimidine metabolism	Tfu_2783	Tfu_2783 thymidylate kinase	19.41	19.13	18.67	18.47	22.51	0.962
METACYC	P1-PWY	purine and pyrimidine metabolism	Tfu_2896	Tfu_2896 hypoxanthine phosphoribosyl transferase		16.7	16.94	16.58	21.76	0.668
METACYC	SO4ASSIM-PWY	sulfate reduction I (assimilatory)	Tfu_1889	Tfu_1889 phosphoadenosine phosphosulfate reductase						
METACYC	PWY-5670	epoxysqualene biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5670	epoxysqualene biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5670	epoxysqualene biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-922	mevalonate pathway I	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-922	mevalonate pathway I	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-922	mevalonate pathway I	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-922	mevalonate pathway I	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-6804	diacylglycerol biosynthesis (PUFA enrichment in oils	Tfu_1855	Tfu_1855 4'-phosphopantetheinyl transferase						
METACYC	PWY-6804	diacylglycerol biosynthesis (PUFA enrichment in oils	Tfu_2817	Tfu_2817 hypothetical protein					18.27	
METACYC	P42-PWY	incomplete reductive TCA cycle	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	P42-PWY	incomplete reductive TCA cycle	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	P42-PWY	incomplete reductive TCA cycle	Tfu_2451	Tfu_2451 succinate dehydrogenase	19.35	19.39	20.29	20.56	23.66	1.002
METACYC	P42-PWY	incomplete reductive TCA cycle	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
METACYC	P42-PWY	incomplete reductive TCA cycle	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
METACYC	P42-PWY	incomplete reductive TCA cycle	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035

METACYC	P42-PWY	incomplete reductive TCA cycle	Tfu_2674	Tfu_2674 2-oxoglutarate ferredoxin oxidoreductase, alph	14.55		17.74	18.16	22.74	1.656
METACYC	P42-PWY	incomplete reductive TCA cycle	Tfu_2675	Tfu_2675 ferrodoxin oxidoreductase beta subunit			17.01	16.7	21.8	
METACYC	PWY-5307	gentiodelphin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5307	gentiodelphin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5307	gentiodelphin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5307	gentiodelphin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5307	gentiodelphin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5307	gentiodelphin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5307	gentiodelphin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5310	superpathway of anthocyanin biosynthesis (from del	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5310	superpathway of anthocyanin biosynthesis (from del	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5310	superpathway of anthocyanin biosynthesis (from del	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6902	chitin degradation II	Tfu_0580	Tfu_0580 chitinase II	17.05	17.75	15.71	15.95	21.45	
METACYC	PWY-6902	chitin degradation II	Tfu_0868	Tfu_0868 hypothetical protein					16.11	
METACYC	PWY-6902	chitin degradation II	Tfu_2486	Tfu_2486 hypothetical protein	16.26	16.75		15.08	20.28	
METACYC	PWY-5844	menaquinol-9 biosynthesis	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY0-1021	alanine biosynthesis III	Tfu_0595	Tfu_0595 putative pyridoxal-phosphate-dependent aminotransferase					16.06	
METACYC	PWY0-1021	alanine biosynthesis III	Tfu_1983	Tfu_1983 cysteine desulphurases, SufS	14.11			13.91	18.52	0.647
METACYC	NONOXIPENT-PWY	pentose phosphate pathway (non-oxidative branch)	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
METACYC	NONOXIPENT-PWY	pentose phosphate pathway (non-oxidative branch)	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
METACYC	NONOXIPENT-PWY	pentose phosphate pathway (non-oxidative branch)	Tfu_2003	Tfu_2003 transaldolase	20.04	20.08	21.54	21.1	24.47	1.211
METACYC	NONOXIPENT-PWY	pentose phosphate pathway (non-oxidative branch)	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
METACYC	PWY-5482	pyruvate fermentation to acetate II	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	PWY-5917	phycocyanobilin biosynthesis	Tfu_2345	Tfu_2345 heme oxygenase (decyclizing)						
METACYC	PWY-6692	Fe(II) oxidation	Tfu_0881	Tfu_0881 cytochrome-c oxidase			17.98	18.28	22.45	
METACYC	PWY-6692	Fe(II) oxidation	Tfu_1015	Tfu_1015 hypothetical protein	20.5	19.96	19.7	20.09	23.2	1.256
METACYC	PWY-6692	Fe(II) oxidation	Tfu_1016	Tfu_1016 cytochrome-c oxidase					20.91	1.146
METACYC	PWY-6692	Fe(II) oxidation	Tfu_1022	Tfu_1022 cytochrome c oxidase subunit III						
METACYC	PWY-6692	Fe(II) oxidation	Tfu_1695	Tfu_1695 cytochrome-c oxidase						
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2682	Tfu_2682 NADH dehydrogenase subunit N	15.55	15.11	17.89	15.78	21.55	1.549
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2683	Tfu_2683 NADH dehydrogenase subunit M	15.96	15.61	18.67	18.21	22.04	1.217
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2684	Tfu_2684 NADH dehydrogenase subunit L	16.72	16.18	19.09	19.32	22.49	1.313
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2685	Tfu_2685 NADH dehydrogenase kappa subunit	15.96	16.12	17.42	17.06	21.01	1.226
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2686	Tfu_2686 NADH dehydrogenase subunit J	14.57		19.26	18.19	22.25	
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2687	Tfu_2687 NADH-quinone oxidoreductase, chain I	17.42	17.05	19.49	19.25	23.17	1.344
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2688	Tfu_2688 NADH dehydrogenase subunit H	16.85	15.81	18.1	18.62	22.74	1.366
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2689	Tfu_2689 NADH dehydrogenase gamma subunit	19.85	19.4	22.2	22.17	25.89	1.474
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2690	Tfu_2690 NADH-quinone oxidoreductase, F subunit	18.4	18.59	21.04	20.94	24.09	1.696
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2691	Tfu_2691 ATP synthase subunit E	18.11	17.48	19.19	19.38	23.19	
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2692	Tfu_2692 NADH dehydrogenase delta subunit	17.85	17.37	21.19	20.56	24.79	1.513
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2693	Tfu_2693 NADH dehydrogenase subunit C	17.89	18.01	20.34	20.17	23.82	1.361
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2694	Tfu_2694 NADH dehydrogenase beta subunit	17.52	17.43	19.51	19.02	23.25	1.847
METACYC	PWY-6692	Fe(II) oxidation	Tfu_2695	Tfu_2695 NADH dehydrogenase alpha subunit	15.61	15.66	16.21	16.57	20.39	
METACYC	PWY-6507	5-dehydro-4-deoxy-D-glucuronate degradation	Tfu_0188	Tfu_0188 2-dehydro-3-deoxyphosphogluconate aldolase	14.36				15.14	
METACYC	PWY-6507	5-dehydro-4-deoxy-D-glucuronate degradation	Tfu_0189	Tfu_0189 putative PfkB-family carbohydrate kinase						
METACYC	PWY-5340	sulfate activation for sulfonation	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
METACYC	PWY-5340	sulfate activation for sulfonation	Tfu_0420	Tfu_0420 Small GTP-binding protein domain:Sulfate adenylyltransferase, l			14.13		18.76	0.81
METACYC	PWY-5340	sulfate activation for sulfonation	Tfu_0425	Tfu_0425 adenylylsulfate kinase					17.66	
METACYC	PWY-6064	methylquercetin biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6064	methylquercetin biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						

METACYC	PWY-5825	dalpatein and dalnigrein biosynthesis	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6419	shikimate degradation II	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6419	shikimate degradation II	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6085	2,4-dichlorophenoxyacetate degradation	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	ECASYN-PWY	enterobacterial common antigen biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	ECASYN-PWY	enterobacterial common antigen biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	ECASYN-PWY	enterobacterial common antigen biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	ECASYN-PWY	enterobacterial common antigen biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	ECASYN-PWY	enterobacterial common antigen biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	ECASYN-PWY	enterobacterial common antigen biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	ECASYN-PWY	enterobacterial common antigen biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	ECASYN-PWY	enterobacterial common antigen biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	ECASYN-PWY	enterobacterial common antigen biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	SPHINGOLIPID-SYN-PWY	sphingolipid metabolism	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	SPHINGOLIPID-SYN-PWY	sphingolipid metabolism	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	SPHINGOLIPID-SYN-PWY	sphingolipid metabolism	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	SPHINGOLIPID-SYN-PWY	sphingolipid metabolism	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5979	3-amino-5-hydroxybenzoate biosynthesis	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
METACYC	PWY-6896	thiamin salvage I	Tfu_0643	Tfu_0643 thiamine monophosphate kinase					14.5	
METACYC	PWY-6724	starch degradation II	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-6724	starch degradation II	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6724	starch degradation II	Tfu_2205	Tfu_2205 glycoside hydrolase, family 77					15.25	
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_1278	Tfu_1278 thiolase						
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6948	sitosterol degradation to androstenedione	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6733	sporopollenin precursor biosynthesis	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-6733	sporopollenin precursor biosynthesis	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6886	1-butanol autotrophic biosynthesis	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	PWY-6886	1-butanol autotrophic biosynthesis	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	PWY-6886	1-butanol autotrophic biosynthesis	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	PWY-6886	1-butanol autotrophic biosynthesis	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	PWY-6886	1-butanol autotrophic biosynthesis	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	PWY-6886	1-butanol autotrophic biosynthesis	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	PWY-6886	1-butanol autotrophic biosynthesis	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	ARGSYN-PWY	arginine biosynthesis I	Tfu_1056	Tfu_1056 carbamoyl-phosphate synthase, small subunit		15.52	17.25	17.26	22.56	0.884
METACYC	ARGSYN-PWY	arginine biosynthesis I	Tfu_1057	Tfu_1057 carbamoyl-phosphate synthase, large subunit,	16.53	16.24	19.8	19.69	24.13	0.99
METACYC	ARGSYN-PWY	arginine biosynthesis I	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
METACYC	ARGSYN-PWY	arginine biosynthesis I	Tfu_2051	Tfu_2051 argininosuccinate lyase	15.68	16.51	18.68	18.9	22.79	

METACYC	ARGSYN-PWY	arginine biosynthesis I	Tfu_2052	Tfu_2052 argininosuccinate synthase	13.3		18.49	17.16	22.53	
METACYC	PWY-6519	7-keto-8-aminopelargonate biosynthesis I	Tfu_1229	Tfu_1229 putative 3-oxoacyl-ACP synthase III						
METACYC	PWY-6519	7-keto-8-aminopelargonate biosynthesis I	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWY-6519	7-keto-8-aminopelargonate biosynthesis I	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWY-6519	7-keto-8-aminopelargonate biosynthesis I	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWY-6519	7-keto-8-aminopelargonate biosynthesis I	Tfu_1974	Tfu_1974 3-oxoacyl-(acyl carrier protein) synthase	14.7	15.5	19.86	19.55	23.27	0.869
METACYC	PWY-6519	7-keto-8-aminopelargonate biosynthesis I	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	PWY-5821	dalcochinin biosynthesis	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6167	flavin biosynthesis II (archaea)	Tfu_0782	Tfu_0782 Cytidyltransferase-related		13.35	14.92	14.18	20.03	
METACYC	PWY-6167	flavin biosynthesis II (archaea)	Tfu_1078	Tfu_1078 Lumazine-binding protein		13.92	16.4	17.05	20.31	
METACYC	PWY-6167	flavin biosynthesis II (archaea)	Tfu_1080	Tfu_1080 bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein						
METACYC	PWY-6167	flavin biosynthesis II (archaea)	Tfu_1081	Tfu_1081 6,7-dimethyl-8-ribityllumazine synthase	15.97	15.69	16.33	16.62	21.62	
METACYC	PWY-5269	cardiolipin biosynthesis II	Tfu_0796	Tfu_0796 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase					15.36	
METACYC	PWY-5269	cardiolipin biosynthesis II	Tfu_1393	Tfu_1393 putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase					15.45	
METACYC	PWY-5269	cardiolipin biosynthesis II	Tfu_2103	Tfu_2103 putative membrane transferase		14.75	15	14.79	18.49	
METACYC	PWY4FS-7	phosphatidylglycerol biosynthesis I (plastidic)	Tfu_0796	Tfu_0796 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase					15.36	
METACYC	PWY4FS-7	phosphatidylglycerol biosynthesis I (plastidic)	Tfu_1393	Tfu_1393 putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase					15.45	
METACYC	PWY4FS-7	phosphatidylglycerol biosynthesis I (plastidic)	Tfu_2103	Tfu_2103 putative membrane transferase		14.75	15	14.79	18.49	
METACYC	PWY-5030	histidine degradation III	Tfu_0821	Tfu_0821 imidazolonepropionase					17.2	
METACYC	PWY-5030	histidine degradation III	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
METACYC	PWY-4381	fatty acid biosynthesis initiation I	Tfu_1229	Tfu_1229 putative 3-oxoacyl-ACP synthase III						
METACYC	PWY-4381	fatty acid biosynthesis initiation I	Tfu_1973	Tfu_1973 acyl-carrier-protein S-malonyltransferase	18.46	18.27	20.02	20.23	23.66	0.61
METACYC	PWY-4381	fatty acid biosynthesis initiation I	Tfu_1974	Tfu_1974 3-oxoacyl-(acyl carrier protein) synthase	14.7	15.5	19.86	19.55	23.27	0.869
METACYC	PWY-2881	cytokinins 7-N-glucoside biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-2881	cytokinins 7-N-glucoside biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-2881	cytokinins 7-N-glucoside biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6309	tryptophan degradation XI (mammalian, via kynuren	Tfu_0922	Tfu_0922 kynureninase	16.91	15.34	13.9	14.63	19.53	1.172
METACYC	PWY-6309	tryptophan degradation XI (mammalian, via kynuren	Tfu_1418	Tfu_1418 hypothetical protein	18.89	18.42	20.57	20.44	23.75	0.572
METACYC	PWY-6309	tryptophan degradation XI (mammalian, via kynuren	Tfu_1722	Tfu_1722 hypothetical protein					14.24	
METACYC	GLYSYN-PWY	glycine biosynthesis I	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
METACYC	PWY-5140	cannabinoid biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5140	cannabinoid biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5140	cannabinoid biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5140	cannabinoid biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5140	cannabinoid biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5140	cannabinoid biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5140	cannabinoid biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6987	lipoate biosynthesis and incorporation III (Bacillus)	Tfu_0991	Tfu_0991 lipoyl synthase					17.9	1.46
METACYC	PWY-6987	lipoate biosynthesis and incorporation III (Bacillus)	Tfu_0992	Tfu_0992 lipoyltransferase					18.24	
METACYC	PWY-6987	lipoate biosynthesis and incorporation III (Bacillus)	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6987	lipoate biosynthesis and incorporation III (Bacillus)	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6987	lipoate biosynthesis and incorporation III (Bacillus)	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6987	lipoate biosynthesis and incorporation III (Bacillus)	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5940	streptomycin biosynthesis	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PWY-6587	pyruvate fermentation to ethanol III	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-6587	pyruvate fermentation to ethanol III	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-6587	pyruvate fermentation to ethanol III	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-6587	pyruvate fermentation to ethanol III	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-7002	4-hydroxyacetophenone degradation	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY-6372	1D-myo-inositol hexakisphosphate biosynthe	Tfu_3099	Tfu_3099 myo-inositol-1-phosphate synthase	16.21	15.62	18.24	18.23	23.01	0.924

METACYC	PWY-102	gibberellin inactivation I (2β-hydroxylation)	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	METHIONINE-DEG1-PWY	methionine degradation I (to homocysteine)	Tfu_1065	Tfu_1065 S-adenosylmethionine synthetase	15.28	15.32	15.74	16.4	20.99	0.962
METACYC	METHIONINE-DEG1-PWY	methionine degradation I (to homocysteine)	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	METHIONINE-DEG1-PWY	methionine degradation I (to homocysteine)	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	METHIONINE-DEG1-PWY	methionine degradation I (to homocysteine)	Tfu_2505	Tfu_2505 S-adenosyl-L-homocysteine hydrolase	18.66	19.01	19.8	19.23	23.56	1.126
METACYC	PWY-5268	salvianin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5268	salvianin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5268	salvianin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5268	salvianin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5268	salvianin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5268	salvianin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5268	salvianin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5668	cardiolipin biosynthesis I	Tfu_0796	Tfu_0796 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase					15.36	
METACYC	PWY-5668	cardiolipin biosynthesis I	Tfu_1393	Tfu_1393 putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase					15.45	
METACYC	PWY-5668	cardiolipin biosynthesis I	Tfu_1855	Tfu_1855 4'-phosphopantetheinyl transferase						
METACYC	PWY-5668	cardiolipin biosynthesis I	Tfu_2103	Tfu_2103 putative membrane transferase		14.75	15	14.79	18.49	
METACYC	PWY-5668	cardiolipin biosynthesis I	Tfu_2817	Tfu_2817 hypothetical protein					18.27	
METACYC	PWY-7033	alkane biosynthesis II	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-7033	alkane biosynthesis II	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-7033	alkane biosynthesis II	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-7033	alkane biosynthesis II	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-5839	menaquinol-7 biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5839	menaquinol-7 biosynthesis	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	FORMASS-PWY	formaldehyde oxidation IV (thiol-independent)	Tfu_3025	Tfu_3025 putative alcohol dehydrogenase	18.7	19.04	16.64	17.19	21.72	
METACYC	PWY-6531	mannitol cycle	Tfu_0928	Tfu_0928 fructokinase	18.37	17.96	18.63	18.42	22.16	0.898
METACYC	PWY-6531	mannitol cycle	Tfu_1037	Tfu_1037 phosphofructokinase	21.14	20.73	24.02	23.83	26.57	0.842
METACYC	PWY-6531	mannitol cycle	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6531	mannitol cycle	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	PWY-6531	mannitol cycle	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-6531	mannitol cycle	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5965	fatty acid biosynthesis initiation III	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5965	fatty acid biosynthesis initiation III	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5965	fatty acid biosynthesis initiation III	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5965	fatty acid biosynthesis initiation III	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5392	reductive TCA cycle II	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	PWY-5392	reductive TCA cycle II	Tfu_0341	Tfu_0341 citryl-CoA lyase	17.85	17.79	17.74	17.05	21.43	
METACYC	PWY-5392	reductive TCA cycle II	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	PWY-5392	reductive TCA cycle II	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5392	reductive TCA cycle II	Tfu_1285	Tfu_1285 citryl-CoA lyase						
METACYC	PWY-5392	reductive TCA cycle II	Tfu_1313	Tfu_1313 putative citrate lyase beta subunit	20.71	20.33	20.94	21.03	24.43	1.292
METACYC	PWY-5392	reductive TCA cycle II	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	PWY-5392	reductive TCA cycle II	Tfu_2451	Tfu_2451 succinate dehydrogenase	19.35	19.39	20.29	20.56	23.66	1.002
METACYC	PWY-5392	reductive TCA cycle II	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
METACYC	PWY-5392	reductive TCA cycle II	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5392	reductive TCA cycle II	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
METACYC	PWY-5392	reductive TCA cycle II	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
METACYC	PWY-5392	reductive TCA cycle II	Tfu_2674	Tfu_2674 2-oxoglutarate ferredoxin oxidoreductase, alph	14.55		17.74	18.16	22.74	1.656
METACYC	PWY-5392	reductive TCA cycle II	Tfu_2675	Tfu_2675 ferrodoxin oxidoreductase beta subunit			17.01	16.7	21.8	
METACYC	PWY-5941	glycogen degradation II	Tfu_0586	Tfu_0586 alpha-glucan phosphorylase					15.86	
METACYC	PWY-5941	glycogen degradation II	Tfu_2205	Tfu_2205 glycoside hydrolase, family 77					15.25	

METACYC	PWY-5941	glycogen degradation II	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	TEICHOICACID-PWY	teichoic acid (poly-glycerol) biosynthesis	Tfu_1855	Tfu_1855 4'-phosphopantetheinyl transferase						
METACYC	TEICHOICACID-PWY	teichoic acid (poly-glycerol) biosynthesis	Tfu_2178	Tfu_2178 similar to Putative glycosyl/glycerophosphate transferase involved in teichoic acid biosynthesis Tag						
METACYC	TEICHOICACID-PWY	teichoic acid (poly-glycerol) biosynthesis	Tfu_2817	Tfu_2817 hypothetical protein					18.27	
METACYC	PWY-5774	saponin biosynthesis IV	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5774	saponin biosynthesis IV	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5774	saponin biosynthesis IV	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5046	branched-chain α-keto acid dehydrogenase co	Tfu_0994	Tfu_0994 dihydrolipoamide dehydrogenase	23.87	23.67	23.96	23.71	27.03	1.154
METACYC	PWY-5046	branched-chain α-keto acid dehydrogenase co	Tfu_2559	Tfu_2559 dihydrolipoamide dehydrogenase	17.62	17.97	18.6	18.7	23.28	1.063
METACYC	PWY-6711	archaeosine biosynthesis	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
METACYC	PWY-6368	3-phosphoinositide degradation	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	P381-PWY	adenosylcobalamin biosynthesis II (late cobalt incor	Tfu_0310	Tfu_0310 precorrin-6x reductase CbiJ/CobK					14.55	
METACYC	P381-PWY	adenosylcobalamin biosynthesis II (late cobalt incor	Tfu_0311	Tfu_0311 cobyrinic acid a,c-diamide synthase CbiA					16.36	
METACYC	P381-PWY	adenosylcobalamin biosynthesis II (late cobalt incor	Tfu_0314	Tfu_0314 SAM (and some other nucleotide) binding motif						
METACYC	P381-PWY	adenosylcobalamin biosynthesis II (late cobalt incor	Tfu_0315	Tfu_0315 precorrin-4 C11-methyltransferase region					19.46	0.814
METACYC	P381-PWY	adenosylcobalamin biosynthesis II (late cobalt incor	Tfu_0316	Tfu_0316 precorrin-3B C17-methyltransferase region:Precorrin-2 C20-methyltransferase						
METACYC	P381-PWY	adenosylcobalamin biosynthesis II (late cobalt incor	Tfu_0317	Tfu_0317 precorrin-8X methylmutase						
METACYC	P381-PWY	adenosylcobalamin biosynthesis II (late cobalt incor	Tfu_0318	Tfu_0318 cobalamin biosynthesis protein CobG, precorrin-3B synthase						
METACYC	P381-PWY	adenosylcobalamin biosynthesis II (late cobalt incor	Tfu_0319	Tfu_0319 cobaltochelatase	18.14	17.88	19.25	19.28	23.66	1.195
METACYC	P381-PWY	adenosylcobalamin biosynthesis II (late cobalt incor	Tfu_0320	Tfu_0320 putative cobF protein, precorrin-6A synthase						
METACYC	HOMOSER-THRESYN-PWY	threonine biosynthesis from homoserine	Tfu_0226	Tfu_0226 threonine synthase	15.9	15.94	18.57	18.65	22.91	1.385
METACYC	HOMOSER-THRESYN-PWY	threonine biosynthesis from homoserine	Tfu_2422	Tfu_2422 homoserine kinase					19.33	0.823
METACYC	HOMOSER-THRESYN-PWY	threonine biosynthesis from homoserine	Tfu_2423	Tfu_2423 threonine synthase	13.86				17.31	
METACYC	PWY-4502	wighteone and luteone biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-4502	wighteone and luteone biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-4502	wighteone and luteone biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6664	di-myo-inositol phosphate biosynthesis	Tfu_3099	Tfu_3099 myo-inositol-1-phosphate synthase	16.21	15.62	18.24	18.23	23.01	0.924
METACYC	PWY-6689	tRNA splicing	Tfu_0243	Tfu_0243 hypothetical protein					16.84	
METACYC	PWY-5155	β-alanine biosynthesis III	Tfu_1862	Tfu_1862 aspartate 1-decarboxylase precursor			14.98		19.99	
METACYC	PWY-6853	ethylene biosynthesis II (microbes)	Tfu_0433	Tfu_0433 delta-1-pyrroline-5-carboxylate dehydrogenas	20.87	20.52	20.5	20.22	24.05	1.051
METACYC	PWY-6978	plastoquinol-9 biosynthesis II	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6978	plastoquinol-9 biosynthesis II	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	HEME-BIOSYNTHESIS-II	heme biosynthesis from uroporphyrinogen-III I	Tfu_1897	Tfu_1897 protoporphyrinogen oxidase			14.61		20.74	1.244
METACYC	HEME-BIOSYNTHESIS-II	heme biosynthesis from uroporphyrinogen-III I	Tfu_1899	Tfu_1899 uroporphyrinogen decarboxylase HemE		14.37	15.41	15.99	20.69	0.856
METACYC	HEME-BIOSYNTHESIS-II	heme biosynthesis from uroporphyrinogen-III I	Tfu_1945	Tfu_1945 ferrochelatase		13.87	18.69	18.79	22.82	1.023
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2033	Tfu_2033 inorganic polyphosphate/ATP-NAD kinase	16.3	16.08	15.21	15.52	19.8	
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2682	Tfu_2682 NADH dehydrogenase subunit N	15.55	15.11	17.89	15.78	21.55	1.549
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2683	Tfu_2683 NADH dehydrogenase subunit M	15.96	15.61	18.67	18.21	22.04	1.217
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2684	Tfu_2684 NADH dehydrogenase subunit L	16.72	16.18	19.09	19.32	22.49	1.313
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2685	Tfu_2685 NADH dehydrogenase kappa subunit	15.96	16.12	17.42	17.06	21.01	1.226
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2686	Tfu_2686 NADH dehydrogenase subunit J	14.57		19.26	18.19	22.25	
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2687	Tfu_2687 NADH-quinone oxidoreductase, chain I	17.42	17.05	19.49	19.25	23.17	1.344
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2688	Tfu_2688 NADH dehydrogenase subunit H	16.85	15.81	18.1	18.62	22.74	1.366
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2689	Tfu_2689 NADH dehydrogenase gamma subunit	19.85	19.4	22.2	22.17	25.89	1.474
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2690	Tfu_2690 NADH-quinone oxidoreductase, F subunit	18.4	18.59	21.04	20.94	24.09	1.696
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2691	Tfu_2691 ATP synthase subunit E	18.11	17.48	19.19	19.38	23.19	
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2692	Tfu_2692 NADH dehydrogenase delta subunit	17.85	17.37	21.19	20.56	24.79	1.513
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2693	Tfu_2693 NADH dehydrogenase subunit C	17.89	18.01	20.34	20.17	23.82	1.361
METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2694	Tfu_2694 NADH dehydrogenase beta subunit	17.52	17.43	19.51	19.02	23.25	1.847

METACYC	PWY-5083	NAD/NADH phosphorylation and dephosphorylation	Tfu_2695	Tfu_2695 NADH dehydrogenase alpha subunit	15.61	15.66	16.21	16.57	20.39	
METACYC	PWY-2723	trehalose degradation V	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	PWY-2723	trehalose degradation V	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	PWY-6559	spermidine biosynthesis II	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1	18.57	18.71	20.61	20.33	23.82	0.982
METACYC	PWY-6559	spermidine biosynthesis II	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
METACYC	PWY-6317	galactose degradation I (Leloir pathway)	Tfu_0169	Tfu_0169 nucleoside-diphosphate-sugar epimerase (UDP	14.49	16.6	18.84	18.16	22.51	0.845
METACYC	PWY-6317	galactose degradation I (Leloir pathway)	Tfu_1622	Tfu_1622 UDP-glucose 4-epimerase						
METACYC	PWY-6317	galactose degradation I (Leloir pathway)	Tfu_2566	Tfu_2566 galactokinase						
METACYC	PWY-6317	galactose degradation I (Leloir pathway)	Tfu_2591	Tfu_2591 UDP-glucose 4-epimerase					14.83	
METACYC	PWY-6317	galactose degradation I (Leloir pathway)	Tfu_2723	Tfu_2723 putative epimerase						
METACYC	P3-PWY	gallate degradation III (anaerobic)	Tfu_0946	Tfu_0946 putative acyl-CoA dehydrogenase	20.62	20.44	21.21	21.21	24.67	0.91
METACYC	P3-PWY	gallate degradation III (anaerobic)	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	P3-PWY	gallate degradation III (anaerobic)	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	P3-PWY	gallate degradation III (anaerobic)	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	P3-PWY	gallate degradation III (anaerobic)	Tfu_1281	Tfu_1281 butyryl-CoA dehydrogenase						
METACYC	P3-PWY	gallate degradation III (anaerobic)	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	P3-PWY	gallate degradation III (anaerobic)	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	P3-PWY	gallate degradation III (anaerobic)	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	PWY-5399	betacyanin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5399	betacyanin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5399	betacyanin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	P221-PWY	octane oxidation	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	P221-PWY	octane oxidation	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	P221-PWY	octane oxidation	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	P221-PWY	octane oxidation	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	P221-PWY	octane oxidation	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	P221-PWY	octane oxidation	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	P221-PWY	octane oxidation	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-7035	(Z)-9-tricosene biosynthesis	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-7035	(Z)-9-tricosene biosynthesis	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-7035	(Z)-9-tricosene biosynthesis	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-7035	(Z)-9-tricosene biosynthesis	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-6859	all-trans-farnesol biosynthesis	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
METACYC	CENTFERM-PWY	pyruvate fermentation to butanoate	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	CENTFERM-PWY	pyruvate fermentation to butanoate	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	CENTFERM-PWY	pyruvate fermentation to butanoate	Tfu_0946	Tfu_0946 putative acyl-CoA dehydrogenase	20.62	20.44	21.21	21.21	24.67	0.91
METACYC	CENTFERM-PWY	pyruvate fermentation to butanoate	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	CENTFERM-PWY	pyruvate fermentation to butanoate	Tfu_1281	Tfu_1281 butyryl-CoA dehydrogenase						
METACYC	CENTFERM-PWY	pyruvate fermentation to butanoate	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	CENTFERM-PWY	pyruvate fermentation to butanoate	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY0-43	conversion of succinate to propionate	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
METACYC	PWY0-43	conversion of succinate to propionate	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
METACYC	PWY0-43	conversion of succinate to propionate	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
METACYC	GLUCUROCAT-PWY	β-D-glucuronide and D-glucuronate degradation	Tfu_0189	Tfu_0189 putative PfkB-family carbohydrate kinase						
METACYC	PWY-5885	wax esters biosynthesis II	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-5885	wax esters biosynthesis II	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-5885	wax esters biosynthesis II	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-5885	wax esters biosynthesis II	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-5475	pentagalloylglucose biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5475	pentagalloylglucose biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						

METACYC	PWY-5475	pentagalloylglucose biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5475	pentagalloylglucose biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	ADENOSYLHOMOCYSCAT-PWY	methionine salvage II (mammalia)	Tfu_1825	Tfu_1825 5-methyltetrahydrofolate--homocysteine methyltransferase					15.39	
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	PWY-5109	2-methylbutyrate biosynthesis	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-6549	glutamine biosynthesis III	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	PWY-6549	glutamine biosynthesis III	Tfu_0863	Tfu_0863 pyruvate phosphate dikinase	17.84	17.11	21.38	21.45	25.04	1.455
METACYC	PWY-6549	glutamine biosynthesis III	Tfu_0982	Tfu_0982 glutamine synthetase type I	16.36	15.34	14.3	15.33	20.84	1.147
METACYC	PWY-6549	glutamine biosynthesis III	Tfu_0988	Tfu_0988 glutamine synthetase type I		16.24	19.93	19.87	23.49	1.247
METACYC	PWY-6549	glutamine biosynthesis III	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	PWY-6549	glutamine biosynthesis III	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	PWY-6549	glutamine biosynthesis III	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
METACYC	PWY-5537	pyruvate fermentation to acetate V	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
METACYC	PWY-5537	pyruvate fermentation to acetate V	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
METACYC	PWY-5768	pyruvate fermentation to acetate VIII	Tfu_1706	Tfu_1706 putative aldehyde dehydrogenase					17.58	
METACYC	PWY-5177	glutaryl-CoA degradation	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-5177	glutaryl-CoA degradation	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-5177	glutaryl-CoA degradation	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-5177	glutaryl-CoA degradation	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-5177	glutaryl-CoA degradation	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-6431	4-hydroxybenzoate biosynthesis IV	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-6431	4-hydroxybenzoate biosynthesis IV	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	SUCROSEUTIL2-PWY	sucrose degradation II	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	SUCROSEUTIL2-PWY	sucrose degradation II	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	SUCROSEUTIL2-PWY	sucrose degradation II	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-1622	formaldehyde assimilation I (serine pathway)	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	PWY-1622	formaldehyde assimilation I (serine pathway)	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	PWY-1622	formaldehyde assimilation I (serine pathway)	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	PWY-1622	formaldehyde assimilation I (serine pathway)	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	PWY-1622	formaldehyde assimilation I (serine pathway)	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	PWY-1622	formaldehyde assimilation I (serine pathway)	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
METACYC	PWY-1622	formaldehyde assimilation I (serine pathway)	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	PWY-1622	formaldehyde assimilation I (serine pathway)	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	PWY-6623	salicylate glucosides biosynthesis II	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6623	salicylate glucosides biosynthesis II	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6623	salicylate glucosides biosynthesis II	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-3841	folate transformations II	Tfu_0372	Tfu_0372 hypothetical protein						
METACYC	PWY-3841	folate transformations II	Tfu_1050	Tfu_1050 5,10-methylenetetrahydrofolate reductase						
METACYC	PWY-3841	folate transformations II	Tfu_1825	Tfu_1825 5-methyltetrahydrofolate--homocysteine methyltransferase					15.39	
METACYC	PWY-3841	folate transformations II	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
METACYC	PWY-3841	folate transformations II	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958

METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_0188	Tfu_0188 2-dehydro-3-deoxyphosphogluconate aldolase	14.36				15.14	
METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_0189	Tfu_0189 putative PfkB-family carbohydrate kinase						
METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-2221	Entner-Doudoroff pathway III (semi-phosphorylative	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	PWY-6763	salicortin biosynthesis	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY-6915	pentalenolactone biosynthesis	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-6932	selenate reduction	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
METACYC	PWY-6932	selenate reduction	Tfu_0420	Tfu_0420 Small GTP-binding protein domain:Sulfate adenylyltransferase, l			14.13		18.76	0.81
METACYC	PWY-6932	selenate reduction	Tfu_0425	Tfu_0425 adenylylsulfate kinase					17.66	
METACYC	PWY-3821	galactose degradation III	Tfu_0169	Tfu_0169 nucleoside-diphosphate-sugar epimerase (UDP	14.49	16.6	18.84	18.16	22.51	0.845
METACYC	PWY-3821	galactose degradation III	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase,	16.85	15	17.24	17.46	22.15	
METACYC	PWY-3821	galactose degradation III	Tfu_1622	Tfu_1622 UDP-glucose 4-epimerase						
METACYC	PWY-3821	galactose degradation III	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
METACYC	PWY-3821	galactose degradation III	Tfu_2566	Tfu_2566 galactokinase						
METACYC	PWY-3821	galactose degradation III	Tfu_2591	Tfu_2591 UDP-glucose 4-epimerase					14.83	
METACYC	PWY-3821	galactose degradation III	Tfu_2723	Tfu_2723 putative epimerase						
METACYC	PWY-6580	L-1-phosphatidyl-inositol biosynthesis (Mycobacteri	Tfu_3099	Tfu_3099 myo-inositol-1-phosphate synthase	16.21	15.62	18.24	18.23	23.01	0.924
METACYC	PWY-5672	ginsenoside biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5672	ginsenoside biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5672	ginsenoside biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5061	6,7,4'-trihydroxyisoflavone biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-5989	stearate biosynthesis II (bacteria and plants)	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWY-5989	stearate biosynthesis II (bacteria and plants)	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWY-5989	stearate biosynthesis II (bacteria and plants)	Tfu_1842	Tfu_1842 enoyl-(acyl carrier protein) reductase	20.49	19.93	21.16	21.07	24.76	1.053
METACYC	PWY-5989	stearate biosynthesis II (bacteria and plants)	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWY-5989	stearate biosynthesis II (bacteria and plants)	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	PWY-3162	tryptophan degradation V (side chain pathway)	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-3162	tryptophan degradation V (side chain pathway)	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-3162	tryptophan degradation V (side chain pathway)	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-3162	tryptophan degradation V (side chain pathway)	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	P163-PWY	lysine fermentation to acetate and butyrate	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	P163-PWY	lysine fermentation to acetate and butyrate	Tfu_0272	Tfu_0272 DUF160	17.82	17.78	20.43	19.91	24.03	1.174
METACYC	P163-PWY	lysine fermentation to acetate and butyrate	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	P163-PWY	lysine fermentation to acetate and butyrate	Tfu_0946	Tfu_0946 putative acyl-CoA dehydrogenase	20.62	20.44	21.21	21.21	24.67	0.91
METACYC	P163-PWY	lysine fermentation to acetate and butyrate	Tfu_1281	Tfu_1281 butyryl-CoA dehydrogenase						
METACYC	P163-PWY	lysine fermentation to acetate and butyrate	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	P163-PWY	lysine fermentation to acetate and butyrate	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	P163-PWY	lysine fermentation to acetate and butyrate	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	PWY-5660	taxol biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5660	taxol biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5660	taxol biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5660	taxol biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6808	dTDP-D-forosamine biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	

METACYC	PWY-5199	factor 420 polyglutamylation	Tfu_2518	Tfu_2518 hypothetical protein			14.93		19.68	
METACYC	PWY-6673	caffeoylglucarate biosynthesis	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-6673	caffeoylglucarate biosynthesis	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-6673	caffeoylglucarate biosynthesis	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY-3661	glycine betaine degradation	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
METACYC	PWY-5921	L-glutamine biosynthesis II (tRNA-dependent)	Tfu_0605	Tfu_0605 aspartyl/glutamyl-tRNA amidotransferase subunit C				14.86	18.24	
METACYC	PWY-5921	L-glutamine biosynthesis II (tRNA-dependent)	Tfu_0606	Tfu_0606 glutamyl-tRNA amidotransferase subunit A	15.37		19.4	18.8	23.02	0.99
METACYC	PWY-5921	L-glutamine biosynthesis II (tRNA-dependent)	Tfu_0609	Tfu_0609 aspartyl/glutamyl-tRNA amidotransferase subu	15.46	16.45	19.76	19.56	23.81	
METACYC	PWY-5508	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_0309	Tfu_0309 cobyric acid synthase					19.41	
METACYC	PWY-5508	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_0312	Tfu_0312 cob(I)yrinic acid a,c-diamide adenosyltransferase					16.96	
METACYC	PWY-5508	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_0996	Tfu_0996 putative cobalamin (5'-phosphate) synthase : adenosylcobinamide-GDP ribazoletransferase						
METACYC	PWY-5508	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_0997	Tfu_0997 adenosylcobinamide kinase / adenosylcobinamide-phos		15.35		15.47	20.21	
METACYC	PWY-5508	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_2222	Tfu_2222 nicotinate-nucleotide-dimethylbenzimidazole p	15.06		15.97	15.99	20.79	0.7
METACYC	PWY-5508	adenosylcobalamin biosynthesis from cobyrinate <i>	Tfu_2224	Tfu_2224 cobalamin biosynthesis protein						
METACYC	PWY-6731	starch degradation III	Tfu_0586	Tfu_0586 alpha-glucan phosphorylase					15.86	
METACYC	PWY-6731	starch degradation III	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PYRIDOXSYN-PWY	pyridoxal 5'-phosphate biosynthesis I	Tfu_0246	Tfu_0246 phosphoserine aminotransferase	19.59	19.46	22.48	21.91	25.76	1.096
METACYC	PYRIDOXSYN-PWY	pyridoxal 5'-phosphate biosynthesis I	Tfu_0248	Tfu_0248 pyridoxamine 5'-phosphate oxidase	15.34	14.98		14.89	18.71	
METACYC	PYRIDOXSYN-PWY	pyridoxal 5'-phosphate biosynthesis I	Tfu_1917	Tfu_1917 1-deoxy-D-xylulose-5-phosphate synthase					16.98	
METACYC	PWY-6695	oxalate degradation II	Tfu_1069	Tfu_1069 CaiB/BaiF family protein					17.39	0.688
METACYC	PWY-7013	L-1,2-propanediol degradation	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-7013	L-1,2-propanediol degradation	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-7013	L-1,2-propanediol degradation	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-7013	L-1,2-propanediol degradation	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-7013	L-1,2-propanediol degradation	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-7013	L-1,2-propanediol degradation	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-7013	L-1,2-propanediol degradation	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-7013	L-1,2-propanediol degradation	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-5891	menaquinol-11 biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5891	menaquinol-11 biosynthesis	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-5135	xanthohumol biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5135	xanthohumol biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5135	xanthohumol biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5135	xanthohumol biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5135	xanthohumol biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-3722	glycine betaine biosynthesis II (Gram-positive bacter	Tfu_0279	Tfu_0279 betaine-aldehyde dehydrogenase	21.7	21.51	19.8	20.02	23.9	0.958
METACYC	PWY-3722	glycine betaine biosynthesis II (Gram-positive bacter	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-3722	glycine betaine biosynthesis II (Gram-positive bacter	Tfu_1287	Tfu_1287 betaine-aldehyde dehydrogenase					18.53	
METACYC	PWY-3722	glycine betaine biosynthesis II (Gram-positive bacter	Tfu_1471	Tfu_1471 betaine-aldehyde dehydrogenase					16.26	
METACYC	PWY-3722	glycine betaine biosynthesis II (Gram-positive bacter	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-3722	glycine betaine biosynthesis II (Gram-positive bacter	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-3722	glycine betaine biosynthesis II (Gram-positive bacter	Tfu_1776	Tfu_1776 betaine-aldehyde dehydrogenase	16	15.03			18.4	
METACYC	PWY-3722	glycine betaine biosynthesis II (Gram-positive bacter	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	ALKANEMONOX-PWY	two-component alkanesulfonate monooxygenase	Tfu_1497	Tfu_1497 alkanesulfonate monooxygenase						
METACYC	ALKANEMONOX-PWY	two-component alkanesulfonate monooxygenase	Tfu_1500	Tfu_1500 alkanesulfonate monooxygenase						
METACYC	ALKANEMONOX-PWY	two-component alkanesulfonate monooxygenase	Tfu_1502	Tfu_1502 alkanesulfonate monooxygenase						
METACYC	PWY-6412	ginsenoside degradation II	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6412	ginsenoside degradation II	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6412	ginsenoside degradation II	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6412	ginsenoside degradation II	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	

METACYC	PWY-6799	fatty acid biosynthesis (plant mitochondria)	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6799	fatty acid biosynthesis (plant mitochondria)	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6799	fatty acid biosynthesis (plant mitochondria)	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-6799	fatty acid biosynthesis (plant mitochondria)	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6799	fatty acid biosynthesis (plant mitochondria)	Tfu_1973	Tfu_1973 acyl-carrier-protein S-malonyltransferase	18.46	18.27	20.02	20.23	23.66	0.61
METACYC	PWY-6799	fatty acid biosynthesis (plant mitochondria)	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6799	fatty acid biosynthesis (plant mitochondria)	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-7018	paromomycin biosynthesis	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-7018	paromomycin biosynthesis	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
METACYC	PWY-7018	paromomycin biosynthesis	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-7018	paromomycin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-7018	paromomycin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-7018	paromomycin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-7018	paromomycin biosynthesis	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-6893	thiamin diphosphate biosynthesis II (Bacillus)	Tfu_0643	Tfu_0643 thiamine monophosphate kinase					14.5	
METACYC	PWY-6893	thiamin diphosphate biosynthesis II (Bacillus)	Tfu_1046	Tfu_1046 thiamine-phosphate pyrophosphorylase		14.35			19.31	
METACYC	PWY-6609	adenine and adenosine salvage III	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY-6609	adenine and adenosine salvage III	Tfu_2563	Tfu_2563 adenosine deaminase					16.67	
METACYC	PWY-6609	adenine and adenosine salvage III	Tfu_2662	Tfu_2662 adenosine deaminase				13.97	19.93	1.018
METACYC	PWY-6609	adenine and adenosine salvage III	Tfu_2896	Tfu_2896 hypoxanthine phosphoribosyl transferase		16.7	16.94	16.58	21.76	0.668
METACYC	PWY-5750	itaconate biosynthesis	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	PWY-5750	itaconate biosynthesis	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	PWY2OL-4	linalool biosynthesis	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
METACYC	PWY-3121	linamarin degradation	Tfu_0937	Tfu_0937 beta-glucosidase	16.92	16.79	21.22	20.91	23.7	2.426
METACYC	PWY-3121	linamarin degradation	Tfu_1607	Tfu_1607 beta-glucosidase						
METACYC	PWY-3121	linamarin degradation	Tfu_1629	Tfu_1629 beta-glucosidase	20.15	19.64	19.92	19.43	23.45	1.12
METACYC	PWY-7045	mithramycin biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-7045	mithramycin biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-7045	mithramycin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-7045	mithramycin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-7045	mithramycin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-7045	mithramycin biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-7045	mithramycin biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-4981	proline biosynthesis II (from arginine)	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
METACYC	PWY-4981	proline biosynthesis II (from arginine)	Tfu_1993	Tfu_1993 arginine deiminase	17.46	16.86	15.61	15.61	20.88	1.353
METACYC	PWY-4981	proline biosynthesis II (from arginine)	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
METACYC	PWY-4981	proline biosynthesis II (from arginine)	Tfu_2708	Tfu_2708 delta 1-pyrroline-5-carboxylate reductase	17.73	17.16	18.03	17.57	21.11	
METACYC	PWY-5312	superpathway of anthocyanin biosynthesis (from pel	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5312	superpathway of anthocyanin biosynthesis (from pel	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5312	superpathway of anthocyanin biosynthesis (from pel	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_0031	Tfu_0031 seryl-tRNA synthetase	19.71	19.5	20.47	20.38	23.8	0.939
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_0212	Tfu_0212 cysteinyl-tRNA synthetase	16.41	14.49	18.9	18.08	23.01	1.169
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_0269	Tfu_0269 arginyl-tRNA synthetase, class Ic	17.72	17.49	20.13	19.85	24.16	1.223
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_0389	Tfu_0389 methionyl-tRNA synthetase	18.09	18	20.33	20.35	23.82	1.106
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_0623	Tfu_0623 glutamyl-tRNA synthetase bacterial/mitochon	18.5	17.36	18.79	19.22	23.34	0.908
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_0759	Tfu_0759 histidine--tRNA ligase	16.98	16.75	18.26	18.29	22.52	0.925
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_0772	Tfu_0772 prolyl-tRNA synthetase	19.32	19.13	19.74	19.37	23.57	1.007
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_0861	Tfu_0861 glycyl-tRNA synthetase	18.27	17.66	19.58	19.58	23.56	1.154
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_1120	Tfu_1120 isoleucyl-tRNA synthetase, class Ia	16.68	16.31	19.54	19.65	23.84	1.694
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_1832	Tfu_1832 cysteinyl-tRNA synthetase	15.91	16.04	18.24	17.09	22.24	1.186

METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_1936	Tfu_1936 valyl-tRNA synthetase	17.79	17.98	19.77	19.27	23.94	1.167
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_2043	Tfu_2043 tyrosyl-tRNA synthetase, class Ib	16.28	16.71	18.6	18.54	22.47	1.194
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_2060	Tfu_2060 phenylalanyl-tRNA synthetase beta subunit	19.74	19.67	20.55	20.4	24.66	1.059
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_2061	Tfu_2061 phenylalanyl-tRNA synthetase alpha subunit	16.56	17.28	19.09	18.91	22.49	0.719
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_2070	Tfu_2070 alanyl-tRNA synthetase	18.51	18.11	19.5	19.52	23.9	1.221
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_2086	Tfu_2086 aspartyl-tRNA synthetase	18.54	17.59	19.9	19.59	23.67	1.015
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_2108	Tfu_2108 threonyl-tRNA synthetase	18.4	18.24	19.7	19.43	23.68	1.178
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_2156	Tfu_2156 leucyl-tRNA synthetase bacterial/mitochondria	20.17	20.38	21.64	21.31	25.2	1.161
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_2376	Tfu_2376 tryptophanyl-tRNA synthetase, class Ib	15.16		16.88	16.16	20.45	
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_2426	Tfu_2426 similar to Arginyl-tRNA synthetase					16.36	
METACYC	TRNA-CHARGING-PWY	tRNA charging	Tfu_2881	Tfu_2881 lysyl-tRNA synthetase, class-2	16.6	16.7	19.01	18.9	23.54	0.997
METACYC	PWY-6125	guanosine nucleotides de novo biosynthesis	Tfu_1062	Tfu_1062 guanylate kinase			14.95	15.22	19.61	
METACYC	PWY-6125	guanosine nucleotides de novo biosynthesis	Tfu_2149	Tfu_2149 ribonucleotide-diphosphate reductase alpha su	14.41		17.19	15.02	21.83	0.68
METACYC	PWY-6125	guanosine nucleotides de novo biosynthesis	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
METACYC	PWY-6125	guanosine nucleotides de novo biosynthesis	Tfu_2440	Tfu_2440 inositol-5-monophosphate dehydrogenase	19.82	19.85	19.51	19.28	23.25	1.113
METACYC	PWY-6125	guanosine nucleotides de novo biosynthesis	Tfu_2589	Tfu_2589 bifunctional GMP synthase/glutamine amidotra	14.94		18.4	18.53	23.34	1.278
METACYC	PWY-6125	guanosine nucleotides de novo biosynthesis	Tfu_2595	Tfu_2595 inositol-5-monophosphate dehydrogenase	18.6	18.73	20.9	20.27	24.94	0.944
METACYC	PWY-6125	guanosine nucleotides de novo biosynthesis	Tfu_2596	Tfu_2596 IMP dehydrogenase	17.6	17.76	20.1	19.82	24.11	1.035
METACYC	PWY-6125	guanosine nucleotides de novo biosynthesis	Tfu_3001	Tfu_3001 ribonucleoside-diphosphate reductase	13.73	13.7	18.55	18.52	22.84	1.196
METACYC	PWY-6125	guanosine nucleotides de novo biosynthesis	Tfu_3002	Tfu_3002 ribonucleoside-diphosphate reductase			18.75	18.62	22.88	0.758
METACYC	PWY-7042	the visual cycle (insects)	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-7042	the visual cycle (insects)	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	CARNMET-PWY	carnitine degradation I	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	CARNMET-PWY	carnitine degradation I	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	CARNMET-PWY	carnitine degradation I	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-5826	hypoglycin biosynthesis	Tfu_1741	Tfu_1741 threonine dehydratase					16.86	
METACYC	ETHYL-PWY	ethylene biosynthesis I (plants)	Tfu_1065	Tfu_1065 S-adenosylmethionine synthetase	15.28	15.32	15.74	16.4	20.99	0.962
METACYC	ARG-PRO-PWY	arginine degradation VI (arginase 2 pathway)	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
METACYC	ARG-PRO-PWY	arginine degradation VI (arginase 2 pathway)	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
METACYC	ARG-PRO-PWY	arginine degradation VI (arginase 2 pathway)	Tfu_2708	Tfu_2708 delta 1-pyrroline-5-carboxylate reductase	17.73	17.16	18.03	17.57	21.11	
METACYC	PWY-5857	ubiquinol-10 biosynthesis (prokaryotic)	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	CITRULLINE-DEG-PWY	citrulline degradation	Tfu_1992	Tfu_1992 ornithine carbamoyltransferase	18.98	18.4	19.1	18.77	22.31	1.14
METACYC	PWY-5400	amaranthin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5400	amaranthin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5400	amaranthin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5400	amaranthin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5400	amaranthin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5400	amaranthin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5400	amaranthin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5209	methyl-coenzyme M oxidation to CO₂	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5209	methyl-coenzyme M oxidation to CO₂	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5209	methyl-coenzyme M oxidation to CO₂	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5209	methyl-coenzyme M oxidation to CO₂	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5209	methyl-coenzyme M oxidation to CO₂	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5209	methyl-coenzyme M oxidation to CO₂	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_1221	Tfu_1221 hypothetical protein						

METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_1278	Tfu_1278 thiolase						
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_2332	Tfu_2332 putative cholesterol oxidase					14.87	
METACYC	PWY-6945	cholesterol degradation to androstenedione I (choles	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-3861	mannitol degradation II	Tfu_0016	Tfu_0016 mannose-6-phosphate isomerase, type I						
METACYC	PWY-3861	mannitol degradation II	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-6661	4-hydroxy-2(1H)-quinolone biosynthesis	Tfu_1386	Tfu_1386 glutamine amidotransferase of anthranilate syr	14.29	15.3	14.48	14.83	21.47	1.207
METACYC	PWY-6791	xyloglucan degradation I (endoglucanase)	Tfu_1615	Tfu_1615 beta-galactosidase					16.26	
METACYC	3-HYDROXYPHENYLACETATE-DEGRADATIO	4-hydroxyphenylacetate degradation	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6366	D-myo-inositol (1,4,5,6)-tetrakisphosphate b	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY0-541	cyclopropane fatty acid (CFA) biosynthesis	Tfu_2160	Tfu_2160 putative cyclopropane fatty acid synthase	20.23	19.76	18.57	18.29	22.69	1.518
METACYC	PWY-6523	intra-aerobic nitrite reduction	Tfu_2794	Tfu_2794 hypothetical protein						
METACYC	CYSTSYN-PWY	cysteine biosynthesis I	Tfu_2368	Tfu_2368 cysteine synthase K/M		14.5	14.44		19.69	
METACYC	PWY-6181	histamine degradation	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-6181	histamine degradation	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-6181	histamine degradation	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-6989	(-)-camphor degradation	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6989	(-)-camphor degradation	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-6989	(-)-camphor degradation	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6989	(-)-camphor degradation	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5120	geranylgeranyldiphosphate biosynthesis	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
METACYC	PWY-7031	undecaprenyl diphosphate-linked heptasaccharide b	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-7031	undecaprenyl diphosphate-linked heptasaccharide b	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-7031	undecaprenyl diphosphate-linked heptasaccharide b	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-7031	undecaprenyl diphosphate-linked heptasaccharide b	Tfu_1855	Tfu_1855 4'-phosphopantetheinyl transferase						
METACYC	PWY-7031	undecaprenyl diphosphate-linked heptasaccharide b	Tfu_2817	Tfu_2817 hypothetical protein					18.27	
METACYC	PWY-6153	autoinducer AI-2 biosynthesis I	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6153	autoinducer AI-2 biosynthesis I	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PPGPPMET-PWY	ppGpp biosynthesis	Tfu_0431	Tfu_0431 putative hydrolase					20.26	
METACYC	PPGPPMET-PWY	ppGpp biosynthesis	Tfu_2090	Tfu_2090 RelA/SpoT protein	12.76			12.64	18.41	
METACYC	PPGPPMET-PWY	ppGpp biosynthesis	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
METACYC	PWY-4661	1D-myo-inositol hexakisphosphate biosynthe	Tfu_3099	Tfu_3099 myo-inositol-1-phosphate synthase	16.21	15.62	18.24	18.23	23.01	0.924
METACYC	ILEUSYN-PWY	isoleucine biosynthesis I (from threonine)	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
METACYC	ILEUSYN-PWY	isoleucine biosynthesis I (from threonine)	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	
METACYC	ILEUSYN-PWY	isoleucine biosynthesis I (from threonine)	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
METACYC	ILEUSYN-PWY	isoleucine biosynthesis I (from threonine)	Tfu_0613	Tfu_0613 ketol-acid reductoisomerase	19.9	19.77	19.96	19.71	23.42	0.799
METACYC	ILEUSYN-PWY	isoleucine biosynthesis I (from threonine)	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	ILEUSYN-PWY	isoleucine biosynthesis I (from threonine)	Tfu_1741	Tfu_1741 threonine dehydratase					16.86	
METACYC	ILEUSYN-PWY	isoleucine biosynthesis I (from threonine)	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	ILEUSYN-PWY	isoleucine biosynthesis I (from threonine)	Tfu_2209	Tfu_2209 dihydroxy-acid dehydratase	14.66	14.56	15.67	16.08	21.64	
METACYC	PWY0-1313	acetate conversion to acetyl-CoA	Tfu_1546	Tfu_1546 putative acyl-CoA synthetase					20.01	
METACYC	PWY0-1313	acetate conversion to acetyl-CoA	Tfu_2808	Tfu_2808 putative acetyl-coenzyme A synthetase			16.12	15.88	21.7	
METACYC	PWY0-1313	acetate conversion to acetyl-CoA	Tfu_2856	Tfu_2856 acetyl-coenzyme A synthetase	24.08	23.76	23.99	23.94	27	1.638
METACYC	PWY-6536	4-aminobutyrate degradation III	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01

METACYC	PWY-6536	4-aminobutyrate degradation III	Tfu_2949	Tfu_2949 succinate-semialdehyde dehydrogenase (NAD(	16.8	17.18	15.55	15.98	20.6	
METACYC	CATECHOL-ORTHO-CLEAVAGE-PWY	catechol degradation to β-ketoadipate	Tfu_0162	Tfu_0162 b-ketoadipate enol-lactone hydrolase				14.37	20.07	
METACYC	CATECHOL-ORTHO-CLEAVAGE-PWY	catechol degradation to β-ketoadipate	Tfu_0874	Tfu_0874 Alpha/beta hydrolase	16.84	15.52	17.31	18.48	22.22	0.937
METACYC	PWY-5343	ajugose biosynthesis II (galactinol-independent)	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5343	ajugose biosynthesis II (galactinol-independent)	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5343	ajugose biosynthesis II (galactinol-independent)	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5996	oleate biosynthesis II (animals)	Tfu_0413	Tfu_0413 stearoyl-CoA 9-desaturase						
METACYC	PWY-5996	oleate biosynthesis II (animals)	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-5996	oleate biosynthesis II (animals)	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-5996	oleate biosynthesis II (animals)	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY-5054	sorbitol biosynthesis I	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	PWY-5054	sorbitol biosynthesis I	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	MENAQUINONESYN-PWY	menaquinol-8 biosynthesis	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-6389	(S)-acetoin biosynthesis	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
METACYC	PWY-6389	(S)-acetoin biosynthesis	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	
METACYC	PWY-6389	(S)-acetoin biosynthesis	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
METACYC	PWY-5160	rose anthocyanin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5160	rose anthocyanin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5160	rose anthocyanin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	DENITRIFICATION-PWY	nitrate reduction I (denitrification)	Tfu_2794	Tfu_2794 hypothetical protein						
METACYC	PWY-6835	6-gingerol biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6835	6-gingerol biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6310	aloesone biosynthesis II	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6310	aloesone biosynthesis II	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6310	aloesone biosynthesis II	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6310	aloesone biosynthesis II	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6714	L-rhamnose degradation III	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6714	L-rhamnose degradation III	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	P162-PWY	glutamate degradation V (via hydroxyglutarate)	Tfu_0946	Tfu_0946 putative acyl-CoA dehydrogenase	20.62	20.44	21.21	21.21	24.67	0.91
METACYC	P162-PWY	glutamate degradation V (via hydroxyglutarate)	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	P162-PWY	glutamate degradation V (via hydroxyglutarate)	Tfu_1281	Tfu_1281 butyryl-CoA dehydrogenase						
METACYC	P162-PWY	glutamate degradation V (via hydroxyglutarate)	Tfu_2481	Tfu_2481 putative NAD-glutamate dehydrogenase	20.96	20.83	21.88	21.73	25.49	1.153
METACYC	PWYG-321	mycolate biosynthesis	Tfu_0224	Tfu_0224 trehalose-phosphatase:HAD-superfamily hydr	14.64	15.78	17.3	17.76	22.74	0.78
METACYC	PWYG-321	mycolate biosynthesis	Tfu_0810	Tfu_0810 ABC-type polar amino acid transport system A	20.65	20.47	19.17	19	22.36	1.163
METACYC	PWYG-321	mycolate biosynthesis	Tfu_0858	Tfu_0858 ABC-type Mn/Zn transport systems ATPase component						
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1100	Tfu_1100 putative regulatory protein						
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1676	Tfu_1676 MoxR-like ATPase					16.26	
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWYG-321	mycolate biosynthesis	Tfu_1976	Tfu_1976 putative 3-oxoacyl-ACP synthase II	18.39	18.02	19.63	19.4	22.79	0.718
METACYC	PWYG-321	mycolate biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWYG-321	mycolate biosynthesis	Tfu_2160	Tfu_2160 putative cyclopropane fatty acid synthase	20.23	19.76	18.57	18.29	22.69	1.518
METACYC	PWYG-321	mycolate biosynthesis	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	PWYG-321	mycolate biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						

METACYC	PWYG-321	mycolate biosynthesis	Tfu_2500	Tfu_2500 ATPase	18.85	18.12	18.16	18.37	22.96	1.114
METACYC	PWYG-321	mycolate biosynthesis	Tfu_2555	Tfu_2555 propionyl-CoA carboxylase complex B subunit	18.59	18.29	18.47	17.99	22.37	0.744
METACYC	PWY-1581	plastoquinol-9 biosynthesis I	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-1581	plastoquinol-9 biosynthesis I	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-5972	stearate biosynthesis I (animals)	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5912	2'-deoxymugineic acid phytosiderophore biosynthes	Tfu_1065	Tfu_1065 S-adenosylmethionine synthetase	15.28	15.32	15.74	16.4	20.99	0.962
METACYC	PWY-6748	nitrate reduction VII (denitrification)	Tfu_2794	Tfu_2794 hypothetical protein						
METACYC	P101-PWY	ectoine biosynthesis	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1	18.57	18.71	20.61	20.33	23.82	0.982
METACYC	P101-PWY	ectoine biosynthesis	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
METACYC	P101-PWY	ectoine biosynthesis	Tfu_0300	Tfu_0300 putative acetyltransferase						
METACYC	P101-PWY	ectoine biosynthesis	Tfu_0301	Tfu_0301 diaminobutyrate--2-oxoglutarate aminotransferase						
METACYC	P101-PWY	ectoine biosynthesis	Tfu_0302	Tfu_0302 putative condensing enzyme					17.04	
METACYC	PWY-6453	stigma estolide biosynthesis	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-6453	stigma estolide biosynthesis	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-6453	stigma estolide biosynthesis	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	HOMOCYSDEGR-PWY	cysteine biosynthesis/homocysteine degradation	Tfu_0438	Tfu_0438 cystathionine beta-synthase	13		14.49	12.98	20.18	
METACYC	PWY-6971	oleandomycin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6971	oleandomycin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6971	oleandomycin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6971	oleandomycin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6971	oleandomycin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6971	oleandomycin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6971	oleandomycin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-7022	paromamine biosynthesis II	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-7022	paromamine biosynthesis II	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-7022	paromamine biosynthesis II	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-7022	paromamine biosynthesis II	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-7022	paromamine biosynthesis II	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	MANNCAT-PWY	D-mannose degradation	Tfu_0016	Tfu_0016 mannose-6-phosphate isomerase, type I						
METACYC	MANNCAT-PWY	D-mannose degradation	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-6199	quercetinsulphates biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6199	quercetinsulphates biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6082	alginate biosynthesis II	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / pl	19.06	18.82	21.97	21.81	25.49	1.131
METACYC	PWY-2941	lysine biosynthesis II	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1	18.57	18.71	20.61	20.33	23.82	0.982
METACYC	PWY-2941	lysine biosynthesis II	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
METACYC	PWY-2941	lysine biosynthesis II	Tfu_0786	Tfu_0786 dihydrodipicolinate reductase	18.87	17.45	19.64	18.4	23.22	0.825
METACYC	PWY-2941	lysine biosynthesis II	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844
METACYC	PWY-2941	lysine biosynthesis II	Tfu_0816	Tfu_0816 diaminopimelate epimerase					18.06	
METACYC	PWY-2941	lysine biosynthesis II	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
METACYC	PWY-2941	lysine biosynthesis II	Tfu_2425	Tfu_2425 diaminopimelate decarboxylase					18.01	

METACYC	PWY-6821	κ-carrageenan degradation	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	GLUTAMINEFUM-PWY	glutamine degradation II	Tfu_1173	Tfu_1173 glutamate synthase (ferredoxin)					19.09	
METACYC	GLUTAMINEFUM-PWY	glutamine degradation II	Tfu_1174	Tfu_1174 glutamate synthase, NADH/NADPH, small subunit 1						
METACYC	PWY0-501	lipoate biosynthesis and incorporation I	Tfu_0991	Tfu_0991 lipoyl synthase					17.9	1.46
METACYC	PWY0-501	lipoate biosynthesis and incorporation I	Tfu_0992	Tfu_0992 lipoyltransferase					18.24	
METACYC	KETOGLUCONMET-PWY	ketogluconate metabolism	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	KETOGLUCONMET-PWY	ketogluconate metabolism	Tfu_1687	Tfu_1687 2,5-didehydrogluconate reductase	19.87	19.39	15.9	16.75	21.51	0.632
METACYC	KETOGLUCONMET-PWY	ketogluconate metabolism	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	TRESYN-PWY	trehalose biosynthesis I	Tfu_0224	Tfu_0224 trehalose-phosphatase:HAD-superfamily hydr	14.64	15.78	17.3	17.76	22.74	0.78
METACYC	TRESYN-PWY	trehalose biosynthesis I	Tfu_0225	Tfu_0225 alpha,alpha-trehalose-phosphate synthase (UD	19.68	19.62	20.81	20.85	24.46	1.199
METACYC	PWY-6708	ubiquinol-8 biosynthesis (prokaryotic)	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-5855	ubiquinol-7 biosynthesis (prokaryotic)	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-6644	fluoroacetate and fluorothreonine biosynthesis	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	ANAGLYCOLYSIS-PWY	glycolysis III (glucokinase)	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-5453	methylglyoxal degradation III	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5453	methylglyoxal degradation III	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	CENTBENZCOA-PWY	benzoyl-CoA degradation II (anaerobic)	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	CENTBENZCOA-PWY	benzoyl-CoA degradation II (anaerobic)	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	CENTBENZCOA-PWY	benzoyl-CoA degradation II (anaerobic)	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	CENTBENZCOA-PWY	benzoyl-CoA degradation II (anaerobic)	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	CENTBENZCOA-PWY	benzoyl-CoA degradation II (anaerobic)	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	CENTBENZCOA-PWY	benzoyl-CoA degradation II (anaerobic)	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY0-1347	NADH to trimethylamine N-oxide electron transfer	Tfu_0340	Tfu_0340 trimethylamine-N-oxide reductase (cytochrom	16.72	15.79	15.16		21.33	
METACYC	PWY-5316	nicotine biosynthesis	Tfu_0575	Tfu_0575 quinolinate synthetase						
METACYC	PWY-5316	nicotine biosynthesis	Tfu_0694	Tfu_0694 putative DNA repair hydrolase						
METACYC	PWY-5316	nicotine biosynthesis	Tfu_1918	Tfu_1918 putative DNA glycosylase						
METACYC	PWY-5316	nicotine biosynthesis	Tfu_2875	Tfu_2875 HhH-GPD:Iron-sulfur cluster loop						
METACYC	PWY-5316	nicotine biosynthesis	Tfu_2883	Tfu_2883 L-aspartate oxidase			15.62	16.95	20.84	
METACYC	HEMESYN2-PWY	heme biosynthesis from uroporphyrinogen-III II	Tfu_0739	Tfu_0739 coproporphyrinogen III oxidase						
METACYC	HEMESYN2-PWY	heme biosynthesis from uroporphyrinogen-III II	Tfu_0835	Tfu_0835 putative oxygen-independent coproporphyrinogen III oxidase						
METACYC	HEMESYN2-PWY	heme biosynthesis from uroporphyrinogen-III II	Tfu_1899	Tfu_1899 uroporphyrinogen decarboxylase HemE		14.37	15.41	15.99	20.69	0.856
METACYC	HEMESYN2-PWY	heme biosynthesis from uroporphyrinogen-III II	Tfu_1945	Tfu_1945 ferrochelatase		13.87	18.69	18.79	22.82	1.023
METACYC	HEMESYN2-PWY	heme biosynthesis from uroporphyrinogen-III II	Tfu_3023	Tfu_3023 similar to Flavodoxin						
METACYC	PWY-4081	glutathione redox reactions I	Tfu_2759	Tfu_2759 similar to Glutathione peroxidase		15.24			20.7	1.126
METACYC	PWY-5479	podophyllotoxin and 6-methoxypodophyllotoxin bios	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5479	podophyllotoxin and 6-methoxypodophyllotoxin bios	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6654	phosphopantothenate biosynthesis III	Tfu_0981	Tfu_0981 3-methyl-2-oxobutanoate hydroxymethyltrans	18.23	17.36	19.12	19.31	23.68	0.787

METACYC	PWY-6297	tuberonate glucoside biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6297	tuberonate glucoside biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6297	tuberonate glucoside biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6061	bile acid biosynthesis, neutral pathway	Tfu_0399	Tfu_0399 putative fatty acid-CoA racemase	16.76	16.16	14.76	15.27	19.11	
METACYC	PWY-5770	phenazine-1-carboxylate biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5770	phenazine-1-carboxylate biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5770	phenazine-1-carboxylate biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6576	dermatan sulfate degradation (metazoa)	Tfu_2486	Tfu_2486 hypothetical protein	16.26	16.75		15.08	20.28	
METACYC	PWY-6610	adenine and adenosine salvage IV	Tfu_2091	Tfu_2091 adenine phosphoribosyltransferase		14.26			19.51	0.761
METACYC	PWY-6610	adenine and adenosine salvage IV	Tfu_2896	Tfu_2896 hypoxanthine phosphoribosyl transferase		16.7	16.94	16.58	21.76	0.668
METACYC	P161-PWY	acetylene degradation	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	P161-PWY	acetylene degradation	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	P161-PWY	acetylene degradation	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	P161-PWY	acetylene degradation	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	P161-PWY	acetylene degradation	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	TRIGLSYN-PWY	triacylglycerol biosynthesis	Tfu_0271	Tfu_0271 Fatty acid synthesis plsX protein		15.01			17.65	
METACYC	TRIGLSYN-PWY	triacylglycerol biosynthesis	Tfu_1036	Tfu_1036 phospholipid/glycerol acyltransferase	18.2	17.54	17.83	17.5	21.56	
METACYC	TRIGLSYN-PWY	triacylglycerol biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	TRIGLSYN-PWY	triacylglycerol biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	TRIGLSYN-PWY	triacylglycerol biosynthesis	Tfu_1417	Tfu_1417 phospholipid/glycerol acyltransferase	13.91	13.6		12.45	17.58	
METACYC	TRIGLSYN-PWY	triacylglycerol biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	TRIGLSYN-PWY	triacylglycerol biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-3981	β-alanine biosynthesis I	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-3981	β-alanine biosynthesis I	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-3981	β-alanine biosynthesis I	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	LEUSYN-PWY	leucine biosynthesis	Tfu_0615	Tfu_0615 3-isopropylmalate dehydrogenase	19.78	19.7	19.64	19.42	23.35	1.025
METACYC	LEUSYN-PWY	leucine biosynthesis	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	LEUSYN-PWY	leucine biosynthesis	Tfu_0617	Tfu_0617 2-isopropylmalate synthase	16.51	16.22	15.8	13.84	20.9	
METACYC	LEUSYN-PWY	leucine biosynthesis	Tfu_0626	Tfu_0626 isopropylmalate isomerase large subunit			15.08	14.46	19.36	
METACYC	LEUSYN-PWY	leucine biosynthesis	Tfu_0627	Tfu_0627 isopropylmalate isomerase small subunit	13.33				18.83	
METACYC	LEUSYN-PWY	leucine biosynthesis	Tfu_0850	Tfu_0850 2-isopropylmalate synthase	16.67	16.9	16.57	16.17	21.98	
METACYC	LEUSYN-PWY	leucine biosynthesis	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	PWY-7047	malate-oxaloacetate shuttle I	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	PWY-5027	phylloquinol biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5027	phylloquinol biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5027	phylloquinol biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_0067	Tfu_0067 enoyl-CoA hydratase	15.28	15.4	15.41		19.86	1.194
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_0276	Tfu_0276 enoyl-CoA hydratase	19.38	19.33	18.51	18.41	22.57	0.956
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_0501	Tfu_0501 enoyl-CoA hydratase					16.87	
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_0590	Tfu_0590 putative enoyl-coA hydratase	19.44	19.48	19.26	19.03	23.62	1.05
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_0875	Tfu_0875 thiolase				13.9	19.26	
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_1259	Tfu_1259 enoyl-CoA hydratase/isomerase-like protein	16.06	15.55	15.86	15.46	20.76	1.057
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_1278	Tfu_1278 thiolase						
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_1280	Tfu_1280 enoyl-CoA hydratase					17.29	
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_1878	Tfu_1878 putative enoyl-CoA hydratase/isomerase	16.84	16.23			19.87	
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_1903	Tfu_1903 thiolase	18.23	17.73	16.48	17.15	21.45	1.443
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_2239	Tfu_2239 hypothetical protein	17.58	17.57	18.21	17.62	22.75	0.874
METACYC	PWY-735	jasmonic acid biosynthesis	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-5987	sorgoleone biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						

METACYC	PWY-5987	sorgoleone biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5987	sorgoleone biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5987	sorgoleone biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5987	sorgoleone biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5987	sorgoleone biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY0-823	arginine degradation III (arginine decarboxylase/agr	Tfu_0058	Tfu_0058 putative agmatinase	15.19	15.1			18.15	1.47
METACYC	PWY-5659	GDP-mannose biosynthesis	Tfu_0016	Tfu_0016 mannose-6-phosphate isomerase, type I						
METACYC	PWY-5659	GDP-mannose biosynthesis	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / pl	19.06	18.82	21.97	21.81	25.49	1.131
METACYC	PWY-5659	GDP-mannose biosynthesis	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	PWY-5659	GDP-mannose biosynthesis	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-5659	GDP-mannose biosynthesis	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PROUT-PWY	proline degradation	Tfu_0433	Tfu_0433 delta-1-pyrroline-5-carboxylate dehydrogenas	20.87	20.52	20.5	20.22	24.05	1.051
METACYC	PROUT-PWY	proline degradation	Tfu_0434	Tfu_0434 proline dehydrogenase	18.28	18.4	17.73	16.85	22.15	1.304
METACYC	PWY-5800	xylan biosynthesis	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
METACYC	PWY-5800	xylan biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5800	xylan biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5800	xylan biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5514	UDP-N-acetyl-D-galactosamine biosynthesis I	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	PWY-5514	UDP-N-acetyl-D-galactosamine biosynthesis I	Tfu_0414	Tfu_0414 UDP-N-acetylglucosamine pyrophosphorylase	19.4	19.37	19.9	19.97	23.72	1.114
METACYC	PWY-5514	UDP-N-acetyl-D-galactosamine biosynthesis I	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	PWY-5514	UDP-N-acetyl-D-galactosamine biosynthesis I	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	PWY-5514	UDP-N-acetyl-D-galactosamine biosynthesis I	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-5687	pyrimidine ribonucleotides interconversion	Tfu_0678	Tfu_0678 uridylate kinase	18.09	18.05	17.82	18.33	22.01	1.02
METACYC	PWY-5687	pyrimidine ribonucleotides interconversion	Tfu_1199	Tfu_1199 CTP synthetase	15.21	15.76	18.58	17.89	22.8	1.201
METACYC	PWY-5687	pyrimidine ribonucleotides interconversion	Tfu_1209	Tfu_1209 cytidylate kinase	15.69	15.43		14.19	19.62	
METACYC	PWY-5687	pyrimidine ribonucleotides interconversion	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
METACYC	PWY-6762	salicylate glucosides biosynthesis IV	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6762	salicylate glucosides biosynthesis IV	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6762	salicylate glucosides biosynthesis IV	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6784	superpathway of cellulose and hemicellulose degrad	Tfu_0082	Tfu_0082 hypothetical protein		13.31			15.38	
METACYC	PWY-6784	superpathway of cellulose and hemicellulose degrad	Tfu_1213	Tfu_1213 hypothetical protein						
METACYC	PWY-6784	superpathway of cellulose and hemicellulose degrad	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6784	superpathway of cellulose and hemicellulose degrad	Tfu_2791	Tfu_2791 hypothetical protein						
METACYC	PWY-6784	superpathway of cellulose and hemicellulose degrad	Tfu_2923	Tfu_2923 hypothetical protein						
METACYC	PWY-6118	glycerol-3-phosphate shuttle	Tfu_2593	Tfu_2593 glycerol-3-phosphate dehydrogenase	19.6	19.46	17.83	17.65	23.22	0.765
METACYC	PWY-4261	glycerol degradation I	Tfu_0787	Tfu_0787 glycerol kinase	18.54	18.3	17.06	16.96	21.42	0.925
METACYC	PWY-4261	glycerol degradation I	Tfu_2593	Tfu_2593 glycerol-3-phosphate dehydrogenase	19.6	19.46	17.83	17.65	23.22	0.765
METACYC	PWY-5372	carbon tetrachloride degradation II	Tfu_2586	Tfu_2586 carbon monoxide dehydrogenase						
METACYC	PWY-5372	carbon tetrachloride degradation II	Tfu_2587	Tfu_2587 molybdopterin dehydrogenase						
METACYC	PWY-6028	acetoin degradation	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-6028	acetoin degradation	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-6028	acetoin degradation	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-6028	acetoin degradation	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-6797	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_0543	Tfu_0543 hypothetical protein			13.59	14.81	19.36	
METACYC	PWY-6797	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_0576	Tfu_0576 hypothetical protein					17.31	
METACYC	PWY-6797	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_2457	Tfu_2457 putative mutT-like protein						
METACYC	PWY-6797	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_2890	Tfu_2890 7, 8-Dihydro-6-hydroxymethylpterin-pyrophosphokinase, HPPK					15.52	
METACYC	PWY-6797	6-hydroxymethyl-dihydropterin diphosphate biosyn	Tfu_2891	Tfu_2891 dihydroneopterin aldolase family:Dihydroneop	14.95	14.62	16	15.74	20.08	
METACYC	PWY-6048	methylthiopropionate degradation I (cleavage)	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-6048	methylthiopropionate degradation I (cleavage)	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						

METACYC	PWY-6048	methylthiopropionate degradation I (cleavage)	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-6048	methylthiopropionate degradation I (cleavage)	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY-6048	methylthiopropionate degradation I (cleavage)	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY0-301	L-ascorbate degradation I (bacterial, anaerobic)	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY-6703	preQ₀ biosynthesis	Tfu_2894	Tfu_2894 GTP cyclohydrolase I		15.85	17.62	17.38	21.27	0.628
METACYC	SERSYN-PWY	serine biosynthesis	Tfu_0136	Tfu_0136 phosphoserine phosphatase SerB:HAD-superfamily hydrolase subfamily IB, PSPas					16.25	
METACYC	SERSYN-PWY	serine biosynthesis	Tfu_0246	Tfu_0246 phosphoserine aminotransferase	19.59	19.46	22.48	21.91	25.76	1.096
METACYC	SERSYN-PWY	serine biosynthesis	Tfu_0614	Tfu_0614 D-3-phosphoglycerate dehydrogenase	20.25	20.04	22.34	22.29	25.26	1.066
METACYC	SERSYN-PWY	serine biosynthesis	Tfu_2259	Tfu_2259 similar to Phosphoglycerate dehydrogenase and related dehydrogenase						
METACYC	PWY-6627	salinosporamide A biosynthesis	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-6627	salinosporamide A biosynthesis	Tfu_1207	Tfu_1207 chorismate mutase of the AroH class						
METACYC	PWY-6627	salinosporamide A biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6627	salinosporamide A biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6627	salinosporamide A biosynthesis	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY-6627	salinosporamide A biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5491	diethylphosphate degradation	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-5491	diethylphosphate degradation	Tfu_1673	Tfu_1673 hypothetical protein						
METACYC	PWY-6842	glutathione-mediated detoxification II	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6842	glutathione-mediated detoxification II	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6842	glutathione-mediated detoxification II	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6842	glutathione-mediated detoxification II	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6842	glutathione-mediated detoxification II	Tfu_2204	Tfu_2204 peptidase M, neutral zinc metallopeptidase, zin	19.26	19.22	19.6	18.89	23.54	1.255
METACYC	PROTOCATECHUATE-ORTHO-CLEAVAGE-PW	protocatechuate degradation II (ortho-cleavage path	Tfu_0162	Tfu_0162 b-ketoadipate enol-lactone hydrolase				14.37	20.07	
METACYC	PROTOCATECHUATE-ORTHO-CLEAVAGE-PW	protocatechuate degradation II (ortho-cleavage path	Tfu_0874	Tfu_0874 Alpha/beta hydrolase	16.84	15.52	17.31	18.48	22.22	0.937
METACYC	PWY490-4	asparagine biosynthesis III (tRNA-dependent)	Tfu_0417	Tfu_0417 peptidyl-tRNA hydrolase	16.17	14.6	16.64	16.59	20.35	
METACYC	PWY490-4	asparagine biosynthesis III (tRNA-dependent)	Tfu_0605	Tfu_0605 aspartyl/glutamyl-tRNA amidotransferase subunit C				14.86	18.24	
METACYC	PWY490-4	asparagine biosynthesis III (tRNA-dependent)	Tfu_0606	Tfu_0606 glutamyl-tRNA amidotransferase subunit A	15.37		19.4	18.8	23.02	0.99
METACYC	PWY490-4	asparagine biosynthesis III (tRNA-dependent)	Tfu_0609	Tfu_0609 aspartyl/glutamyl-tRNA amidotransferase sub	15.46	16.45	19.76	19.56	23.81	
METACYC	NPGLUCAT-PWY	Entner-Doudoroff pathway II (non-phosphorylative)	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	NPGLUCAT-PWY	Entner-Doudoroff pathway II (non-phosphorylative)	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	NPGLUCAT-PWY	Entner-Doudoroff pathway II (non-phosphorylative)	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	NPGLUCAT-PWY	Entner-Doudoroff pathway II (non-phosphorylative)	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	NPGLUCAT-PWY	Entner-Doudoroff pathway II (non-phosphorylative)	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-5451	acetone degradation I (to methylglyoxal)	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5451	acetone degradation I (to methylglyoxal)	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6527	stachyose degradation	Tfu_0169	Tfu_0169 nucleoside-diphosphate-sugar epimerase (UDP	14.49	16.6	18.84	18.16	22.51	0.845
METACYC	PWY-6527	stachyose degradation	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase,	16.85	15	17.24	17.46	22.15	
METACYC	PWY-6527	stachyose degradation	Tfu_1622	Tfu_1622 UDP-glucose 4-epimerase						
METACYC	PWY-6527	stachyose degradation	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6527	stachyose degradation	Tfu_2566	Tfu_2566 galactokinase						
METACYC	PWY-6527	stachyose degradation	Tfu_2591	Tfu_2591 UDP-glucose 4-epimerase					14.83	
METACYC	PWY-6527	stachyose degradation	Tfu_2723	Tfu_2723 putative epimerase						
METACYC	PWY-4321	glutamate degradation IV	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
METACYC	PWY-6427	rot-2'-enonate biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6427	rot-2'-enonate biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6123	inosine-5'-phosphate biosynthesis I	Tfu_2546	Tfu_2546 1-(5-Phosphoribosyl)-5-amino-4-imidazole- ca	17.46	17.22	17.98	17.21	21.62	
METACYC	PWY-6123	inosine-5'-phosphate biosynthesis I	Tfu_2547	Tfu_2547 phosphoribosylaminoimidazole carboxylase, ATPase subunit					18.27	
METACYC	PWY-6123	inosine-5'-phosphate biosynthesis I	Tfu_2572	Tfu_2572 bifunctional phosphoribosylaminoimidazoleca	19.86	19.04	20.76	20.79	24.53	0.912
METACYC	PWY-6123	inosine-5'-phosphate biosynthesis I	Tfu_3014	Tfu_3014 adenylosuccinate lyase	18.68	18.68	20.17	19.69	23.57	0.954
METACYC	PWY-6123	inosine-5'-phosphate biosynthesis I	Tfu_3015	Tfu_3015 phosphoribosylaminoimidazole-succinocarbox	17.2	16.06	17.97	17.67	21.89	0.805

METACYC	PWY-5851	demethylmenaquinol-9 biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5892	menaquinol-12 biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5892	menaquinol-12 biosynthesis	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-6613	tetrahydrofolate salvage from 5,10-methenyltetrahyd	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
METACYC	PWY-6613	tetrahydrofolate salvage from 5,10-methenyltetrahyd	Tfu_2573	Tfu_2573 phosphoribosylglycinamide formyltransferase	14.49	14.7	17.07	16.78	21.38	
METACYC	PWY-841	purine nucleotides de novo biosynthesis II	Tfu_2440	Tfu_2440 inositol-5-monophosphate dehydrogenase	19.82	19.85	19.51	19.28	23.25	1.113
METACYC	PWY-841	purine nucleotides de novo biosynthesis II	Tfu_2589	Tfu_2589 bifunctional GMP synthase/glutamine amidotra	14.94		18.4	18.53	23.34	1.278
METACYC	PWY-841	purine nucleotides de novo biosynthesis II	Tfu_2595	Tfu_2595 inositol-5-monophosphate dehydrogenase	18.6	18.73	20.9	20.27	24.94	0.944
METACYC	PWY-841	purine nucleotides de novo biosynthesis II	Tfu_2596	Tfu_2596 IMP dehydrogenase	17.6	17.76	20.1	19.82	24.11	1.035
METACYC	PWY-841	purine nucleotides de novo biosynthesis II	Tfu_3012	Tfu_3012 adenylosuccinate synthetase	15.75	15.57	18.76	18.61	22.25	0.954
METACYC	PWY-841	purine nucleotides de novo biosynthesis II	Tfu_3014	Tfu_3014 adenylosuccinate lyase	18.68	18.68	20.17	19.69	23.57	0.954
METACYC	PWY-882	ascorbate biosynthesis I (L-galactose pathway)	Tfu_0016	Tfu_0016 mannose-6-phosphate isomerase, type I						
METACYC	PWY-882	ascorbate biosynthesis I (L-galactose pathway)	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-882	ascorbate biosynthesis I (L-galactose pathway)	Tfu_1394	Tfu_1394 mannose-1-phosphate guanylyltransferase / pl	19.06	18.82	21.97	21.81	25.49	1.131
METACYC	PWY-882	ascorbate biosynthesis I (L-galactose pathway)	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-882	ascorbate biosynthesis I (L-galactose pathway)	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PWY-6682	dehydrophos biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6682	dehydrophos biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6682	dehydrophos biosynthesis	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-6682	dehydrophos biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6682	dehydrophos biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5782	2-keto-L-gulonate biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5782	2-keto-L-gulonate biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-4681	kievitone biosynthesis	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
METACYC	PWY-6545	pyrimidine deoxyribonucleotides de novo bio	Tfu_1387	Tfu_1387 thymidylate synthase complementing protein ThyX			16.01	15.73	20.7	0.764
METACYC	PWY-6545	pyrimidine deoxyribonucleotides de novo bio	Tfu_1935	Tfu_1935 deoxyUTP pyrophosphatase subfamily 1					16.91	
METACYC	PWY-6545	pyrimidine deoxyribonucleotides de novo bio	Tfu_2149	Tfu_2149 ribonucleotide-diphosphate reductase alpha su	14.41		17.19	15.02	21.83	0.68
METACYC	PWY-6545	pyrimidine deoxyribonucleotides de novo bio	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
METACYC	PWY-6545	pyrimidine deoxyribonucleotides de novo bio	Tfu_2783	Tfu_2783 thymidylate kinase	19.41	19.13	18.67	18.47	22.51	0.962
METACYC	PWY-6545	pyrimidine deoxyribonucleotides de novo bio	Tfu_2932	Tfu_2932 deoxycytidine triphosphate deaminase					19.21	
METACYC	PWY-6545	pyrimidine deoxyribonucleotides de novo bio	Tfu_3001	Tfu_3001 ribonucleoside-diphosphate reductase	13.73	13.7	18.55	18.52	22.84	1.196
METACYC	PWY-6545	pyrimidine deoxyribonucleotides de novo bio	Tfu_3002	Tfu_3002 ribonucleoside-diphosphate reductase			18.75	18.62	22.88	0.758
METACYC	PWY-6349	CDP-archaeol biosynthesis	Tfu_2533	Tfu_2533 putative glycerol 1-phosphate dehydrogenase					17.86	
METACYC	PWY-581	IAA biosynthesis I	Tfu_2207	Tfu_2207 amidase					14.6	
METACYC	PWY-5741	ethylmalonyl pathway	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-5741	ethylmalonyl pathway	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-5741	ethylmalonyl pathway	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-5741	ethylmalonyl pathway	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-6990	(+)-camphor biosynthesis	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-6814	chitin degradation III (carnivorous plants)	Tfu_0580	Tfu_0580 chitinase II	17.05	17.75	15.71	15.95	21.45	
METACYC	PWY-6814	chitin degradation III (carnivorous plants)	Tfu_0868	Tfu_0868 hypothetical protein					16.11	
METACYC	PWY-621	sucrose degradation III	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase,	16.85	15	17.24	17.46	22.15	
METACYC	PWY-621	sucrose degradation III	Tfu_0928	Tfu_0928 fructokinase	18.37	17.96	18.63	18.42	22.16	0.898
METACYC	PWY-621	sucrose degradation III	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	PWY-621	sucrose degradation III	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-621	sucrose degradation III	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PWY-6312	barbaloin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6312	barbaloin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6312	barbaloin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6312	barbaloin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	

METACYC	PWY-6906	chitin derivatives degradation	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6906	chitin derivatives degradation	Tfu_2473	Tfu_2473 n-acetylglucosamine-6-phosphate deacetylase	14.21				17.55	
METACYC	PWY-4621	arsenate detoxification II (glutaredoxin)	Tfu_1521	Tfu_1521 similar to Arsenate reductase and related proteins glutaredoxin family					17.85	
METACYC	PWY-4621	arsenate detoxification II (glutaredoxin)	Tfu_1554	Tfu_1554 Low molecular weight phosphotyrosine protei	12.56	12.64	14.42	12.86	16.39	
METACYC	PWY-6631	O -methylation of tricetin	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6631	O -methylation of tricetin	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5485	pyruvate fermentation to acetate IV	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_1037	Tfu_1037 phosphofructokinase	21.14	20.73	24.02	23.83	26.57	0.842
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	PWY-1042	glycolysis IV (plant cytosol)	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-6470	peptidoglycan biosynthesis V (β-lactam resistar	Tfu_1104	Tfu_1104 peptidoglycan glycosyltransferase						
METACYC	PWY-6470	peptidoglycan biosynthesis V (β-lactam resistar	Tfu_1107	Tfu_1107 phospho-N-acetylmuramoyl-pentapeptide- transferase					17.98	
METACYC	PWY-6470	peptidoglycan biosynthesis V (β-lactam resistar	Tfu_1110	Tfu_1110 N-acetylglucosaminyl transferase	19.15	18.71	18.79	18.53	22.9	0.735
METACYC	PWY-6470	peptidoglycan biosynthesis V (β-lactam resistar	Tfu_3064	Tfu_3064 hypothetical protein	17.05	16.02	15.7	15.59	20.75	
METACYC	PWY-5290	secologanin and strictosidine biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5290	secologanin and strictosidine biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5290	secologanin and strictosidine biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5290	secologanin and strictosidine biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5290	secologanin and strictosidine biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5290	secologanin and strictosidine biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5290	secologanin and strictosidine biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-2622	trehalose biosynthesis IV	Tfu_0584	Tfu_0584 alpha amylase, catalytic subdomain						
METACYC	TRPCAT-PWY	tryptophan degradation I (via anthranilate)	Tfu_0921	Tfu_0921 putative tryptophan 2,3-dioxygenase	13.54	14.16			17.35	
METACYC	TRPCAT-PWY	tryptophan degradation I (via anthranilate)	Tfu_0922	Tfu_0922 kynureninase	16.91	15.34	13.9	14.63	19.53	1.172
METACYC	TRPCAT-PWY	tryptophan degradation I (via anthranilate)	Tfu_1418	Tfu_1418 hypothetical protein	18.89	18.42	20.57	20.44	23.75	0.572
METACYC	TRPCAT-PWY	tryptophan degradation I (via anthranilate)	Tfu_1722	Tfu_1722 hypothetical protein					14.24	
METACYC	DETOX1-PWY	superoxide radicals degradation	Tfu_0957	Tfu_0957 superoxide dismutase	22.64	22.53	22.08	22.69	25.05	0.848
METACYC	DETOX1-PWY	superoxide radicals degradation	Tfu_1649	Tfu_1649 catalase	20.13	19.98	21.56	21.24	24.73	0.727
METACYC	DETOX1-PWY	superoxide radicals degradation	Tfu_2766	Tfu_2766 hypothetical protein	17.21	16.85	15.75	15.26	19.61	
METACYC	PWY-6320	phaselate biosynthesis	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-6320	phaselate biosynthesis	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-6320	phaselate biosynthesis	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY-6558	heparan sulfate biosynthesis (late stages)	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY-5068	chlorophyll cycle	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5068	chlorophyll cycle	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5068	chlorophyll cycle	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	FASYN-ELONG-PWY	fatty acid elongation -- saturated	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	FASYN-ELONG-PWY	fatty acid elongation -- saturated	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	FASYN-ELONG-PWY	fatty acid elongation -- saturated	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	FASYN-ELONG-PWY	fatty acid elongation -- saturated	Tfu_1842	Tfu_1842 enoyl-(acyl carrier protein) reductase	20.49	19.93	21.16	21.07	24.76	1.053
METACYC	FASYN-ELONG-PWY	fatty acid elongation -- saturated	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	FASYN-ELONG-PWY	fatty acid elongation -- saturated	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	

METACYC	P344-PWY	acrylonitrile degradation	Tfu_2207	Tfu_2207 amidase					14.6	
METACYC	PWY-6922	L-N^δ-acetylornithine bios	Tfu_0434	Tfu_0434 proline dehydrogenase	18.28	18.4	17.73	16.85	22.15	1.304
METACYC	PWY-6922	L-N^δ-acetylornithine bios	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6922	L-N^δ-acetylornithine bios	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6922	L-N^δ-acetylornithine bios	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
METACYC	PWY-6922	L-N^δ-acetylornithine bios	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6922	L-N^δ-acetylornithine bios	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6922	L-N^δ-acetylornithine bios	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
METACYC	PWY-6055	dimethylsulfoniopropionate biosynthesis II (Spartina	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-6055	dimethylsulfoniopropionate biosynthesis II (Spartina	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-6055	dimethylsulfoniopropionate biosynthesis II (Spartina	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	GLYCOLYSIS	glycolysis I	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	GLYCOLYSIS	glycolysis I	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
METACYC	GLYCOLYSIS	glycolysis I	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	GLYCOLYSIS	glycolysis I	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	GLYCOLYSIS	glycolysis I	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	GLYCOLYSIS	glycolysis I	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	GLYCOLYSIS	glycolysis I	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
METACYC	GLYCOLYSIS	glycolysis I	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	GLYCOLYSIS	glycolysis I	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	GLYCOLYSIS	glycolysis I	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	GLYCOLYSIS	glycolysis I	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	GLYCOLYSIS	glycolysis I	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	GLYCOLYSIS	glycolysis I	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-4821	UDP-D-xylose and UDP-D-glucuronate biosynthesis	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
METACYC	PWY0-166	pyrimidine deoxyribonucleotides de novo bio	Tfu_1935	Tfu_1935 deoxyUTP pyrophosphatase subfamily 1					16.91	
METACYC	PWY0-166	pyrimidine deoxyribonucleotides de novo bio	Tfu_2149	Tfu_2149 ribonucleotide-diphosphate reductase alpha su	14.41		17.19	15.02	21.83	0.68
METACYC	PWY0-166	pyrimidine deoxyribonucleotides de novo bio	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
METACYC	PWY0-166	pyrimidine deoxyribonucleotides de novo bio	Tfu_2783	Tfu_2783 thymidylate kinase	19.41	19.13	18.67	18.47	22.51	0.962
METACYC	PWY0-166	pyrimidine deoxyribonucleotides de novo bio	Tfu_2932	Tfu_2932 deoxycytidine triphosphate deaminase					19.21	
METACYC	PWY0-166	pyrimidine deoxyribonucleotides de novo bio	Tfu_3001	Tfu_3001 ribonucleoside-diphosphate reductase	13.73	13.7	18.55	18.52	22.84	1.196
METACYC	PWY0-166	pyrimidine deoxyribonucleotides de novo bio	Tfu_3002	Tfu_3002 ribonucleoside-diphosphate reductase			18.75	18.62	22.88	0.758
METACYC	PWY-6717	(1,4)-β-xylan degradation	Tfu_1213	Tfu_1213 hypothetical protein						
METACYC	PWY-6717	(1,4)-β-xylan degradation	Tfu_1616	Tfu_1616 alpha-L-arabinofuranosidase	18.6	18.38			20.92	1.664
METACYC	PWY-6717	(1,4)-β-xylan degradation	Tfu_2791	Tfu_2791 hypothetical protein						
METACYC	PWY-6717	(1,4)-β-xylan degradation	Tfu_2923	Tfu_2923 hypothetical protein						
METACYC	QUINATEDEG-PWY	quinate degradation I	Tfu_1635	Tfu_1635 dehydroquinase, class II					16.28	
METACYC	PWY-5791	1,4-dihydroxy-2-naphthoate biosynthesis II (plants)	Tfu_0960	Tfu_0960 n-acylamino acid racemase : O-succinylbenzoate-CoA synthase					19.49	
METACYC	PWY-5791	1,4-dihydroxy-2-naphthoate biosynthesis II (plants)	Tfu_1408	Tfu_1408 putative ortho-succinylbenzoate-CoA synthetase						
METACYC	PWY-5791	1,4-dihydroxy-2-naphthoate biosynthesis II (plants)	Tfu_1409	Tfu_1409 naphthoate synthase	16.03	15.45	18.71	18.23	22.53	
METACYC	PWY-5791	1,4-dihydroxy-2-naphthoate biosynthesis II (plants)	Tfu_1410	Tfu_1410 O-succinylbenzoate synthase					15.48	
METACYC	PWY-5791	1,4-dihydroxy-2-naphthoate biosynthesis II (plants)	Tfu_1411	Tfu_1411 Menaquinone biosynthesis protein					16.81	
METACYC	PWY-5791	1,4-dihydroxy-2-naphthoate biosynthesis II (plants)	Tfu_1413	Tfu_1413 isochorismate synthase						
METACYC	PWY-5791	1,4-dihydroxy-2-naphthoate biosynthesis II (plants)	Tfu_1872	Tfu_1872 isochorismate synthase					17.85	
METACYC	PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_0633	Tfu_0633 D-alanylalanine synthetase	15.85	14.68	13.91		19.95	0.685
METACYC	PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_1105	Tfu_1105 UDP-N-acetylmuramyl-tripeptide synthetase	15.32	14.97	16.06	15.77	20.43	0.647
METACYC	PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_1106	Tfu_1106 UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diamino	13.98	15.35	14.44		21.31	0.824
METACYC	PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_1108	Tfu_1108 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase					18.55	
METACYC	PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_1111	Tfu_1111 UDP-N-acetylmuramate--alanine ligase			14.68	15.53	20.38	1.128
METACYC	PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_1640	Tfu_1640 D-alanine--D-alanine ligase					15.9	

METACYC	PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_2162	Tfu_2162 glutamate racemase						
METACYC	PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_2664	Tfu_2664 UDP-N-acetylenolpyruvoylglucosamine reducta	13.88				20.85	
METACYC	PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosyn	Tfu_3016	Tfu_3016 UDP-N-acetylglucosamine 1-carboxyvinyltransferase		14.48	17.9	17.73	22.19	1.204
METACYC	PWY-6720	toyocamycin biosynthesis	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-6720	toyocamycin biosynthesis	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
METACYC	PWY-5675	nitrate reduction V (assimilatory)	Tfu_0982	Tfu_0982 glutamine synthetase type I	16.36	15.34	14.3	15.33	20.84	1.147
METACYC	PWY-5675	nitrate reduction V (assimilatory)	Tfu_0988	Tfu_0988 glutamine synthetase type I		16.24	19.93	19.87	23.49	1.247
METACYC	PWY-5675	nitrate reduction V (assimilatory)	Tfu_1371	Tfu_1371 glutamate dehydrogenase	13.87		17.06	16.78	21.17	1.233
METACYC	PWY-5265	peptidoglycan biosynthesis II (staphylococci)	Tfu_1104	Tfu_1104 peptidoglycan glycosyltransferase						
METACYC	PWY-5265	peptidoglycan biosynthesis II (staphylococci)	Tfu_1107	Tfu_1107 phospho-N-acetylmuramoyl-pentapeptide- transferase					17.98	
METACYC	PWY-5265	peptidoglycan biosynthesis II (staphylococci)	Tfu_1110	Tfu_1110 N-acetylglucosaminyl transferase	19.15	18.71	18.79	18.53	22.9	0.735
METACYC	PWY-5265	peptidoglycan biosynthesis II (staphylococci)	Tfu_2903	Tfu_2903 hypothetical protein					17.09	
METACYC	PWY-5265	peptidoglycan biosynthesis II (staphylococci)	Tfu_3064	Tfu_3064 hypothetical protein	17.05	16.02	15.7	15.59	20.75	
METACYC	GLUGLNSYN-PWY	glutamate biosynthesis IV	Tfu_1173	Tfu_1173 glutamate synthase (ferredoxin)					19.09	
METACYC	GLUGLNSYN-PWY	glutamate biosynthesis IV	Tfu_1174	Tfu_1174 glutamate synthase, NADH/NADPH, small subunit 1						
METACYC	PWY-6596	adenosine nucleotides degradation I	Tfu_2440	Tfu_2440 inositol-5-monophosphate dehydrogenase	19.82	19.85	19.51	19.28	23.25	1.113
METACYC	PWY-6596	adenosine nucleotides degradation I	Tfu_2581	Tfu_2581 inosine-uridine preferring nucleoside hydrolas	16.93	16.72	16.96	15.37	21.32	
METACYC	PWY-6596	adenosine nucleotides degradation I	Tfu_2595	Tfu_2595 inositol-5-monophosphate dehydrogenase	18.6	18.73	20.9	20.27	24.94	0.944
METACYC	PWY-6596	adenosine nucleotides degradation I	Tfu_2596	Tfu_2596 IMP dehydrogenase	17.6	17.76	20.1	19.82	24.11	1.035
METACYC	P345-PWY	aldoxime degradation	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	P345-PWY	aldoxime degradation	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	P224-PWY	sulfate reduction V (dissimilatory)	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
METACYC	P224-PWY	sulfate reduction V (dissimilatory)	Tfu_0420	Tfu_0420 Small GTP-binding protein domain:Sulfate adenylyltransferase, l			14.13		18.76	0.81
METACYC	P224-PWY	sulfate reduction V (dissimilatory)	Tfu_0425	Tfu_0425 adenylylsulfate kinase					17.66	
METACYC	4TOLCARBDEG-PWY	4-toluenecarboxylate degradation	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	4TOLCARBDEG-PWY	4-toluenecarboxylate degradation	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-842	starch degradation I	Tfu_0584	Tfu_0584 alpha amylase, catalytic subdomain						
METACYC	PWY-842	starch degradation I	Tfu_0586	Tfu_0586 alpha-glucan phosphorylase					15.86	
METACYC	PWY-842	starch degradation I	Tfu_0833	Tfu_0833 alpha amylase, catalytic subdomain	15.71	15.55	14.92	15.54	20.77	0.845
METACYC	PWY-842	starch degradation I	Tfu_0985	Tfu_0985 hypothetical protein						
METACYC	PWY-842	starch degradation I	Tfu_2205	Tfu_2205 glycoside hydrolase, family 77					15.25	
METACYC	PWY-842	starch degradation I	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PWY-1186	homomethionine biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-1186	homomethionine biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5853	demethylmenaquinol-6 biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-381	nitrate reduction II (assimilatory)	Tfu_0982	Tfu_0982 glutamine synthetase type I	16.36	15.34	14.3	15.33	20.84	1.147
METACYC	PWY-381	nitrate reduction II (assimilatory)	Tfu_0988	Tfu_0988 glutamine synthetase type I		16.24	19.93	19.87	23.49	1.247
METACYC	PWY-381	nitrate reduction II (assimilatory)	Tfu_1888	Tfu_1888 putative nitrite/sulphite reductase	16.01	13.98	17.79	17.82	22.36	1.384
METACYC	PWY-5342	ajugose biosynthesis I (galactinol-dependent)	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5342	ajugose biosynthesis I (galactinol-dependent)	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5342	ajugose biosynthesis I (galactinol-dependent)	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6122	5-aminoimidazole ribonucleotide biosynthesis II	Tfu_0156	Tfu_0156 phosphoribosylformylglycinamidine synthase I			15.57	15.14	21.14	0.902
METACYC	PWY-6122	5-aminoimidazole ribonucleotide biosynthesis II	Tfu_0158	Tfu_0158 phosphoribosylformylglycinamidine synthase s	13.89	15.06	17.93	18.1	22.88	0.924
METACYC	PWY-6122	5-aminoimidazole ribonucleotide biosynthesis II	Tfu_0178	Tfu_0178 phosphoribosylformylglycinamidine synthase					17.74	
METACYC	PWY-6122	5-aminoimidazole ribonucleotide biosynthesis II	Tfu_2747	Tfu_2747 amidophosphoribosyltransferase						
METACYC	PWY-6122	5-aminoimidazole ribonucleotide biosynthesis II	Tfu_2748	Tfu_2748 phosphoribosylaminoimidazole synthetase	14.77		17.56	17.33	20.81	0.689
METACYC	PWY-6122	5-aminoimidazole ribonucleotide biosynthesis II	Tfu_3013	Tfu_3013 phosphoribosylglycinamide synthetase			17.63	17.26	21.77	
METACYC	PWY-5161	6'-deoxychalcone metabolism	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5161	6'-deoxychalcone metabolism	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5161	6'-deoxychalcone metabolism	Tfu_1764	Tfu_1764 putative glycosyl transferase						

METACYC	PWY0-1264	biotin-carboxyl carrier protein assembly	Tfu_0947	Tfu_0947 putative acetyl/propionyl CoA carboxylase alpl	20.64	20.68	21.06	20.9	24.61	1.056
METACYC	PWY0-1264	biotin-carboxyl carrier protein assembly	Tfu_1228	Tfu_1228 putative acyl-CoA carboxylase complex A subunit						
METACYC	PWY0-1264	biotin-carboxyl carrier protein assembly	Tfu_2553	Tfu_2553 biotin--acetyl-CoA-carboxylase ligase						
METACYC	PWY0-1264	biotin-carboxyl carrier protein assembly	Tfu_2557	Tfu_2557 putative acyl-CoA carboxylase, alpha subunit	16.42	15.3	17.56	17.37	22.48	
METACYC	GLUTSYN-PWY	glutamate biosynthesis I	Tfu_1173	Tfu_1173 glutamate synthase (ferredoxin)					19.09	
METACYC	GLUTSYN-PWY	glutamate biosynthesis I	Tfu_1174	Tfu_1174 glutamate synthase, NADH/NADPH, small subunit 1						
METACYC	PWY-5271	phaseic acid biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5271	phaseic acid biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6200	2,4,5-trichlorophenoxyacetate degradation	Tfu_1234	Tfu_1234 putative hydrolase			13.82	13	20.38	
METACYC	PWY-6823	molybdenum cofactor biosynthesis	Tfu_0595	Tfu_0595 putative pyridoxal-phosphate-dependent aminotransferase					16.06	
METACYC	PWY-6823	molybdenum cofactor biosynthesis	Tfu_1983	Tfu_1983 cysteine desulphurases, SufS	14.11			13.91	18.52	0.647
METACYC	GLNSYN-PWY	glutamine biosynthesis I	Tfu_0982	Tfu_0982 glutamine synthetase type I	16.36	15.34	14.3	15.33	20.84	1.147
METACYC	GLNSYN-PWY	glutamine biosynthesis I	Tfu_0988	Tfu_0988 glutamine synthetase type I		16.24	19.93	19.87	23.49	1.247
METACYC	RUMP-PWY	formaldehyde oxidation I	Tfu_0003	Tfu_0003 6-phosphogluconate dehydrogenase	20.18	20.31	19.92	19.72	23.9	0.655
METACYC	RUMP-PWY	formaldehyde oxidation I	Tfu_2004	Tfu_2004 glucose-6-phosphate isomerase	20.74	20.34	21.85	21.77	25.29	0.989
METACYC	RUMP-PWY	formaldehyde oxidation I	Tfu_2005	Tfu_2005 glucose-6-phosphate 1-dehydrogenase	16.6	15.74	16.81	16.27	21.46	
METACYC	RUMP-PWY	formaldehyde oxidation I	Tfu_2007	Tfu_2007 6-phosphogluconolactonase	18.7	19.13	18.21	17.98	22.37	0.913
METACYC	RUMP-PWY	formaldehyde oxidation I	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-5025	IAA biosynthesis IV	Tfu_2207	Tfu_2207 amidase					14.6	
METACYC	PWY-5994	palmitate biosynthesis I (animals)	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWY-5994	palmitate biosynthesis I (animals)	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWY-5994	palmitate biosynthesis I (animals)	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWY-5994	palmitate biosynthesis I (animals)	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	PWY-5197	lactate biosynthesis (archaea)	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-5197	lactate biosynthesis (archaea)	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6018	seed germination protein turnover	Tfu_0503	Tfu_0503 leucyl aminopeptidase	19.88	19.54	19.89	19.71	24.09	0.912
METACYC	PWY-6018	seed germination protein turnover	Tfu_0995	Tfu_0995 leucyl aminopeptidase	22.3	22.22	21.93	22.33	25.29	1.048
METACYC	PWY0-1314	fructose degradation	Tfu_0696	Tfu_0696 putative 6-phosphofructokinase : 1-phosphofructokinase						
METACYC	PWY-4061	glutathione-mediated detoxification	Tfu_2204	Tfu_2204 peptidase M, neutral zinc metallopeptidase, zin	19.26	19.22	19.6	18.89	23.54	1.255
METACYC	PWY-5057	valine degradation II	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	PWY-5057	valine degradation II	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-5057	valine degradation II	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-5057	valine degradation II	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-5057	valine degradation II	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	PWY-5057	valine degradation II	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	P105-PWY	TCA cycle IV (2-oxoglutarate decarboxylase)	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	P105-PWY	TCA cycle IV (2-oxoglutarate decarboxylase)	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	P105-PWY	TCA cycle IV (2-oxoglutarate decarboxylase)	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	P105-PWY	TCA cycle IV (2-oxoglutarate decarboxylase)	Tfu_0819	Tfu_0819 malate synthase	20.71	20.65	20.77	20.84	24.52	0.986
METACYC	P105-PWY	TCA cycle IV (2-oxoglutarate decarboxylase)	Tfu_1377	Tfu_1377 isocitrate lyase	17.24	15.99	17.23	17.21	21.54	
METACYC	P105-PWY	TCA cycle IV (2-oxoglutarate decarboxylase)	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	P105-PWY	TCA cycle IV (2-oxoglutarate decarboxylase)	Tfu_2451	Tfu_2451 succinate dehydrogenase	19.35	19.39	20.29	20.56	23.66	1.002
METACYC	P105-PWY	TCA cycle IV (2-oxoglutarate decarboxylase)	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
METACYC	P105-PWY	TCA cycle IV (2-oxoglutarate decarboxylase)	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
METACYC	PWY-5079	phenylalanine degradation III	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-5079	phenylalanine degradation III	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-5079	phenylalanine degradation III	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-5079	phenylalanine degradation III	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY-4801	aloesone biosynthesis I	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-4801	aloesone biosynthesis I	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						

METACYC	PWY-4801	aloesone biosynthesis I	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-4801	aloesone biosynthesis I	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6416	quinate degradation II	Tfu_1635	Tfu_1635 dehydroquinase, class II					16.28	
METACYC	PWY-6585	2-tridecanone biosynthesis	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-6585	2-tridecanone biosynthesis	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-6585	2-tridecanone biosynthesis	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY66-366	flavin biosynthesis IV (mammalian)	Tfu_0782	Tfu_0782 Cytidyltransferase-related		13.35	14.92	14.18	20.03	
METACYC	PWY-4421	curcumin glucoside biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-4421	curcumin glucoside biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-4421	curcumin glucoside biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5760	β-alanine biosynthesis IV	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-5760	β-alanine biosynthesis IV	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-5760	β-alanine biosynthesis IV	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-6499	D-glucarate degradation II	Tfu_1718	Tfu_1718 putative 5-dehydro-4-deoxyglucarate dehydratase						
METACYC	PWY-6691	plaunotol biosynthesis	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
METACYC	PWY-6955	lincomycin biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6955	lincomycin biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	GLUCONSUPER-PWY	D-gluconate degradation	Tfu_2114	Tfu_2114 carbohydrate kinase, thermoresistant glucokin	15.34		15.45	14.87	18.89	
METACYC	PWY-5695	urate biosynthesis/inosine 5'-phosphate degradatior	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY-5695	urate biosynthesis/inosine 5'-phosphate degradatior	Tfu_2440	Tfu_2440 inositol-5-monophosphate dehydrogenase	19.82	19.85	19.51	19.28	23.25	1.113
METACYC	PWY-5695	urate biosynthesis/inosine 5'-phosphate degradatior	Tfu_2595	Tfu_2595 inositol-5-monophosphate dehydrogenase	18.6	18.73	20.9	20.27	24.94	0.944
METACYC	PWY-5695	urate biosynthesis/inosine 5'-phosphate degradatior	Tfu_2596	Tfu_2596 IMP dehydrogenase	17.6	17.76	20.1	19.82	24.11	1.035
METACYC	PWY-6365	D-myo-inositol (3,4,5,6)-tetrakisphosphate bi	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-7000	kanamycin biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-7000	kanamycin biosynthesis	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-7000	kanamycin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-7000	kanamycin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-7000	kanamycin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-7000	kanamycin biosynthesis	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-7000	kanamycin biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5104	isoleucine biosynthesis IV	Tfu_0553	Tfu_0553 acetolactate synthase large subunit	16.69	17.48	15.1	15.46	20.92	1.604
METACYC	PWY-5104	isoleucine biosynthesis IV	Tfu_0611	Tfu_0611 acetolactate synthase I large subunit					17.68	
METACYC	PWY-5104	isoleucine biosynthesis IV	Tfu_0612	Tfu_0612 acetolactate synthase, small subunit	15.34		14.92		19.66	1.005
METACYC	PWY-5104	isoleucine biosynthesis IV	Tfu_0613	Tfu_0613 ketol-acid reductoisomerase	19.9	19.77	19.96	19.71	23.42	0.799
METACYC	PWY-5104	isoleucine biosynthesis IV	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	PWY-5104	isoleucine biosynthesis IV	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	PWY-5104	isoleucine biosynthesis IV	Tfu_2209	Tfu_2209 dihydroxy-acid dehydratase	14.66	14.56	15.67	16.08	21.64	
METACYC	P23-PWY	reductive TCA cycle I	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	P23-PWY	reductive TCA cycle I	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	P23-PWY	reductive TCA cycle I	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	P23-PWY	reductive TCA cycle I	Tfu_2451	Tfu_2451 succinate dehydrogenase	19.35	19.39	20.29	20.56	23.66	1.002
METACYC	P23-PWY	reductive TCA cycle I	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
METACYC	P23-PWY	reductive TCA cycle I	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	P23-PWY	reductive TCA cycle I	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
METACYC	P23-PWY	reductive TCA cycle I	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
METACYC	P23-PWY	reductive TCA cycle I	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
METACYC	P23-PWY	reductive TCA cycle I	Tfu_2674	Tfu_2674 2-oxoglutarate ferredoxin oxidoreductase, alph	14.55		17.74	18.16	22.74	1.656
METACYC	P23-PWY	reductive TCA cycle I	Tfu_2675	Tfu_2675 ferrodoxin oxidoreductase beta subunit			17.01	16.7	21.8	
METACYC	PWY0-1471	uracil degradation III	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY0-1471	uracil degradation III	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	

METACYC	SAM-PWY	S-adenosyl-L-methionine biosynthesis	Tfu_1065	Tfu_1065 S-adenosylmethionine synthetase	15.28	15.32	15.74	16.4	20.99	0.962
METACYC	SULFMETII-PWY	sulfate reduction II (assimilatory)	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
METACYC	SULFMETII-PWY	sulfate reduction II (assimilatory)	Tfu_0420	Tfu_0420 Small GTP-binding protein domain:Sulfate adenylyltransferase, l			14.13		18.76	0.81
METACYC	SULFMETII-PWY	sulfate reduction II (assimilatory)	Tfu_0425	Tfu_0425 adenylylsulfate kinase					17.66	
METACYC	SULFMETII-PWY	sulfate reduction II (assimilatory)	Tfu_1888	Tfu_1888 putative nitrite/sulphite reductase	16.01	13.98	17.79	17.82	22.36	1.384
METACYC	PEPTIDOGLYCANSYN-PWY	peptidoglycan biosynthesis I (<I>meso</I>-diaminor	Tfu_1104	Tfu_1104 peptidoglycan glycosyltransferase						
METACYC	PEPTIDOGLYCANSYN-PWY	peptidoglycan biosynthesis I (<I>meso</I>-diaminor	Tfu_1107	Tfu_1107 phospho-N-acetylmuramoyl-pentapeptide- transferase					17.98	
METACYC	PEPTIDOGLYCANSYN-PWY	peptidoglycan biosynthesis I (<I>meso</I>-diaminor	Tfu_1110	Tfu_1110 N-acetylglucosaminyl transferase	19.15	18.71	18.79	18.53	22.9	0.735
METACYC	PEPTIDOGLYCANSYN-PWY	peptidoglycan biosynthesis I (<I>meso</I>-diaminor	Tfu_2903	Tfu_2903 hypothetical protein					17.09	
METACYC	PEPTIDOGLYCANSYN-PWY	peptidoglycan biosynthesis I (<I>meso</I>-diaminor	Tfu_3064	Tfu_3064 hypothetical protein	17.05	16.02	15.7	15.59	20.75	
METACYC	PWY-6655	xanthan biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6655	xanthan biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6655	xanthan biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6818	ornithine lipid biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6818	ornithine lipid biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6818	ornithine lipid biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6818	ornithine lipid biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	UDPNAGSYN-PWY	UDP-N-acetyl-D-glucosamine biosynthesis I	Tfu_0414	Tfu_0414 UDP-N-acetylglucosamine pyrophosphorylase	19.4	19.37	19.9	19.97	23.72	1.114
METACYC	UDPNAGSYN-PWY	UDP-N-acetyl-D-glucosamine biosynthesis I	Tfu_2611	Tfu_2611 D-fructose-6-phosphate amidotransferase	16.46	16.09	18.53	18.54	22.75	1.101
METACYC	UDPNAGSYN-PWY	UDP-N-acetyl-D-glucosamine biosynthesis I	Tfu_2612	Tfu_2612 phosphoglucosamine mutase		12.2	15.38	14.97	20.13	0.827
METACYC	PWY-6605	adenine and adenosine salvage II	Tfu_2091	Tfu_2091 adenine phosphoribosyltransferase		14.26			19.51	0.761
METACYC	PWY-5467	gramine biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-5467	gramine biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-1901	aurone biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-1901	aurone biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-1901	aurone biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-3881	mannitol biosynthesis	Tfu_0016	Tfu_0016 mannose-6-phosphate isomerase, type I						
METACYC	PWY-3881	mannitol biosynthesis	Tfu_2508	Tfu_2508 hypothetical protein	15.7	15.27	15.1	15.93	20.53	
METACYC	PWY-5664	tetrahydrobiopterin biosynthesis II	Tfu_2894	Tfu_2894 GTP cyclohydrolase I		15.85	17.62	17.38	21.27	0.628
METACYC	PWY-5976	dhurrin degradation	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-5132	humulone biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5132	humulone biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5132	humulone biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	ALADEG-PWY	alanine degradation I	Tfu_2606	Tfu_2606 alanine racemase region	16.31	14.93	16.54	16.55	20.86	
METACYC	PWY-5874	heme degradation	Tfu_2345	Tfu_2345 heme oxygenase (decyclizing)						
METACYC	CYCLOHEXANOL-OXIDATION-PWY	cyclohexanol degradation	Tfu_1490	Tfu_1490 putative monooxygenase					16.06	
METACYC	CYCLOHEXANOL-OXIDATION-PWY	cyclohexanol degradation	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY-6352	3-phosphoinositide biosynthesis	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-5653	NAD biosynthesis from 2-amino-3-carboxymuconate	Tfu_0983	Tfu_0983 NAD+ synthase	16.91	16.85	17.72	17.22	22.21	0.82
METACYC	PWY-5653	NAD biosynthesis from 2-amino-3-carboxymuconate	Tfu_2171	Tfu_2171 nicotinic acid mononucleotide adenyltransferase					18.95	
METACYC	PWY-5653	NAD biosynthesis from 2-amino-3-carboxymuconate	Tfu_2883	Tfu_2883 L-aspartate oxidase			15.62	16.95	20.84	
METACYC	PWY-40	putrescine biosynthesis I	Tfu_0058	Tfu_0058 putative agmatinase	15.19	15.1			18.15	1.47
METACYC	PWY-6972	oleandomycin activation/inactivation	Tfu_0810	Tfu_0810 ABC-type polar amino acid transport system A	20.65	20.47	19.17	19	22.36	1.163
METACYC	PWY-6972	oleandomycin activation/inactivation	Tfu_0858	Tfu_0858 ABC-type Mn/Zn transport systems ATPase component						
METACYC	PWY-6972	oleandomycin activation/inactivation	Tfu_1100	Tfu_1100 putative regulatory protein						
METACYC	PWY-6972	oleandomycin activation/inactivation	Tfu_1676	Tfu_1676 MoxR-like ATPase					16.26	
METACYC	PWY-6972	oleandomycin activation/inactivation	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6972	oleandomycin activation/inactivation	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6972	oleandomycin activation/inactivation	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6972	oleandomycin activation/inactivation	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	

METACYC	PWY-6972	oleandomycin activation/inactivation	Tfu_2500	Tfu_2500 ATPase	18.85	18.12	18.16	18.37	22.96	1.114
METACYC	BGALACT-PWY	lactose degradation III	Tfu_1615	Tfu_1615 beta-galactosidase					16.26	
METACYC	PWY-561	superpathway of glyoxylate cycle and fatty acid degr	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	PWY-561	superpathway of glyoxylate cycle and fatty acid degr	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	GLUDEG-II-PWY	glutamate degradation VII (to butanoate)	Tfu_1546	Tfu_1546 putative acyl-CoA synthetase					20.01	
METACYC	GLUDEG-II-PWY	glutamate degradation VII (to butanoate)	Tfu_2808	Tfu_2808 putative acetyl-coenzyme A synthetase			16.12	15.88	21.7	
METACYC	GLUDEG-II-PWY	glutamate degradation VII (to butanoate)	Tfu_2856	Tfu_2856 acetyl-coenzyme A synthetase	24.08	23.76	23.99	23.94	27	1.638
METACYC	PWY-5901	2,3-dihydroxybenzoate biosynthesis	Tfu_1413	Tfu_1413 isochorismate synthase						
METACYC	PWY-5901	2,3-dihydroxybenzoate biosynthesis	Tfu_1870	Tfu_1870 isochorismatase						
METACYC	PWY-5901	2,3-dihydroxybenzoate biosynthesis	Tfu_1872	Tfu_1872 isochorismate synthase					17.85	
METACYC	PWY-5901	2,3-dihydroxybenzoate biosynthesis	Tfu_1873	Tfu_1873 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase					14.76	
METACYC	PWY-7025	gentamicin biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-7025	gentamicin biosynthesis	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
METACYC	PWY-7025	gentamicin biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-5926	afrormosin conjugates interconversion	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5926	afrormosin conjugates interconversion	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5926	afrormosin conjugates interconversion	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY0-1337	oleate β-oxidation	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY0-1337	oleate β-oxidation	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY0-1337	oleate β-oxidation	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	BETA-ALA-DEGRADATION-I-PWY	β-alanine degradation I	Tfu_0687	Tfu_0687 methylmalonate-semialdehyde dehydrogenase	18.43	17.24	18.03	18.14	22.37	1.017
METACYC	BETA-ALA-DEGRADATION-I-PWY	β-alanine degradation I	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
METACYC	PWY-6344	ornithine degradation II (Stickland reaction)	Tfu_2247	Tfu_2247 ornithine aminotransferase	17.14	16.93			19.08	0.774
METACYC	PWY-6344	ornithine degradation II (Stickland reaction)	Tfu_2708	Tfu_2708 delta 1-pyrroline-5-carboxylate reductase	17.73	17.16	18.03	17.57	21.11	
METACYC	1CMET2-PWY	formylTHF biosynthesis I	Tfu_1050	Tfu_1050 5,10-methylenetetrahydrofolate reductase						
METACYC	1CMET2-PWY	formylTHF biosynthesis I	Tfu_1825	Tfu_1825 5-methyltetrahydrofolate--homocysteine methyltransferase					15.39	
METACYC	1CMET2-PWY	formylTHF biosynthesis I	Tfu_2190	Tfu_2190 folylpolyglutamate synthetase					19.35	
METACYC	1CMET2-PWY	formylTHF biosynthesis I	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
METACYC	1CMET2-PWY	formylTHF biosynthesis I	Tfu_2356	Tfu_2356 formyltetrahydrofolate deformylase					15.81	
METACYC	1CMET2-PWY	formylTHF biosynthesis I	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
METACYC	PWY-6707	gallate biosynthesis	Tfu_1635	Tfu_1635 dehydroquinase, class II					16.28	
METACYC	PWY-7015	ribostamycin biosynthesis	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-7015	ribostamycin biosynthesis	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
METACYC	DISSULFRED-PWY	sulfate reduction IV (dissimilatory)	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
METACYC	DISSULFRED-PWY	sulfate reduction IV (dissimilatory)	Tfu_0420	Tfu_0420 Small GTP-binding protein domain:Sulfate adenylyltransferase, l			14.13		18.76	0.81
METACYC	DISSULFRED-PWY	sulfate reduction IV (dissimilatory)	Tfu_0425	Tfu_0425 adenylylsulfate kinase					17.66	
METACYC	PWY-6307	tryptophan degradation X (mammalian, via tryptami	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-6307	tryptophan degradation X (mammalian, via tryptami	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-6307	tryptophan degradation X (mammalian, via tryptami	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-5035	gibberellin biosynthesis III (early C-13 hydroxylation	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-6305	putrescine biosynthesis IV	Tfu_0058	Tfu_0058 putative agmatinase	15.19	15.1			18.15	1.47
METACYC	PWY-6305	putrescine biosynthesis IV	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
METACYC	PWY-6575	juvenile hormone III biosynthesis I	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-6575	juvenile hormone III biosynthesis I	Tfu_0543	Tfu_0543 hypothetical protein			13.59	14.81	19.36	
METACYC	PWY-6575	juvenile hormone III biosynthesis I	Tfu_0576	Tfu_0576 hypothetical protein					17.31	
METACYC	PWY-6575	juvenile hormone III biosynthesis I	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-6575	juvenile hormone III biosynthesis I	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6575	juvenile hormone III biosynthesis I	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-6575	juvenile hormone III biosynthesis I	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6575	juvenile hormone III biosynthesis I	Tfu_2457	Tfu_2457 putative mutT-like protein						

METACYC	PWY-6575	juvenile hormone III biosynthesis I	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	GLYCOCAT-PWY	glycogen degradation I	Tfu_0273	Tfu_0273 glucokinase ROK		12.38			18.77	
METACYC	GLYCOCAT-PWY	glycogen degradation I	Tfu_0586	Tfu_0586 alpha-glucan phosphorylase					15.86	
METACYC	GLYCOCAT-PWY	glycogen degradation I	Tfu_0833	Tfu_0833 alpha amylase, catalytic subdomain	15.71	15.55	14.92	15.54	20.77	0.845
METACYC	GLYCOCAT-PWY	glycogen degradation I	Tfu_1033	Tfu_1033 glucokinase ROK					19.34	
METACYC	GLYCOCAT-PWY	glycogen degradation I	Tfu_2205	Tfu_2205 glycoside hydrolase, family 77					15.25	
METACYC	GLYCOCAT-PWY	glycogen degradation I	Tfu_2510	Tfu_2510 phosphomannomutase	21.34	20.97	20.46	20.55	24.59	0.926
METACYC	PWY66-162	ethanol degradation IV	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY66-162	ethanol degradation IV	Tfu_1546	Tfu_1546 putative acyl-CoA synthetase					20.01	
METACYC	PWY66-162	ethanol degradation IV	Tfu_1649	Tfu_1649 catalase	20.13	19.98	21.56	21.24	24.73	0.727
METACYC	PWY66-162	ethanol degradation IV	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY66-162	ethanol degradation IV	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY66-162	ethanol degradation IV	Tfu_2808	Tfu_2808 putative acetyl-coenzyme A synthetase			16.12	15.88	21.7	
METACYC	PWY66-162	ethanol degradation IV	Tfu_2856	Tfu_2856 acetyl-coenzyme A synthetase	24.08	23.76	23.99	23.94	27	1.638
METACYC	PWY-5480	pyruvate fermentation to ethanol I	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	PWY-5480	pyruvate fermentation to ethanol I	Tfu_1489	Tfu_1489 oxidoreductase						
METACYC	PWY-5480	pyruvate fermentation to ethanol I	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	PWY-5480	pyruvate fermentation to ethanol I	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PWY1F-353	glycine betaine biosynthesis III (plants)	Tfu_0279	Tfu_0279 betaine-aldehyde dehydrogenase	21.7	21.51	19.8	20.02	23.9	0.958
METACYC	PWY1F-353	glycine betaine biosynthesis III (plants)	Tfu_1287	Tfu_1287 betaine-aldehyde dehydrogenase					18.53	
METACYC	PWY1F-353	glycine betaine biosynthesis III (plants)	Tfu_1471	Tfu_1471 betaine-aldehyde dehydrogenase					16.26	
METACYC	PWY1F-353	glycine betaine biosynthesis III (plants)	Tfu_1776	Tfu_1776 betaine-aldehyde dehydrogenase	16	15.03			18.4	
METACYC	GLUDEG-I-PWY	glutamate degradation III (via 4-aminobutyrate)	Tfu_0690	Tfu_0690 4-aminobutyrate aminotransferase	19.09	18.64	18.39	18.87	22.58	1.01
METACYC	PWY-6318	phenylalanine degradation IV (mammalian, via side c	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-6318	phenylalanine degradation IV (mammalian, via side c	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-3462	phenylalanine biosynthesis II	Tfu_1207	Tfu_1207 chorismate mutase of the AroH class						
METACYC	PWY-2724	alkane oxidation	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-2724	alkane oxidation	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-2724	alkane oxidation	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-6767	4,4'-diapolycopenedioate biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-6767	4,4'-diapolycopenedioate biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-6767	4,4'-diapolycopenedioate biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-7036	very long chain fatty acid biosynthesis II	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-7036	very long chain fatty acid biosynthesis II	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-7036	very long chain fatty acid biosynthesis II	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-7036	very long chain fatty acid biosynthesis II	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-7036	very long chain fatty acid biosynthesis II	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-7036	very long chain fatty acid biosynthesis II	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-7036	very long chain fatty acid biosynthesis II	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-5064	chlorophyll a biosynthesis II	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5064	chlorophyll a biosynthesis II	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5064	chlorophyll a biosynthesis II	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	CODH-PWY	reductive acetyl coenzyme A pathway	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	CODH-PWY	reductive acetyl coenzyme A pathway	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	CODH-PWY	reductive acetyl coenzyme A pathway	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
METACYC	PWY-5538	pyruvate fermentation to acetate VI	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
METACYC	PWY-5538	pyruvate fermentation to acetate VI	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
METACYC	PWY-6578	7-keto-8-aminopelargonate biosynthesis II	Tfu_1302	Tfu_1302 probable 6-carboxyhexanoate--COA ligase					15.64	
METACYC	ETOH-ACETYLCOA-ANA-PWY	ethanol degradation I	Tfu_1270	Tfu_1270 alcohol dehydrogenase class III						
METACYC	ETOH-ACETYLCOA-ANA-PWY	ethanol degradation I	Tfu_1489	Tfu_1489 oxidoreductase						

METACYC	ETOH-ACETYLCOA-ANA-PWY	ethanol degradation I	Tfu_1775	Tfu_1775 putative alcohol dehydrogenase (zinc-binding)					15.94	
METACYC	ETOH-ACETYLCOA-ANA-PWY	ethanol degradation I	Tfu_2771	Tfu_2771 putative dehydrogenase	21.14	20.48	22.73	22.45	25.79	2.16
METACYC	PLPSAL-PWY	pyridoxal 5'-phosphate salvage pathway	Tfu_0248	Tfu_0248 pyridoxamine 5'-phosphate oxidase	15.34	14.98		14.89	18.71	
METACYC	PWY-5108	isoleucine biosynthesis V	Tfu_0616	Tfu_0616 branched-chain amino acid aminotransferase	20.25	19.96	22.08	21.99	24.87	0.982
METACYC	PWY-5108	isoleucine biosynthesis V	Tfu_2112	Tfu_2112 putative aminotransferase	20.47	20.18	20.21	20.11	23.77	0.849
METACYC	PWY-5743	3-hydroxypropionate cycle	Tfu_2395	Tfu_2395 hypothetical protein	16.89	15.73	15.47	16.56	21.77	0.591
METACYC	PWY-5743	3-hydroxypropionate cycle	Tfu_2555	Tfu_2555 propionyl-CoA carboxylase complex B subunit	18.59	18.29	18.47	17.99	22.37	0.744
METACYC	PWY-5743	3-hydroxypropionate cycle	Tfu_2761	Tfu_2761 methylmalonyl-CoA mutase	14.63	15.17	14.22	13.56	21.09	1.143
METACYC	PWY-5743	3-hydroxypropionate cycle	Tfu_2762	Tfu_2762 methylmalonyl-CoA mutase	15.39	14.9	15.16	13.96	20.57	
METACYC	PWY-5743	3-hydroxypropionate cycle	Tfu_2811	Tfu_2811 methylmalonyl-CoA mutase, N-terminal	20.3	20.06	22.95	22.73	26.27	0.706
METACYC	PWY-6039	chlorogenic acid biosynthesis I	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-6039	chlorogenic acid biosynthesis I	Tfu_0966	Tfu_0966 caffeoyl-CoA O-methyltransferase		13.62			16.15	
METACYC	PWY-6039	chlorogenic acid biosynthesis I	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-6039	chlorogenic acid biosynthesis I	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY-5913	TCA cycle VI (obligate autotrophs)	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	PWY-5913	TCA cycle VI (obligate autotrophs)	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	PWY-5913	TCA cycle VI (obligate autotrophs)	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	PWY-5913	TCA cycle VI (obligate autotrophs)	Tfu_1371	Tfu_1371 glutamate dehydrogenase	13.87		17.06	16.78	21.17	1.233
METACYC	PWY-5913	TCA cycle VI (obligate autotrophs)	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	PWY-5913	TCA cycle VI (obligate autotrophs)	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	PWY-5913	TCA cycle VI (obligate autotrophs)	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
METACYC	PWY-5913	TCA cycle VI (obligate autotrophs)	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
METACYC	PWY-5913	TCA cycle VI (obligate autotrophs)	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
METACYC	P321-PWY	benzoyl-CoA degradation III (anaerobic)	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	P321-PWY	benzoyl-CoA degradation III (anaerobic)	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	P321-PWY	benzoyl-CoA degradation III (anaerobic)	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	P321-PWY	benzoyl-CoA degradation III (anaerobic)	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-2601	isethionate degradation	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-2601	isethionate degradation	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	P562-PWY	<I>myo</I>-inositol degradation	Tfu_0687	Tfu_0687 methylmalonate-semialdehyde dehydrogenase	18.43	17.24	18.03	18.14	22.37	1.017
METACYC	PWY-4702	phytate degradation I	Tfu_1212	Tfu_1212 archaeal fructose-1 6-bisphosphatase and relat	14.95	15.73	15.51	15.72	20.15	0.894
METACYC	PWY-4702	phytate degradation I	Tfu_1943	Tfu_1943 inositol-1(or 4)-monophosphatase	16.16	15.99			19.17	0.652
METACYC	PWY-6363	D-myo-inositol (1,4,5)-trisphosphate degrada	Tfu_1212	Tfu_1212 archaeal fructose-1 6-bisphosphatase and relat	14.95	15.73	15.51	15.72	20.15	0.894
METACYC	PWY-6363	D-myo-inositol (1,4,5)-trisphosphate degrada	Tfu_1943	Tfu_1943 inositol-1(or 4)-monophosphatase	16.16	15.99			19.17	0.652
METACYC	GALACTUROCAT-PWY	D-galacturonate degradation I	Tfu_0189	Tfu_0189 putative PfkB-family carbohydrate kinase						
METACYC	PWY-3961	phosphopantothenate biosynthesis II	Tfu_1788	Tfu_1788 hypothetical protein	19.06	18.7	19.67	19.63	23.68	1.295
METACYC	PWY-3961	phosphopantothenate biosynthesis II	Tfu_1796	Tfu_1796 putative proteasome component	14.51	14.96	17.7	16.83	22.14	
METACYC	PWY-3961	phosphopantothenate biosynthesis II	Tfu_2610	Tfu_2610 pantothenate kinase			14.28		19	
METACYC	PWY-3961	phosphopantothenate biosynthesis II	Tfu_2882	Tfu_2882 Bvg accessory factor	15.79	15.26	16.09	15.65	20.23	
METACYC	PWY-6543	4-aminobenzoate biosynthesis	Tfu_1666	Tfu_1666 para-aminobenzoate synthase, component I:Glutamine amidotransferase of anthranilate synthase						
METACYC	PWY-5988	wound-induced proteolysis I	Tfu_0503	Tfu_0503 leucyl aminopeptidase	19.88	19.54	19.89	19.71	24.09	0.912
METACYC	PWY-5988	wound-induced proteolysis I	Tfu_0995	Tfu_0995 leucyl aminopeptidase	22.3	22.22	21.93	22.33	25.29	1.048
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2149	Tfu_2149 ribonucleotide-diphosphate reductase alpha su	14.41		17.19	15.02	21.83	0.68
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2188	Tfu_2188 nucleoside-diphosphate kinase	18.19	17.66	18.86	19.13	21.68	0.935
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2406	Tfu_2406 H+-transporting two-sector ATPase, delta/epsi	17.61	17.4	18.54	18.5	21.47	
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2407	Tfu_2407 ATP synthase F1, beta subunit	21.37	21.44	23.04	22.88	26.22	1.194
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2408	Tfu_2408 H+-transporting two-sector ATPase, gamma su	20.11	19.39	21.19	20.62	23.67	
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2409	Tfu_2409 ATP synthase subunit A	21.64	21.69	23.06	22.63	26.34	1.138
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2410	Tfu_2410 H+-transporting two-sector ATPase, delta (OSC	20.66	20.14	21.77	21.25	24.88	0.912
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2411	Tfu_2411 ATP synthase F0, subunit B	20.75	20.59	21	21.14	24.9	0.695

METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2412	Tfu_2412 ATP synthase F0, C subunit						
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2413	Tfu_2413 H+-transporting two-sector ATPase, A subunit						
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_2625	Tfu_2625 adenylate kinase, subfamily	19.36	20.27	22.16	21.48	24.95	0.736
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_3001	Tfu_3001 ribonucleoside-diphosphate reductase	13.73	13.7	18.55	18.52	22.84	1.196
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_3002	Tfu_3002 ribonucleoside-diphosphate reductase			18.75	18.62	22.88	0.758
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_3012	Tfu_3012 adenylosuccinate synthetase	15.75	15.57	18.76	18.61	22.25	0.954
METACYC	PWY-6126	adenosine nucleotides de novo biosynthesis	Tfu_3014	Tfu_3014 adenylosuccinate lyase	18.68	18.68	20.17	19.69	23.57	0.954
METACYC	HOMOSERSYN-PWY	homoserine biosynthesis	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1	18.57	18.71	20.61	20.33	23.82	0.982
METACYC	HOMOSERSYN-PWY	homoserine biosynthesis	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
METACYC	HOMOSERSYN-PWY	homoserine biosynthesis	Tfu_2424	Tfu_2424 homoserine dehydrogenase					18.67	1.062
METACYC	REDCITCYC	TCA cycle III (helicobacter)	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	REDCITCYC	TCA cycle III (helicobacter)	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	REDCITCYC	TCA cycle III (helicobacter)	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	REDCITCYC	TCA cycle III (helicobacter)	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
METACYC	REDCITCYC	TCA cycle III (helicobacter)	Tfu_2674	Tfu_2674 2-oxoglutarate ferredoxin oxidoreductase, alph	14.55		17.74	18.16	22.74	1.656
METACYC	REDCITCYC	TCA cycle III (helicobacter)	Tfu_2675	Tfu_2675 ferrodoxin oxidoreductase beta subunit			17.01	16.7	21.8	
METACYC	7ALPHADEHYDROX-PWY	cholate degradation (bacteria, anaerobic)	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	7ALPHADEHYDROX-PWY	cholate degradation (bacteria, anaerobic)	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PHENYLALANINE-DEG1-PWY	phenylalanine degradation I (aerobic)	Tfu_1547	Tfu_1547 pterin-4-alpha-carbinolamine dehydratase						
METACYC	CALVIN-PWY	Calvin-Benson-Bassham cycle	Tfu_0464	Tfu_0464 GlpX	18.98	18.91	19.97	19.41	23.31	1.007
METACYC	CALVIN-PWY	Calvin-Benson-Bassham cycle	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
METACYC	CALVIN-PWY	Calvin-Benson-Bassham cycle	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
METACYC	CALVIN-PWY	Calvin-Benson-Bassham cycle	Tfu_2015	Tfu_2015 triosephosphate isomerase	20.47	20.1	23.01	23.04	25.98	0.888
METACYC	CALVIN-PWY	Calvin-Benson-Bassham cycle	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	CALVIN-PWY	Calvin-Benson-Bassham cycle	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
METACYC	CALVIN-PWY	Calvin-Benson-Bassham cycle	Tfu_3010	Tfu_3010 fructose-bisphosphate aldolase	22.67	22.42	24.39	24.08	27.01	1.158
METACYC	PWY-6901	xylose degradation IV	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	PWY-6901	xylose degradation IV	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	PWY-6901	xylose degradation IV	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	PWY-6901	xylose degradation IV	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	PWY-6901	xylose degradation IV	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
METACYC	PWY-6901	xylose degradation IV	Tfu_2016	Tfu_2016 phosphoglycerate kinase	22.45	22.34	24.21	24.29	27.12	1.009
METACYC	PWY-6901	xylose degradation IV	Tfu_2017	Tfu_2017 glyceraldehyde-3-phosphate dehydrogenase, ty	23.03	22.77	25.37	25.33	28.17	1.113
METACYC	PWY-6901	xylose degradation IV	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	PWY-6901	xylose degradation IV	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078
METACYC	PYRUVDEHYD-PWY	acetyl-CoA biosynthesis I (pyruvate dehydrogenase c	Tfu_0180	Tfu_0180 pyruvate dehydrogenase (lipoamide)	20.47	20.54	21.95	22.05	25.45	0.974
METACYC	PYRUVDEHYD-PWY	acetyl-CoA biosynthesis I (pyruvate dehydrogenase c	Tfu_0181	Tfu_0181 putative branched-chain alpha keto acid dehyd	21.52	21.2	22.35	22.16	25.65	0.999
METACYC	PYRUVDEHYD-PWY	acetyl-CoA biosynthesis I (pyruvate dehydrogenase c	Tfu_0182	Tfu_0182 putative dihydrolipoamide acyltransferase con	22.33	22.24	22.85	22.66	25.78	1.092
METACYC	PYRUVDEHYD-PWY	acetyl-CoA biosynthesis I (pyruvate dehydrogenase c	Tfu_0994	Tfu_0994 dihydrolipoamide dehydrogenase	23.87	23.67	23.96	23.71	27.03	1.154
METACYC	PYRUVDEHYD-PWY	acetyl-CoA biosynthesis I (pyruvate dehydrogenase c	Tfu_2559	Tfu_2559 dihydrolipoamide dehydrogenase	17.62	17.97	18.6	18.7	23.28	1.063
METACYC	PYRUVDEHYD-PWY	acetyl-CoA biosynthesis I (pyruvate dehydrogenase c	Tfu_3049	Tfu_3049 pyruvate dehydrogenase (lipoamide)	20.31	19.75	20.61	20.78	24.41	1.167
METACYC	PYRUVDEHYD-PWY	acetyl-CoA biosynthesis I (pyruvate dehydrogenase c	Tfu_3050	Tfu_3050 dehydrogenase complex, E1 component, beta s	20.68	20.22	21.86	21.38	24.75	1.231
METACYC	PYRUVDEHYD-PWY	acetyl-CoA biosynthesis I (pyruvate dehydrogenase c	Tfu_3051	Tfu_3051 pyruvate dehydrogenase complex, E2 compone	21.68	21.7	22.67	22.41	25.66	1.062
METACYC	PWY-2781	cis-zeatin biosynthesis	Tfu_0815	Tfu_0815 tRNA delta(2)-isopentenylpyrophosphate transferase					18.28	
METACYC	PWY-6086	4-chloro-2-methylphenoxyacetate degradation	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	PWY-6593	sulfoacetate degradation	Tfu_1300	Tfu_1300 DitJ-like CoA ligase (AMP forming), possibly rel	16.49	15.45			20.78	
METACYC	PWY-6593	sulfoacetate degradation	Tfu_2248	Tfu_2248 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6693	galactose degradation IV	Tfu_0928	Tfu_0928 fructokinase	18.37	17.96	18.63	18.42	22.16	0.898
METACYC	PWY-6693	galactose degradation IV	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6693	galactose degradation IV	Tfu_2530	Tfu_2530 hypothetical protein					15.24	

METACYC	PWY-5123	trans, trans-farnesyl diphosphate biosynthesi	Tfu_1051	Tfu_1051 putative polyprenyl synthase / dimethylallyltranstransferase					19.26	
METACYC	PWY-5313	superpathway of anthocyanin biosynthesis (from cya	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5313	superpathway of anthocyanin biosynthesis (from cya	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-5313	superpathway of anthocyanin biosynthesis (from cya	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5313	superpathway of anthocyanin biosynthesis (from cya	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5313	superpathway of anthocyanin biosynthesis (from cya	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5313	superpathway of anthocyanin biosynthesis (from cya	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5313	superpathway of anthocyanin biosynthesis (from cya	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6760	xylose degradation III	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY-6908	thiamin diphosphate biosynthesis IV (eukaryotes)	Tfu_1046	Tfu_1046 thiamine-phosphate pyrophosphorylase		14.35			19.31	
METACYC	PWY-6736	sulfur volatiles biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6736	sulfur volatiles biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6562	norspermidine biosynthesis	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1	18.57	18.71	20.61	20.33	23.82	0.982
METACYC	PWY-6562	norspermidine biosynthesis	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
METACYC	PWY-6562	norspermidine biosynthesis	Tfu_0301	Tfu_0301 diaminobutyrate--2-oxoglutarate aminotransferase						
METACYC	PWY-6920	6-gingerol analog biosynthesis	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-6920	6-gingerol analog biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6920	6-gingerol analog biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6920	6-gingerol analog biosynthesis	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-6920	6-gingerol analog biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6920	6-gingerol analog biosynthesis	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6920	6-gingerol analog biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6920	6-gingerol analog biosynthesis	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-6920	6-gingerol analog biosynthesis	Tfu_2239	Tfu_2239 hypothetical protein	17.58	17.57	18.21	17.62	22.75	0.874
METACYC	PWY-6984	lipoate salvage II	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-6984	lipoate salvage II	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-6121	5-aminoimidazole ribonucleotide biosynthesis I	Tfu_0156	Tfu_0156 phosphoribosylformylglycinamidine synthase I			15.57	15.14	21.14	0.902
METACYC	PWY-6121	5-aminoimidazole ribonucleotide biosynthesis I	Tfu_0158	Tfu_0158 phosphoribosylformylglycinamidine synthase s	13.89	15.06	17.93	18.1	22.88	0.924
METACYC	PWY-6121	5-aminoimidazole ribonucleotide biosynthesis I	Tfu_0178	Tfu_0178 phosphoribosylformylglycinamidine synthase					17.74	
METACYC	PWY-6121	5-aminoimidazole ribonucleotide biosynthesis I	Tfu_2573	Tfu_2573 phosphoribosylglycinamide formyltransferase	14.49	14.7	17.07	16.78	21.38	
METACYC	PWY-6121	5-aminoimidazole ribonucleotide biosynthesis I	Tfu_2747	Tfu_2747 amidophosphoribosyltransferase						
METACYC	PWY-6121	5-aminoimidazole ribonucleotide biosynthesis I	Tfu_2748	Tfu_2748 phosphoribosylaminoimidazole synthetase	14.77		17.56	17.33	20.81	0.689
METACYC	PWY-6121	5-aminoimidazole ribonucleotide biosynthesis I	Tfu_3013	Tfu_3013 phosphoribosylglycinamide synthetase			17.63	17.26	21.77	
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_0169	Tfu_0169 nucleoside-diphosphate-sugar epimerase (UDP	14.49	16.6	18.84	18.16	22.51	0.845
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_1154	Tfu_1154 imidazole glycerol phosphate synthase subunit HisH						
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_1622	Tfu_1622 UDP-glucose 4-epimerase						
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_2591	Tfu_2591 UDP-glucose 4-epimerase					14.83	
METACYC	PWY-6397	mycolyl-arabinogalactan-peptidoglycan complex bio	Tfu_2723	Tfu_2723 putative epimerase						
METACYC	PWY-5981	CDP-diacylglycerol biosynthesis III	Tfu_0631	Tfu_0631 glycerol-3-phosphate dehydrogenase (NAD(P)	14.3	15.55	14.47		20.42	
METACYC	PWY-5981	CDP-diacylglycerol biosynthesis III	Tfu_0680	Tfu_0680 phosphatidate cytidylyltransferase	15.69	15.29	15.87	15.37	19.59	
METACYC	PWY-5981	CDP-diacylglycerol biosynthesis III	Tfu_1036	Tfu_1036 phospholipid/glycerol acyltransferase	18.2	17.54	17.83	17.5	21.56	
METACYC	PWY-5981	CDP-diacylglycerol biosynthesis III	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-5981	CDP-diacylglycerol biosynthesis III	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						

METACYC	PWY-5981	CDP-diacylglycerol biosynthesis III	Tfu_1417	Tfu_1417 phospholipid/glycerol acyltransferase	13.91	13.6		12.45	17.58	
METACYC	PWY-5981	CDP-diacylglycerol biosynthesis III	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-5981	CDP-diacylglycerol biosynthesis III	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-6374	vibriobactin biosynthesis	Tfu_1871	Tfu_1871 2,3-dihydroxybenzoate-AMP ligase			14.18	14.93	21.25	0.737
METACYC	PWY-6286	spheroidene and spheroidenone biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6286	spheroidene and spheroidenone biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6409	pyoverdine I biosynthesis	Tfu_0301	Tfu_0301 diaminobutyrate--2-oxoglutarate aminotransferase						
METACYC	COLANSYN-PWY	colanic acid building blocks biosynthesis	Tfu_0169	Tfu_0169 nucleoside-diphosphate-sugar epimerase (UDF	14.49	16.6	18.84	18.16	22.51	0.845
METACYC	COLANSYN-PWY	colanic acid building blocks biosynthesis	Tfu_0373	Tfu_0373 UTP--glucose-1-phosphate uridylyltransferase,	16.85	15	17.24	17.46	22.15	
METACYC	COLANSYN-PWY	colanic acid building blocks biosynthesis	Tfu_1622	Tfu_1622 UDP-glucose 4-epimerase						
METACYC	COLANSYN-PWY	colanic acid building blocks biosynthesis	Tfu_2544	Tfu_2544 UDP-glucose 6-dehydrogenase			15.09		19.86	
METACYC	COLANSYN-PWY	colanic acid building blocks biosynthesis	Tfu_2566	Tfu_2566 galactokinase						
METACYC	COLANSYN-PWY	colanic acid building blocks biosynthesis	Tfu_2591	Tfu_2591 UDP-glucose 4-epimerase					14.83	
METACYC	COLANSYN-PWY	colanic acid building blocks biosynthesis	Tfu_2723	Tfu_2723 putative epimerase						
METACYC	PWY-5971	palmitate biosynthesis II (bacteria and plants)	Tfu_1682	Tfu_1682 3-ketoacyl-(acyl-carrier-protein) reductase	16.81	16.46	15.51	15.71	20.33	
METACYC	PWY-5971	palmitate biosynthesis II (bacteria and plants)	Tfu_1841	Tfu_1841 putative 3-ketoacyl-CoA reductase	17.48	17.54	16.08	15.25	21.31	
METACYC	PWY-5971	palmitate biosynthesis II (bacteria and plants)	Tfu_1842	Tfu_1842 enoyl-(acyl carrier protein) reductase	20.49	19.93	21.16	21.07	24.76	1.053
METACYC	PWY-5971	palmitate biosynthesis II (bacteria and plants)	Tfu_1843	Tfu_1843 3-oxoacyl-(acyl-carrier-protein) reductase	16.14	16.8	18.38	18.62	22.77	1.118
METACYC	PWY-5971	palmitate biosynthesis II (bacteria and plants)	Tfu_2308	Tfu_2308 hypothetical protein	18.27	17.95	17.32	16.68	21.64	
METACYC	PWY-6825	phosphatidylcholine biosynthesis V	Tfu_0735	Tfu_0735 ubiquinone/menaquinone biosynthesis methyltransferase						
METACYC	DAPLYSINESYN-PWY	lysine biosynthesis I	Tfu_0042	Tfu_0042 aspartate-semialdehyde dehydrogenase, USG-1	18.57	18.71	20.61	20.33	23.82	0.982
METACYC	DAPLYSINESYN-PWY	lysine biosynthesis I	Tfu_0043	Tfu_0043 aspartate kinase	17	16.12	20.07	19.6	23.96	1.121
METACYC	DAPLYSINESYN-PWY	lysine biosynthesis I	Tfu_0494	Tfu_0494 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N	20.98	20.36	20.57	20.17	24.7	0.791
METACYC	DAPLYSINESYN-PWY	lysine biosynthesis I	Tfu_0495	Tfu_0495 succinyl-diaminopimelate desuccinylase	16.35	16.43	16.49	16.87	20.83	0.501
METACYC	DAPLYSINESYN-PWY	lysine biosynthesis I	Tfu_0568	Tfu_0568 hypothetical protein					18.2	
METACYC	DAPLYSINESYN-PWY	lysine biosynthesis I	Tfu_0786	Tfu_0786 dihydrodipicolinate reductase	18.87	17.45	19.64	18.4	23.22	0.825
METACYC	DAPLYSINESYN-PWY	lysine biosynthesis I	Tfu_0791	Tfu_0791 dihydrodipicolinate synthase	18.66	18.47	18.44	17.89	22.07	0.844
METACYC	DAPLYSINESYN-PWY	lysine biosynthesis I	Tfu_0816	Tfu_0816 diaminopimelate epimerase					18.06	
METACYC	DAPLYSINESYN-PWY	lysine biosynthesis I	Tfu_1715	Tfu_1715 dihydrodipicolinate synthase					14.89	
METACYC	DAPLYSINESYN-PWY	lysine biosynthesis I	Tfu_2425	Tfu_2425 diaminopimelate decarboxylase					18.01	
METACYC	PWY-6418	4-hydroxycoumarin biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-6418	4-hydroxycoumarin biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-6418	4-hydroxycoumarin biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-6418	4-hydroxycoumarin biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-801	homocysteine and cysteine interconversion	Tfu_0438	Tfu_0438 cystathionine beta-synthase	13		14.49	12.98	20.18	
METACYC	PWY-6897	thiamin salvage II	Tfu_0643	Tfu_0643 thiamine monophosphate kinase					14.5	
METACYC	PWY-6897	thiamin salvage II	Tfu_1046	Tfu_1046 thiamine-phosphate pyrophosphorylase		14.35			19.31	
METACYC	PWY-5188	tetrapyrrole biosynthesis I	Tfu_0623	Tfu_0623 glutamyl-tRNA synthetase bacterial/mitochon	18.5	17.36	18.79	19.22	23.34	0.908
METACYC	PWY-5188	tetrapyrrole biosynthesis I	Tfu_2726	Tfu_2726 glutamate-1-semialdehyde aminotransferase	17.89	17.41	18.76	18.54	22.7	
METACYC	PWY-5188	tetrapyrrole biosynthesis I	Tfu_2730	Tfu_2730 porphobilinogen synthase					18.56	
METACYC	PWY-5188	tetrapyrrole biosynthesis I	Tfu_2731	Tfu_2731 putative uroporphyrin-III C-methyltransferase	19.75	19.58	19.91	19.51	24.15	1.231
METACYC	PWY-5188	tetrapyrrole biosynthesis I	Tfu_2732	Tfu_2732 porphobilinogen deaminase	13.44				19.8	
METACYC	PWY-5188	tetrapyrrole biosynthesis I	Tfu_2733	Tfu_2733 glutamyl-tRNA reductase						
METACYC	MANNOSYL-CHITO-DOLICHOL-BIOSYNTHESI	dolichyl-diphosphooligosaccharide biosynthesis	Tfu_1850	Tfu_1850 dolichyl-phosphate beta-D-mannosyltransferas	17.8	17.7	16.81	17.93	21.31	0.842
METACYC	PWY-5793	maysin biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5793	maysin biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5793	maysin biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6857	retinol biosynthesis	Tfu_0155	Tfu_0155 esterase / lipase						
METACYC	PWY-6857	retinol biosynthesis	Tfu_0882	Tfu_0882 hypothetical protein						
METACYC	PWY-6857	retinol biosynthesis	Tfu_0883	Tfu_0883 hypothetical protein						

METACYC	PWY-6857	retinol biosynthesis	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2682	Tfu_2682 NADH dehydrogenase subunit N	15.55	15.11	17.89	15.78	21.55	1.549
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2683	Tfu_2683 NADH dehydrogenase subunit M	15.96	15.61	18.67	18.21	22.04	1.217
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2684	Tfu_2684 NADH dehydrogenase subunit L	16.72	16.18	19.09	19.32	22.49	1.313
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2685	Tfu_2685 NADH dehydrogenase kappa subunit	15.96	16.12	17.42	17.06	21.01	1.226
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2686	Tfu_2686 NADH dehydrogenase subunit J	14.57		19.26	18.19	22.25	
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2687	Tfu_2687 NADH-quinone oxidoreductase, chain I	17.42	17.05	19.49	19.25	23.17	1.344
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2688	Tfu_2688 NADH dehydrogenase subunit H	16.85	15.81	18.1	18.62	22.74	1.366
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2689	Tfu_2689 NADH dehydrogenase gamma subunit	19.85	19.4	22.2	22.17	25.89	1.474
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2690	Tfu_2690 NADH-quinone oxidoreductase, F subunit	18.4	18.59	21.04	20.94	24.09	1.696
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2691	Tfu_2691 ATP synthase subunit E	18.11	17.48	19.19	19.38	23.19	
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2692	Tfu_2692 NADH dehydrogenase delta subunit	17.85	17.37	21.19	20.56	24.79	1.513
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2693	Tfu_2693 NADH dehydrogenase subunit C	17.89	18.01	20.34	20.17	23.82	1.361
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2694	Tfu_2694 NADH dehydrogenase beta subunit	17.52	17.43	19.51	19.02	23.25	1.847
METACYC	PWY0-1335	NADH to cytochrome bo oxidase electron tra	Tfu_2695	Tfu_2695 NADH dehydrogenase alpha subunit	15.61	15.66	16.21	16.57	20.39	
METACYC	PWY-6696	oxalate degradation III	Tfu_1737	Tfu_1737 oxidoreductase alpha (molybdopterin) subunit			14.39	13.79	19.93	
METACYC	PWY-5837	1,4-dihydroxy-2-naphthoate biosynthesis I	Tfu_0960	Tfu_0960 n-acylamino acid racemase : O-succinylbenzoate-CoA synthase					19.49	
METACYC	PWY-5837	1,4-dihydroxy-2-naphthoate biosynthesis I	Tfu_1408	Tfu_1408 putative ortho-succinylbenzoate-CoA synthetase						
METACYC	PWY-5837	1,4-dihydroxy-2-naphthoate biosynthesis I	Tfu_1409	Tfu_1409 naphthoate synthase	16.03	15.45	18.71	18.23	22.53	
METACYC	PWY-5837	1,4-dihydroxy-2-naphthoate biosynthesis I	Tfu_1410	Tfu_1410 O-succinylbenzoate synthase					15.48	
METACYC	PWY-5837	1,4-dihydroxy-2-naphthoate biosynthesis I	Tfu_1411	Tfu_1411 Menaquinone biosynthesis protein					16.81	
METACYC	PWY-5837	1,4-dihydroxy-2-naphthoate biosynthesis I	Tfu_1413	Tfu_1413 isochorismate synthase						
METACYC	PWY-5837	1,4-dihydroxy-2-naphthoate biosynthesis I	Tfu_1872	Tfu_1872 isochorismate synthase					17.85	
METACYC	GALACTITOLCAT-PWY	galactitol degradation	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	GALACTITOLCAT-PWY	galactitol degradation	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	THIOREDOX-PWY	thioredoxin pathway	Tfu_3108	Tfu_3108 thioredoxin reductase	16.25	15.17	16.88	17.34	22.36	1.054
METACYC	PWY-702	methionine biosynthesis II	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-702	methionine biosynthesis II	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-702	methionine biosynthesis II	Tfu_2422	Tfu_2422 homoserine kinase					19.33	0.823
METACYC	PWY-702	methionine biosynthesis II	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6803	phosphatidylcholine acyl editing	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-6803	phosphatidylcholine acyl editing	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-6803	phosphatidylcholine acyl editing	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6803	phosphatidylcholine acyl editing	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY66-368	ketolysis	Tfu_0081	Tfu_0081 3-hydroxybutyrate dehydrogenase	21.11	21.46	19.94	20.31	23.95	1.187
METACYC	PWY66-368	ketolysis	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY66-368	ketolysis	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY66-368	ketolysis	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY66-368	ketolysis	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	NADPHOS-DEPHOS-PWY	NAD phosphorylation and dephosphorylation	Tfu_2033	Tfu_2033 inorganic polyphosphate/ATP-NAD kinase	16.3	16.08	15.21	15.52	19.8	
METACYC	PWY-5339	chalcone 2'-O-glucoside biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5339	chalcone 2'-O-glucoside biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5339	chalcone 2'-O-glucoside biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWYQT-4429	CO₂ fixation into oxaloacetate (anapleu	Tfu_2132	Tfu_2132 carbonic anhydrase, putative					20.01	
METACYC	PWYQT-4429	CO₂ fixation into oxaloacetate (anapleu	Tfu_2554	Tfu_2554 phosphoenolpyruvate carboxylase	18.7	18.31	21.35	20.84	24.95	1.372
METACYC	M-CRESOL-DEGRADATION-PWY	<I>m</I>-cresol degradation	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	M-CRESOL-DEGRADATION-PWY	<I>m</I>-cresol degradation	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY4FS-8	phosphatidylglycerol biosynthesis II (non-plastidic)	Tfu_0796	Tfu_0796 CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase					15.36	
METACYC	PWY4FS-8	phosphatidylglycerol biosynthesis II (non-plastidic)	Tfu_1393	Tfu_1393 putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase					15.45	
METACYC	PWY4FS-8	phosphatidylglycerol biosynthesis II (non-plastidic)	Tfu_2103	Tfu_2103 putative membrane transferase		14.75	15	14.79	18.49	

METACYC	BSUBPOLYAMSYN-PWY	spermidine biosynthesis I	Tfu_2234	Tfu_2234 spermidine synthase						
METACYC	ARG-GLU-PWY	arginine degradation VII (arginase 3 pathway)	Tfu_1543	Tfu_1543 arginase	16.88	16.58		15.07	16.68	
METACYC	PWY-6614	tetrahydrofolate biosynthesis	Tfu_1314	Tfu_1314 dihydropteroate synthase	16.71	16.84	17.22	16.91	22.57	1.071
METACYC	PWY-6614	tetrahydrofolate biosynthesis	Tfu_2190	Tfu_2190 folylpolyglutamate synthetase					19.35	
METACYC	PWY-6614	tetrahydrofolate biosynthesis	Tfu_2893	Tfu_2893 dihydropteroate synthase	18.01	17.46	18.35	17.82	21.56	1.133
METACYC	PWY-5404	betaxanthin biosynthesis (via dopaxanthin)	Tfu_0637	Tfu_0637 cytochrome bd ubiquinol oxidase, subunit II			18.7	17.36	23.03	2.71
METACYC	PWY-5404	betaxanthin biosynthesis (via dopaxanthin)	Tfu_0638	Tfu_0638 putative cytochrome oxidase subunit I			19.89	19.95	23.08	
METACYC	PWY-5404	betaxanthin biosynthesis (via dopaxanthin)	Tfu_0766	Tfu_0766 highly similar to cytochrome D ubiquinol oxidase subunit I						
METACYC	PWY1-3	polyhydroxybutyrate biosynthesis	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY1-3	polyhydroxybutyrate biosynthesis	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY1-3	polyhydroxybutyrate biosynthesis	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY1-3	polyhydroxybutyrate biosynthesis	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY1-3	polyhydroxybutyrate biosynthesis	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY1-3	polyhydroxybutyrate biosynthesis	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY1-3	polyhydroxybutyrate biosynthesis	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY1-3	polyhydroxybutyrate biosynthesis	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-5816	all trans undecaprenyl diphosphate biosynth	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-5816	all trans undecaprenyl diphosphate biosynth	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-5816	all trans undecaprenyl diphosphate biosynth	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-5380	A series fagopyritols biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5380	A series fagopyritols biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5380	A series fagopyritols biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-6406	salicylate biosynthesis I	Tfu_1413	Tfu_1413 isochorismate synthase						
METACYC	PWY-6406	salicylate biosynthesis I	Tfu_1872	Tfu_1872 isochorismate synthase					17.85	
METACYC	PWY-3542	choline biosynthesis II	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-3542	choline biosynthesis II	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6607	guanosine nucleotides degradation I	Tfu_2581	Tfu_2581 inosine-uridine preferring nucleoside hydrolas	16.93	16.72	16.96	15.37	21.32	
METACYC	PWY-5198	factor 420 biosynthesis	Tfu_0629	Tfu_0629 hypothetical protein						
METACYC	PWY-5198	factor 420 biosynthesis	Tfu_2517	Tfu_2517 LPPG:Fo 2-phospho-L-lactate transferase			14.64	15.51	20.71	
METACYC	PWY-6138	CMP-N-acetylneuraminate biosynthesis I (eu	Tfu_0009	Tfu_0009 putative transferase						
METACYC	PWY-5379	B series fagopyritols biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5379	B series fagopyritols biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5379	B series fagopyritols biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5094	naringenin glycoside biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5094	naringenin glycoside biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5094	naringenin glycoside biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5278	sulfite oxidation III	Tfu_0419	Tfu_0419 sulfate adenylyltransferase subunit 2					17.31	0.911
METACYC	PWY-5278	sulfite oxidation III	Tfu_0420	Tfu_0420 Small GTP-binding protein domain:Sulfate adenylyltransferase, l			14.13		18.76	0.81
METACYC	PWY-5278	sulfite oxidation III	Tfu_0425	Tfu_0425 adenylylsulfate kinase					17.66	
METACYC	GLYCEROLMETAB-PWY	glycerol degradation V	Tfu_2801	Tfu_2801 glycerol dehydrogenase					18.62	
METACYC	METH-ACETATE-PWY	methanogenesis from acetate	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	METH-ACETATE-PWY	methanogenesis from acetate	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	METH-ACETATE-PWY	methanogenesis from acetate	Tfu_2971	Tfu_2971 acetate kinase					13.64	
METACYC	PWY-2301	myo-inositol biosynthesis	Tfu_1212	Tfu_1212 archaeal fructose-1 6-bisphosphatase and relat	14.95	15.73	15.51	15.72	20.15	0.894
METACYC	PWY-2301	myo-inositol biosynthesis	Tfu_1943	Tfu_1943 inositol-1(or 4)-monophosphatase	16.16	15.99			19.17	0.652
METACYC	PWY-2301	myo-inositol biosynthesis	Tfu_3099	Tfu_3099 myo-inositol-1-phosphate synthase	16.21	15.62	18.24	18.23	23.01	0.924
METACYC	PWY-6637	sulfolactate degradation II	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6637	sulfolactate degradation II	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-7027	hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosyr	Tfu_0531	Tfu_0531 acyl-CoA thioesterase	17.1	17.29		17.28	20.25	0.851
METACYC	PWY-7027	hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosyr	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						

METACYC	PWY-7027	hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosyr	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-7027	hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosyr	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-7027	hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosyr	Tfu_1299	Tfu_1299 dihydroxynaphthoic acid synthase						
METACYC	PWY-7027	hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosyr	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-7027	hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosyr	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-7027	hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosyr	Tfu_2213	Tfu_2213 hypothetical protein						
METACYC	PWY-7027	hentriaconta-3,6,9,12,15,19,22,25,28-nonaene biosyr	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_0819	Tfu_0819 malate synthase	20.71	20.65	20.77	20.84	24.52	0.986
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_1377	Tfu_1377 isocitrate lyase	17.24	15.99	17.23	17.21	21.54	
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_2451	Tfu_2451 succinate dehydrogenase	19.35	19.39	20.29	20.56	23.66	1.002
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_2452	Tfu_2452 succinate dehydrogenase	21.35	21.31	22.55	22.42	25.77	1.417
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_2674	Tfu_2674 2-oxoglutarate ferredoxin oxidoreductase, alph	14.55		17.74	18.16	22.74	1.656
METACYC	PWY-6969	TCA cycle V (2-oxoglutarate:ferredoxin oxidoreducta	Tfu_2675	Tfu_2675 ferrodoxin oxidoreductase beta subunit			17.01	16.7	21.8	
METACYC	PWY-6385	peptidoglycan biosynthesis III (mycobacteria)	Tfu_1104	Tfu_1104 peptidoglycan glycosyltransferase						
METACYC	PWY-6385	peptidoglycan biosynthesis III (mycobacteria)	Tfu_1110	Tfu_1110 N-acetylglucosaminyl transferase	19.15	18.71	18.79	18.53	22.9	0.735
METACYC	PWY-6385	peptidoglycan biosynthesis III (mycobacteria)	Tfu_1855	Tfu_1855 4'-phosphopantetheinyl transferase						
METACYC	PWY-6385	peptidoglycan biosynthesis III (mycobacteria)	Tfu_2817	Tfu_2817 hypothetical protein					18.27	
METACYC	PWY-6385	peptidoglycan biosynthesis III (mycobacteria)	Tfu_3064	Tfu_3064 hypothetical protein	17.05	16.02	15.7	15.59	20.75	
METACYC	GLYCOLATEMET-PWY	glycolate and glyoxylate degradation I	Tfu_1010	Tfu_1010 glycerate kinase			14.48		20.4	
METACYC	GLYCOLATEMET-PWY	glycolate and glyoxylate degradation I	Tfu_1265	Tfu_1265 2-hydroxy-3-oxopropionate reductase			15.84	13.26	19.37	
METACYC	PWY-7029	terminal olefins biosynthesis II	Tfu_1218	Tfu_1218 actinorhodin polyketide beta-ketoacyl synthase alpha subunit / 3-oxoacyl-ACP synthase I						
METACYC	PWY-7029	terminal olefins biosynthesis II	Tfu_1219	Tfu_1219 actinorhodin polyketide beta-ketoacyl synthase beta subunit / 3-oxoacyl-ACP synthase II						
METACYC	PWY-7029	terminal olefins biosynthesis II	Tfu_1762	Tfu_1762 Apolipoprotein N-acyltransferase						
METACYC	PWY-7029	terminal olefins biosynthesis II	Tfu_2102	Tfu_2102 lipid A biosynthesis lauroyl acyltransferase	15.9	14.47	14.39		19.54	
METACYC	PWY-5506	methanol oxidation to formaldehyde IV	Tfu_1649	Tfu_1649 catalase	20.13	19.98	21.56	21.24	24.73	0.727
METACYC	PWY-5807	heptaprenyl diphosphate biosynthesis	Tfu_2681	Tfu_2681 trans-hexaprenyltranstransferase					20.84	0.581
METACYC	RIBOKIN-PWY	ribose degradation	Tfu_0259	Tfu_0259 ribokinase, bacterial					17.88	
METACYC	PWY-5872	ubiquinol-10 biosynthesis (eukaryotic)	Tfu_2697	Tfu_2697 ubiquinone/menaquinone biosynthesis methyltransferase			14.88		20.19	1.1
METACYC	PWY-6722	candicidin biosynthesis	Tfu_1666	Tfu_1666 para-aminobenzoate synthase, component I:Glutamine amidotransferase of anthranilate synthase						
METACYC	PWY-6650	juvenile hormone III biosynthesis II	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-6650	juvenile hormone III biosynthesis II	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6650	juvenile hormone III biosynthesis II	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-6650	juvenile hormone III biosynthesis II	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6650	juvenile hormone III biosynthesis II	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-6788	cellulose degradation II (fungi)	Tfu_0620	Tfu_0620 hypothetical protein						
METACYC	PWY-6788	cellulose degradation II (fungi)	Tfu_0901	Tfu_0901 hypothetical protein						
METACYC	PWY-6788	cellulose degradation II (fungi)	Tfu_0937	Tfu_0937 beta-glucosidase	16.92	16.79	21.22	20.91	23.7	2.426
METACYC	PWY-6788	cellulose degradation II (fungi)	Tfu_1074	Tfu_1074 hypothetical protein						
METACYC	PWY-6788	cellulose degradation II (fungi)	Tfu_1607	Tfu_1607 beta-glucosidase						
METACYC	PWY-6788	cellulose degradation II (fungi)	Tfu_1627	Tfu_1627 hypothetical protein						
METACYC	PWY-6788	cellulose degradation II (fungi)	Tfu_1629	Tfu_1629 beta-glucosidase	20.15	19.64	19.92	19.43	23.45	1.12
METACYC	PWY-6788	cellulose degradation II (fungi)	Tfu_1959	Tfu_1959 hypothetical protein					15.56	
METACYC	PWY-6788	cellulose degradation II (fungi)	Tfu_2176	Tfu_2176 hypothetical protein						

METACYC	PWY-6788	cellulose degradation II (fungi)	Tfu_2712	Tfu_2712 hypothetical protein						
METACYC	PWY-6910	hydroxymethylpyrimidine salvage	Tfu_2250	Tfu_2250 phosphomethylpyrimidine kinase	16.07	16.41	14.97		19.92	1.225
METACYC	PWY-6497	D-galactarate degradation II	Tfu_1718	Tfu_1718 putative 5-dehydro-4-deoxyglucarate dehydratase						
METACYC	PWY-6749	CMP-legionaminate biosynthesis	Tfu_1891	Tfu_1891 glycogen debranching enzyme GlgX					17.84	
METACYC	PWY-6749	CMP-legionaminate biosynthesis	Tfu_2611	Tfu_2611 D-fructose-6-phosphate amidotransferase	16.46	16.09	18.53	18.54	22.75	1.101
METACYC	PWY-6749	CMP-legionaminate biosynthesis	Tfu_2612	Tfu_2612 phosphoglucosamine mutase		12.2	15.38	14.97	20.13	0.827
METACYC	PWY-6982	umbelliferone biosynthesis	Tfu_1427	Tfu_1427 putative DNA repair protein						
METACYC	TCA	TCA cycle I (prokaryotic)	Tfu_0092	Tfu_0092 malate dehydrogenase	17.7	18.22	21.32	21.47	24.64	1.069
METACYC	TCA	TCA cycle I (prokaryotic)	Tfu_0247	Tfu_0247 citrate synthase	21.54	21.3	22.96	22.96	26.13	
METACYC	TCA	TCA cycle I (prokaryotic)	Tfu_0459	Tfu_0459 fumarate hydratase	20.7	20.61	21.56	21.22	25.47	1.097
METACYC	TCA	TCA cycle I (prokaryotic)	Tfu_1925	Tfu_1925 aconitate hydratase	22.76	22.69	23.21	22.98	26.34	1.403
METACYC	TCA	TCA cycle I (prokaryotic)	Tfu_2568	Tfu_2568 isocitrate dehydrogenase	21.24	20.88	22.43	22.41	25.78	1.131
METACYC	TCA	TCA cycle I (prokaryotic)	Tfu_2576	Tfu_2576 succinyl-CoA synthetase alpha subunit	16.28	16.29	19.3	18.97	22.83	1.631
METACYC	TCA	TCA cycle I (prokaryotic)	Tfu_2577	Tfu_2577 succinyl-CoA synthetase subunit beta	20.18	20.31	21.94	22.07	25.19	1.035
METACYC	PWY-5784	IAA conjugate biosynthesis II	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-5784	IAA conjugate biosynthesis II	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-5784	IAA conjugate biosynthesis II	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-5784	IAA conjugate biosynthesis II	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PWY-5784	IAA conjugate biosynthesis II	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-0	putrescine degradation III	Tfu_0744	Tfu_0744 aldehyde dehydrogenase (NAD+)	19.26	19.32	19.15	19.33	23.26	0.861
METACYC	PWY-0	putrescine degradation III	Tfu_1688	Tfu_1688 aldehyde dehydrogenase family protein						
METACYC	PWY-0	putrescine degradation III	Tfu_2590	Tfu_2590 succinic semialdehyde dehydrogenase	19.52	19.17	15.57	14.77	20.37	0.822
METACYC	PWY-6583	pyruvate fermentation to butanol I	Tfu_0253	Tfu_0253 acetyl-CoA acetyltransferase		13.98	15.22	14.68	20.31	
METACYC	PWY-6583	pyruvate fermentation to butanol I	Tfu_0436	Tfu_0436 acetyl-CoA acetyltransferase	18.45	18.03	17.95	17.39	21.73	0.811
METACYC	PWY-6583	pyruvate fermentation to butanol I	Tfu_0946	Tfu_0946 putative acyl-CoA dehydrogenase	20.62	20.44	21.21	21.21	24.67	0.91
METACYC	PWY-6583	pyruvate fermentation to butanol I	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6583	pyruvate fermentation to butanol I	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6583	pyruvate fermentation to butanol I	Tfu_1281	Tfu_1281 butyryl-CoA dehydrogenase						
METACYC	PWY-6583	pyruvate fermentation to butanol I	Tfu_1520	Tfu_1520 thiolase					15.67	
METACYC	PWY-6583	pyruvate fermentation to butanol I	Tfu_2394	Tfu_2394 acetyl-CoA acetyltransferase	18.25	18.23	19.37	18.71	22.26	0.829
METACYC	PWY-6583	pyruvate fermentation to butanol I	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-6974	dTDP-L-olivose biosynthesis	Tfu_1221	Tfu_1221 hypothetical protein						
METACYC	PWY-6974	dTDP-L-olivose biosynthesis	Tfu_1222	Tfu_1222 actinorhodin polyketide synthase bifunctional cyclase/dehydratase					17.63	
METACYC	PWY-6974	dTDP-L-olivose biosynthesis	Tfu_2530	Tfu_2530 hypothetical protein					15.24	
METACYC	PWY-2681	trans-zeatin biosynthesis	Tfu_0694	Tfu_0694 putative DNA repair hydrolase						
METACYC	PWY-2681	trans-zeatin biosynthesis	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-2681	trans-zeatin biosynthesis	Tfu_1918	Tfu_1918 putative DNA glycosylase						
METACYC	PWY-2681	trans-zeatin biosynthesis	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-2681	trans-zeatin biosynthesis	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-2681	trans-zeatin biosynthesis	Tfu_2875	Tfu_2875 HhH-GPD:Iron-sulfur cluster loop						
METACYC	PWY-6303	methyl indole-3-acetate interconversion	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-6303	methyl indole-3-acetate interconversion	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6303	methyl indole-3-acetate interconversion	Tfu_2427	Tfu_2427 putative carboxylesterase	17.77	18.01	19.35	18.61	23.12	0.567
METACYC	PWY-2201	folate transformations I	Tfu_0372	Tfu_0372 hypothetical protein						
METACYC	PWY-2201	folate transformations I	Tfu_1050	Tfu_1050 5,10-methylenetetrahydrofolate reductase						
METACYC	PWY-2201	folate transformations I	Tfu_1825	Tfu_1825 5-methyltetrahydrofolate--homocysteine methyltransferase					15.39	
METACYC	PWY-2201	folate transformations I	Tfu_2353	Tfu_2353 glycine hydroxymethyltransferase	13.62		16	15.62	20.34	1.09
METACYC	PWY-2201	folate transformations I	Tfu_2356	Tfu_2356 formyltetrahydrofolate deformylase					15.81	
METACYC	PWY-2201	folate transformations I	Tfu_2571	Tfu_2571 methenyltetrahydrofolate cyclohydrolase	18.59	18.89	19.66	19.54	23.7	0.958
METACYC	RIBOSYN2-PWY	flavin biosynthesis I (bacteria and plants)	Tfu_0782	Tfu_0782 Cytidyltransferase-related		13.35	14.92	14.18	20.03	

METACYC	RIBOSYN2-PWY	flavin biosynthesis I (bacteria and plants)	Tfu_0876	Tfu_0876 5-amino-6-(5-phosphoribosylamino)uracil reductase					18.52	
METACYC	RIBOSYN2-PWY	flavin biosynthesis I (bacteria and plants)	Tfu_0877	Tfu_0877 hypothetical protein					17.13	
METACYC	RIBOSYN2-PWY	flavin biosynthesis I (bacteria and plants)	Tfu_1078	Tfu_1078 Lumazine-binding protein		13.92	16.4	17.05	20.31	
METACYC	RIBOSYN2-PWY	flavin biosynthesis I (bacteria and plants)	Tfu_1080	Tfu_1080 bifunctional 3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II protein						
METACYC	RIBOSYN2-PWY	flavin biosynthesis I (bacteria and plants)	Tfu_1081	Tfu_1081 6,7-dimethyl-8-ribityllumazine synthase	15.97	15.69	16.33	16.62	21.62	
METACYC	PWY-6899	base-degraded thiamin salvage	Tfu_1336	Tfu_1336 putative Sir2 family regulator						
METACYC	PWY-6899	base-degraded thiamin salvage	Tfu_2374	Tfu_2374 putative pyrazinamidase / nicotinamidase		14.58			19.52	
METACYC	PWY-6899	base-degraded thiamin salvage	Tfu_2953	Tfu_2953 putative transcriptional regulator	15.38	15.61	16.42	14.9	19.48	1.394
METACYC	PWY-5785	di-trans,poly-cis-undecaprenyl phosp	Tfu_0853	Tfu_0853 di-trans-poly-cis-decaprenylcistransferase	16.33	16.31	16	16.58	20.43	0.931
METACYC	PWY-6001	linoleate biosynthesis II (animals)	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-6001	linoleate biosynthesis II (animals)	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-6001	linoleate biosynthesis II (animals)	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6001	linoleate biosynthesis II (animals)	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-4021	β-alanine betaine biosynthesis	Tfu_1089	Tfu_1089 hypothetical protein						
METACYC	PWY-4021	β-alanine betaine biosynthesis	Tfu_2418	Tfu_2418 modification methylase HemK						
METACYC	PWY-6793	demethylmenaquinol-8 biosynthesis III	Tfu_0694	Tfu_0694 putative DNA repair hydrolase						
METACYC	PWY-6793	demethylmenaquinol-8 biosynthesis III	Tfu_0788	Tfu_0788 1,4-dihydroxy-2-naphthoate octaprenyltransferase,				14.99	19.36	
METACYC	PWY-6793	demethylmenaquinol-8 biosynthesis III	Tfu_1918	Tfu_1918 putative DNA glycosylase						
METACYC	PWY-6793	demethylmenaquinol-8 biosynthesis III	Tfu_2001	Tfu_2001 protoheme IX farnesyltransferase						
METACYC	PWY-6793	demethylmenaquinol-8 biosynthesis III	Tfu_2519	Tfu_2519 hypothetical protein					15.29	
METACYC	PWY-6793	demethylmenaquinol-8 biosynthesis III	Tfu_2875	Tfu_2875 HhH-GPD:Iron-sulfur cluster loop						
METACYC	PWY0-1296	purine ribonucleosides degradation to ribose-1-phos	Tfu_2242	Tfu_2242 purine nucleoside phosphorylase	14.64	15.63	15.08	14.86	19.9	
METACYC	PWY0-1296	purine ribonucleosides degradation to ribose-1-phos	Tfu_2563	Tfu_2563 adenosine deaminase					16.67	
METACYC	PWY0-1296	purine ribonucleosides degradation to ribose-1-phos	Tfu_2662	Tfu_2662 adenosine deaminase				13.97	19.93	1.018
METACYC	PWY-6657	polyhydroxydecanoate biosynthesis	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6657	polyhydroxydecanoate biosynthesis	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6657	polyhydroxydecanoate biosynthesis	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	PHESYN	phenylalanine biosynthesis I	Tfu_1207	Tfu_1207 chorismate mutase of the AroH class						
METACYC	PHESYN	phenylalanine biosynthesis I	Tfu_3053	Tfu_3053 prephenate dehydratase					16.06	
METACYC	PWY-6873	long chain fatty acid ester synthesis for microdiesel p	Tfu_1031	Tfu_1031 long-chain fatty-acid-CoA ligase	23.81	23.6	21.68	21.58	25	1.032
METACYC	PWY-6873	long chain fatty acid ester synthesis for microdiesel p	Tfu_1733	Tfu_1733 putative acyl-CoA synthetase, long-chain-fatty acid:CoA ligase				14.51	18.82	1.08
METACYC	PWY-6873	long chain fatty acid ester synthesis for microdiesel p	Tfu_1998	Tfu_1998 putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase						
METACYC	PWY-6873	long chain fatty acid ester synthesis for microdiesel p	Tfu_2158	Tfu_2158 putative long-chain-fatty-acid-CoA ligase	22.39	22.15	20.82	20.24	23.82	0.959
METACYC	PWY-6686	mannosylglucosylglycerate biosynthesis I	Tfu_0135	Tfu_0135 hypothetical protein					16.99	
METACYC	PWY-6686	mannosylglucosylglycerate biosynthesis I	Tfu_1730	Tfu_1730 hypothetical protein						
METACYC	PWY-6686	mannosylglucosylglycerate biosynthesis I	Tfu_1732	Tfu_1732 hypothetical protein						
METACYC	PWY-6686	mannosylglucosylglycerate biosynthesis I	Tfu_1764	Tfu_1764 putative glycosyl transferase						
METACYC	GLUTSYNIII-PWY	glutamate biosynthesis III	Tfu_1371	Tfu_1371 glutamate dehydrogenase	13.87		17.06	16.78	21.17	1.233
METACYC	PWY-5723	Rubisco shunt	Tfu_0428	Tfu_0428 phosphopyruvate hydratase	23.25	22.98	24.42	24.33	27.37	0.77
METACYC	PWY-5723	Rubisco shunt	Tfu_1077	Tfu_1077 ribulose-phosphate 3-epimerase		14.39	15.83		19.81	0.938
METACYC	PWY-5723	Rubisco shunt	Tfu_1179	Tfu_1179 pyruvate kinase	18.4	18.5	20.1	20.03	23.97	0.859
METACYC	PWY-5723	Rubisco shunt	Tfu_1837	Tfu_1837 putative phosphatase	16.43	15.7			20.75	
METACYC	PWY-5723	Rubisco shunt	Tfu_1953	Tfu_1953 hypothetical protein					16.39	
METACYC	PWY-5723	Rubisco shunt	Tfu_2002	Tfu_2002 transketolase	21.4	21.23	22.57	22.4	25.65	1.081
METACYC	PWY-5723	Rubisco shunt	Tfu_2003	Tfu_2003 transaldolase	20.04	20.08	21.54	21.1	24.47	1.211
METACYC	PWY-5723	Rubisco shunt	Tfu_2169	Tfu_2169 putative phosphoglycerate mutase	14.67		16.19	16.66	20.89	1.296
METACYC	PWY-5723	Rubisco shunt	Tfu_2202	Tfu_2202 ribose-5-phosphate isomerase B	19.07	18.85	20.54	20.44	24.2	
METACYC	PWY-5723	Rubisco shunt	Tfu_2911	Tfu_2911 phosphoglyceromutase	18.77	19.23	21.05	21.13	24.72	1.078

Appendix - E - Proteomics Data No HOV

CLASS	HOV	HOV-description	locus	locus-description	AV	AVR	CB	CBR	CB2D	iTRAQ
NONE	X	NO-HOV	Tfu_2872	Tfu_2872 hypothetical protein		14.03	14.01	13.58	18.85	
NONE	X	NO-HOV	Tfu_1754	Tfu_1754 hypothetical protein					17.54	
NONE	X	NO-HOV	Tfu_0560	Tfu_0560 putative anti-sigma factor	18.06	17.68	17.05	17.91	21.05	0.666
NONE	X	NO-HOV	Tfu_2670	Tfu_2670 hypothetical protein	11.69			13.29	18.47	
NONE	X	NO-HOV	Tfu_1590	Tfu_1590 CRISPR-associated CT1975 family protein	21.76	20.85	20.67	20.56	24.31	1.279
NONE	X	NO-HOV	Tfu_2830	Tfu_2830 putative TetR-family transcriptional regulator					17.74	
NONE	X	NO-HOV	Tfu_2203	Tfu_2203 hypothetical protein	16.45	16.06	17.49	17.28	20.09	
NONE	X	NO-HOV	Tfu_1360	Tfu_1360 helix-turn-helix motif	14.57				15.77	
NONE	X	NO-HOV	Tfu_2127	Tfu_2127 hypothetical protein					18.25	
NONE	X	NO-HOV	Tfu_2155	Tfu_2155 hypothetical protein					17.93	
NONE	X	NO-HOV	Tfu_2358	Tfu_2358 hypothetical protein	17.52	17.25	15.76	15.96	20.59	1.409
NONE	X	NO-HOV	Tfu_0209	Tfu_0209 hypothetical protein					15.13	
NONE	X	NO-HOV	Tfu_3103	Tfu_3103 hypothetical protein					19.58	
NONE	X	NO-HOV	Tfu_0814	Tfu_0814 hypothetical protein					17.14	
NONE	X	NO-HOV	Tfu_0441	Tfu_0441 hypothetical protein					18.11	
NONE	X	NO-HOV	Tfu_0939	Tfu_0939 hypothetical protein	14.84				18.59	0.59
NONE	X	NO-HOV	Tfu_1534	Tfu_1534 hypothetical protein					14.68	
NONE	X	NO-HOV	Tfu_1900	Tfu_1900 hypothetical protein	15.07				17.81	
NONE	X	NO-HOV	Tfu_0763	Tfu_0763 hypothetical protein					14.15	
NONE	X	NO-HOV	Tfu_0392	Tfu_0392 helix-turn-helix motif					17.97	
NONE	X	NO-HOV	Tfu_3072	Tfu_3072 hypothetical protein	17.66	17.46	16.99	17.21	19.85	
NONE	X	NO-HOV	Tfu_0383	Tfu_0383 hypothetical protein					16.23	
NONE	X	NO-HOV	Tfu_0025	Tfu_0025 hypothetical protein					16.49	
NONE	X	NO-HOV	Tfu_0641	Tfu_0641 hypothetical protein	16.13	16.1	14.74	14.58	17.66	
NONE	X	NO-HOV	Tfu_0727	Tfu_0727 hypothetical protein					17.44	
NONE	X	NO-HOV	Tfu_0008	Tfu_0008 hypothetical protein	16.79	16.38	16.43	16.43	20.38	
NONE	X	NO-HOV	Tfu_1097	Tfu_1097 hypothetical protein					18.19	
NONE	X	NO-HOV	Tfu_0053	Tfu_0053 hypothetical protein	21.79	21.79	21.91	21.57	24.97	0.972
NONE	X	NO-HOV	Tfu_2459	Tfu_2459 hypothetical protein	19.16	19.06	14.77	14.67	20.23	
NONE	X	NO-HOV	Tfu_2715	Tfu_2715 hypothetical protein					16.72	
NONE	X	NO-HOV	Tfu_2899	Tfu_2899 hypothetical protein	17.77	17.35	15.38	15.95	19.3	
NONE	X	NO-HOV	Tfu_2957	Tfu_2957 hypothetical protein				15.27	19.41	
NONE	X	NO-HOV	Tfu_0869	Tfu_0869 hypthetical protein		14.24			17.27	
NONE	X	NO-HOV	Tfu_3017	Tfu_3017 hypothetical protein	18.64	17.92	18.13	18.6	23.31	0.963

NONE	X	NO-HOV	Tfu_1458	Tfu_1458 hypothetical protein		13.46			18.83	
NONE	X	NO-HOV	Tfu_2819	Tfu_2819 hypothetical protein	16.85	15.9	15.37		19.42	
NONE	X	NO-HOV	Tfu_2983	Tfu_2983 hypothetical protein					15.54	
NONE	X	NO-HOV	Tfu_2367	Tfu_2367 hypothetical protein	16.9	16.52	17.97	17.45	21.89	1.111
NONE	X	NO-HOV	Tfu_1240	Tfu_1240 hypothetical protein	15.06				17.8	
NONE	X	NO-HOV	Tfu_2528	Tfu_2528 hypothetical protein	15.53	16.23	15.21	13.22	20.54	
NONE	X	NO-HOV	Tfu_0789	Tfu_0789 hypothetical protein					18.56	
NONE	X	NO-HOV	Tfu_2843	Tfu_2843 TPR repeat	18.81	18.76	18.28	17.92	22.26	0.801
NONE	X	NO-HOV	Tfu_0138	Tfu_0138 hypothetical protein					16.22	
NONE	X	NO-HOV	Tfu_1442	Tfu_1442 hypothetical protein					18.89	
NONE	X	NO-HOV	Tfu_2319	Tfu_2319 hypothetical protein	18.56	18.02	14.78	14.78	19.72	
NONE	X	NO-HOV	Tfu_0020	Tfu_0020 hypothetical protein	17.69	17.46	17.02	17.03	20.74	1.006
NONE	X	NO-HOV	Tfu_1167	Tfu_1167 hypothetical protein					16.95	
NONE	X	NO-HOV	Tfu_2391	Tfu_2391 hypothetical protein					18.03	
NONE	X	NO-HOV	Tfu_0192	Tfu_0192 hypothetical protein	20.66	20.34	20.57	20.13	24.12	1.095
NONE	X	NO-HOV	Tfu_0071	Tfu_0071 hypothetical protein	21.16	21.14	20.88	21.24	24.32	0.493
NONE	X	NO-HOV	Tfu_2256	Tfu_2256 hypothetical protein					14.39	
NONE	X	NO-HOV	Tfu_0232	Tfu_0232 hypothetical protein					16.73	
NONE	X	NO-HOV	Tfu_1597	Tfu_1597 CRISPR-associated CT1976 family protein	15.22	14.62	13.94		19.99	
NONE	X	NO-HOV	Tfu_2088	Tfu_2088 hypothetical protein	19.65	19.52	20.66	20.27	24.1	0.893
NONE	X	NO-HOV	Tfu_0165	Tfu_0165 hypothetical protein					16.29	
NONE	X	NO-HOV	Tfu_0762	Tfu_0762 hypothetical protein					17.48	
NONE	X	NO-HOV	Tfu_2992	Tfu_2992 hypothetical protein					17.54	
NONE	X	NO-HOV	Tfu_1460	Tfu_1460 hypothetical protein					18.87	
NONE	X	NO-HOV	Tfu_2076	Tfu_2076 hypothetical protein					16.27	
NONE	X	NO-HOV	Tfu_0474	Tfu_0474 hypothetical protein				15.75	20.59	1.192
NONE	X	NO-HOV	Tfu_0709	Tfu_0709 bacteriophage (phiC31) resistance gene pglY	20.64	20.26	19.93	19.76	24.19	1.096
NONE	X	NO-HOV	Tfu_1645	Tfu_1645 hypothetical protein	18.45	17.42	17.93	17.8	22.78	0.703
NONE	X	NO-HOV	Tfu_1588	Tfu_1588 hypothetical protein	18.48	18.68	17.29	17.49	21.54	
NONE	X	NO-HOV	Tfu_2142	Tfu_2142 hypothetical protein					15.27	
NONE	X	NO-HOV	Tfu_0063	Tfu_0063 hypothetical protein					17.41	
NONE	X	NO-HOV	Tfu_0487	Tfu_0487 hypothetical protein	15.12	14.7	14.34	14.18	18.3	
NONE	X	NO-HOV	Tfu_2405	Tfu_2405 putative secreted/membrane protein					14.81	
NONE	X	NO-HOV	Tfu_1082	Tfu_1082 hypothetical protein					15.33	
NONE	X	NO-HOV	Tfu_1045	Tfu_1045 hypothetical protein			15.15		19.38	
NONE	X	NO-HOV	Tfu_2721	Tfu_2721 hypothetical protein	17.92	17.49	15.93	16.89	20.98	1.04
NONE	X	NO-HOV	Tfu_3105	Tfu_3105 hypothetical protein	14.09	13.49	13.38		20.44	0.773
NONE	X	NO-HOV	Tfu_2889	Tfu_2889 possible secreted protein					18.85	
NONE	X	NO-HOV	Tfu_2700	Tfu_2700 hypothetical protein					18.45	

NONE	X	NO-HOV	Tfu_0149	Tfu_0149 putative integral membrane protein			19.55	18.78	22.46	0.823
NONE	X	NO-HOV	Tfu_0860	Tfu_0860 hypothetical protein					19.5	
NONE	X	NO-HOV	Tfu_0270	Tfu_0270 hypothetical protein					15.2	
NONE	X	NO-HOV	Tfu_2198	Tfu_2198 hypothetical protein			12.49		16.28	
NONE	X	NO-HOV	Tfu_2935	Tfu_2935 hypothetical protein				13.97	19.13	1.448
NONE	X	NO-HOV	Tfu_0596	Tfu_0596 hypothetical protein		15.01		16.99	20.98	0.983
NONE	X	NO-HOV	Tfu_1614	Tfu_1614 hypothetical protein	16.14	16.41			20.01	
NONE	X	NO-HOV	Tfu_0870	Tfu_0870 hypothetical protein	14.94				20.25	
NONE	X	NO-HOV	Tfu_2098	Tfu_2098 hypothetical protein					15.21	
NONE	X	NO-HOV	Tfu_2805	Tfu_2805 hypothetical protein			15.68	14.51	20.66	0.853
NONE	X	NO-HOV	Tfu_0549	Tfu_0549 anti-sigma factor					17.94	
NONE	X	NO-HOV	Tfu_3019	Tfu_3019 hypothetical protein					15.13	
NONE	X	NO-HOV	Tfu_1836	Tfu_1836 hypothetical protein	16.3	16.29	15.86	15.97	21.49	0.774
NONE	X	NO-HOV	Tfu_2558	Tfu_2558 hypothetical protein	20.98	20.14	19.08	19.01	23.08	0.92
NONE	X	NO-HOV	Tfu_2998	Tfu_2998 hypothetical protein					16.88	
NONE	X	NO-HOV	Tfu_2987	Tfu_2987 hypothetical protein	14.51	14.42			17.5	
NONE	X	NO-HOV	Tfu_0798	Tfu_0798 helix-turn-helix motif					15.39	
NONE	X	NO-HOV	Tfu_0095	Tfu_0095 hypothetical protein					18.62	
NONE	X	NO-HOV	Tfu_2516	Tfu_2516 hypothetical protein	17.26	16.8			19.74	
NONE	X	NO-HOV	Tfu_1934	Tfu_1934 hypothetical protein	18.9	18.76	18.34	18.32	22.63	1.464
NONE	X	NO-HOV	Tfu_1814	Tfu_1814 hypothetical protein	17.88	17.69	16.37	16.2	21.78	0.557
NONE	X	NO-HOV	Tfu_1453	Tfu_1453 hypothetical protein					16.19	
NONE	X	NO-HOV	Tfu_2859	Tfu_2859 hypothetical protein					15.84	
NONE	X	NO-HOV	Tfu_1997	Tfu_1997 putative transcriptional regulator					17.27	
NONE	X	NO-HOV	Tfu_2483	Tfu_2483 hypothetical protein	17.04	16.41	15.12	14.92	20.36	
NONE	X	NO-HOV	Tfu_0891	Tfu_0891 hypothetical protein	17.46	16.1	14.62		19.01	
NONE	X	NO-HOV	Tfu_0342	Tfu_0342 hypothetical protein	18.62	18.01		15.72	19.69	
NONE	X	NO-HOV	Tfu_0660	Tfu_0660 hypothetical protein	18.54	17.97	17.41	16.73	21.15	0.641
NONE	X	NO-HOV	Tfu_2964	Tfu_2964 hypothetical protein					16.35	
NONE	X	NO-HOV	Tfu_1269	Tfu_1269 hypothetical protein					17.03	
NONE	X	NO-HOV	Tfu_2371	Tfu_2371 hypothetical protein					18.55	
NONE	X	NO-HOV	Tfu_0356	Tfu_0356 putative integral membrane protein					16.46	
NONE	X	NO-HOV	Tfu_1052	Tfu_1052 helix-turn-helix motif	20.71	20.51	21.01	19.48	24.12	0.779
NONE	X	NO-HOV	Tfu_2792	Tfu_2792 hypothetical protein	21.05	20.96	20.78	20.39	24.72	0.945
NONE	X	NO-HOV	Tfu_0929	Tfu_0929 hypothetical protein	17.07	17.17			18.72	0.812
NONE	X	NO-HOV	Tfu_1600	Tfu_1600 hypothetical protein	15.84	16.02	15.7	14.39	20.27	
NONE	X	NO-HOV	Tfu_0977	Tfu_0977 helix-turn-helix motif					17.55	
NONE	X	NO-HOV	Tfu_1426	Tfu_1426 hypothetical protein	17.64	16.88	16	15.46	21.72	
NONE	X	NO-HOV	Tfu_2442	Tfu_2442 hypothetical protein		15.57			19.1	

NONE	X	NO-HOV	Tfu_1801	Tfu_1801 helix-turn-helix motif					14.92	
NONE	X	NO-HOV	Tfu_3011	Tfu_3011 hypothetical protein	18.42	18.01	17.2	17.2	20.97	0.582
NONE	X	NO-HOV	Tfu_0774	Tfu_0774 hypothetical protein					16.29	
NONE	X	NO-HOV	Tfu_1220	Tfu_1220 actinorhodin polyketide synthase acyl carrier protein / 3-oxoacyl-ACP synthase					17.63	
NONE	X	NO-HOV	Tfu_1574	Tfu_1574 hypothetical protein					18	
NONE	X	NO-HOV	Tfu_0502	Tfu_0502 hypothetical protein	19.89	16.33	18.1	17.81	20.35	
NONE	X	NO-HOV	Tfu_1007	Tfu_1007 hypothetical protein	18.41	18.25	14.37	16.19	20.13	
NONE	X	NO-HOV	Tfu_2718	Tfu_2718 hypothetical protein	14.08				19.21	0.785
NONE	X	NO-HOV	Tfu_1177	Tfu_1177 hypothetical protein	17.73	17.92	17.05	16.14	21.61	
NONE	X	NO-HOV	Tfu_2431	Tfu_2431 hypothetical protein					16.69	1.418
NONE	X	NO-HOV	Tfu_2164	Tfu_2164 hypothetical protein					17.44	
NONE	X	NO-HOV	Tfu_1524	Tfu_1524 hypothetical protein					15.29	
NONE	X	NO-HOV	Tfu_2607	Tfu_2607 hypothetical protein		15.56			17.89	
NONE	X	NO-HOV	Tfu_2498	Tfu_2498 putative integral membrane protein	14.89	14.68	14.31		19.15	
NONE	X	NO-HOV	Tfu_1405	Tfu_1405 hypothetical protein	17.38	17.28	19.42	18.9	22.75	1.128
NONE	X	NO-HOV	Tfu_2241	Tfu_2241 hypothetical protein					16.35	
NONE	X	NO-HOV	Tfu_0565	Tfu_0565 hypothetical protein					18.01	
NONE	X	NO-HOV	Tfu_2286	Tfu_2286 hypothetical protein	16.17	15.68	15.42		19.62	
NONE	X	NO-HOV	Tfu_0607	Tfu_0607 hypothetical protein	18.02	17.79	16.63	17.3	21.47	0.764
NONE	X	NO-HOV	Tfu_1592	Tfu_1592 hypothetical protein	17.49	17.54	18.35	17.58	22.51	1.105
NONE	X	NO-HOV	Tfu_0463	Tfu_0463 hypothetical protein	13.96	18.61		16.68	20.74	0.706
NONE	X	NO-HOV	Tfu_2118	Tfu_2118 hypothetical protein	13.93	13.99			16.28	
NONE	X	NO-HOV	Tfu_0489	Tfu_0489 hypothetical protein					15.71	
NONE	X	NO-HOV	Tfu_1146	Tfu_1146 hypothetical protein					15.36	
NONE	X	NO-HOV	Tfu_1589	Tfu_1589 CRISPR-associated CT1976 family protein	17.53	17.11	18.28	17.72	21.75	1
NONE	X	NO-HOV	Tfu_2252	Tfu_2252 putative molybdopterin-guanine dinucleotide biosynthesis protein					19.21	
NONE	X	NO-HOV	Tfu_0730	Tfu_0730 hypothetical protein					16.57	
NONE	X	NO-HOV	Tfu_2079	Tfu_2079 hypothetical protein	15.47	14.37			19.85	
NONE	X	NO-HOV	Tfu_1009	Tfu_1009 hypothetical protein					16.02	
NONE	X	NO-HOV	Tfu_2705	Tfu_2705 excisionase/Xis, DNA-binding			14.1		17.64	1.197
NONE	X	NO-HOV	Tfu_0859	Tfu_0859 hypothetical protein					18.04	
NONE	X	NO-HOV	Tfu_0490	Tfu_0490 hypothetical protein					15.69	
NONE	X	NO-HOV	Tfu_2977	Tfu_2977 putative Lsr2-like protein	18.07	18.07	18.77	18.15	22.27	1.384
NONE	X	NO-HOV	Tfu_2119	Tfu_2119 hypothetical protein		14.34			17.52	
NONE	X	NO-HOV	Tfu_1659	Tfu_1659 hypothetical protein	15.62	16.77	15.05		19.01	1.154
NONE	X	NO-HOV	Tfu_0378	Tfu_0378 hypothetical protein					15.58	
NONE	X	NO-HOV	Tfu_2042	Tfu_2042 hypothetical protein			17.33	15.47	22.56	0.931
NONE	X	NO-HOV	Tfu_1264	Tfu_1264 hypothetical protein				14.48	19.68	
NONE	X	NO-HOV	Tfu_1445	Tfu_1445 hypothetical protein	14.78				17.8	

NONE	X	NO-HOV	Tfu_0479	Tfu_0479 hypothetical protein					16.75	
NONE	X	NO-HOV	Tfu_0581	Tfu_0581 hypothetical protein		15.21	15.17		20.11	1.119
NONE	X	NO-HOV	Tfu_0098	Tfu_0098 hypothetical protein	16.4	15.67	13.94	13.26	17.8	0.904
NONE	X	NO-HOV	Tfu_0710	Tfu_0710 bacteriophage (phiC31) resistance gene pglZ	18.94	17.84	17.28	16.23	22.25	0.817
NONE	X	NO-HOV	Tfu_1245	Tfu_1245 hypothetical protein	16	16.59	16.54	16.68	21.95	
NONE	X	NO-HOV	Tfu_1399	Tfu_1399 hypothetical protein					16.37	
NONE	X	NO-HOV	Tfu_0699	Tfu_0699 hypothetical protein	14.86				19.07	
NONE	X	NO-HOV	Tfu_3021	Tfu_3021 hypothetical protein					16.9	
NONE	X	NO-HOV	Tfu_0517	Tfu_0517 hypothetical protein	19.6	19.53	18.76	18.82	22.27	1.032
NONE	X	NO-HOV	Tfu_2812	Tfu_2812 hypothetical protein					17.03	
NONE	X	NO-HOV	Tfu_2706	Tfu_2706 hypothetical protein	17.22	16.94	16.04	16.47	20.55	
NONE	X	NO-HOV	Tfu_1003	Tfu_1003 hypothetical protein					20.39	
NONE	X	NO-HOV	Tfu_1381	Tfu_1381 hypothetical protein					16.16	
NONE	X	NO-HOV	Tfu_2652	Tfu_2652 hypothetical protein			15.18	14.82	20.74	
NONE	X	NO-HOV	Tfu_2208	Tfu_2208 hypothetical protein	15.55				19.44	0.824
NONE	X	NO-HOV	Tfu_2729	Tfu_2729 hypothetical protein					16.9	
NONE	X	NO-HOV	Tfu_0332	Tfu_0332 putative integral membrane protein	16.42	12.54		13.91	18.4	
NONE	X	NO-HOV	Tfu_0695	Tfu_0695 hypothetical protein	15.31				18.38	
NONE	X	NO-HOV	Tfu_2036	Tfu_2036 hypothetical protein	17.9	16.65	17.8	17.46	21.8	0.769
NONE	X	NO-HOV	Tfu_2220	Tfu_2220 putative ABC transporter	17.47	15.72	15.52	15.3	21.24	1.118
NONE	X	NO-HOV	Tfu_1598	Tfu_1598 CRISPR-associated CT1975 family protein	19.9	19.86	19.9	19.14	23.92	0.978
NONE	X	NO-HOV	Tfu_1767	Tfu_1767 hypothetical protein	16.87	15.99		11.08	19.52	
NONE	X	NO-HOV	Tfu_2868	Tfu_2868 putative Lsr2-like protein		15.3	15.7	16.05	21.25	
NONE	X	NO-HOV	Tfu_0990	Tfu_0990 putative integral membrane protein	17.38	17.3	17.52	17.66	21.87	1.071
NONE	X	NO-HOV	Tfu_1061	Tfu_1061 hypothetical protein	21.67	21.51	21.83	21.49	24.92	1.727
NONE	X	NO-HOV	Tfu_2615	Tfu_2615 hypothetical protein					16.83	
NONE	X	NO-HOV	Tfu_1131	Tfu_1131 hypothetical protein	16.51	17	14.65		19.53	3.193
NONE	X	NO-HOV	Tfu_2153	Tfu_2153 hypothetical protein		13.24			16.04	
NONE	X	NO-HOV	Tfu_1759	Tfu_1759 hypothetical protein					17.26	
NONE	X	NO-HOV	Tfu_1827	Tfu_1827 hypothetical protein	20.91	20.81	19.98	19.65	23.2	0.738
NONE	X	NO-HOV	Tfu_2838	Tfu_2838 hypothetical protein					14.92	
NONE	X	NO-HOV	Tfu_2135	Tfu_2135 hypothetical protein					17.12	
NONE	X	NO-HOV	Tfu_1005	Tfu_1005 putative integral membrane protein				15.04	18.45	0.974
NONE	X	NO-HOV	Tfu_1085	Tfu_1085 hypothetical protein	16.82	16.26			19.16	
NONE	X	NO-HOV	Tfu_2010	Tfu_2010 hypothetical protein					16.55	
NONE	X	NO-HOV	Tfu_0466	Tfu_0466 hypothetical protein					17.06	
NONE	X	NO-HOV	Tfu_0054	Tfu_0054 hypothetical protein	17.82	16.72	15.48	14.12	21.53	
NONE	X	NO-HOV	Tfu_0493	Tfu_0493 hypothetical protein	16.45	14.63	15.05		20.36	
NONE	X	NO-HOV	Tfu_1088	Tfu_1088 hypothetical protein					18.24	

NONE	X	NO-HOV	Tfu_0847	Tfu_0847 hypothetical protein		13.81			20.79	
NONE	X	NO-HOV	Tfu_1591	Tfu_1591 hypothetical protein	18.78	19.17	18.52	18.51	23.71	
NONE	X	NO-HOV	Tfu_2318	Tfu_2318 hypothetical protein					15.5	
NONE	X	NO-HOV	Tfu_2306	Tfu_2306 helix-turn-helix motif	12.04				17.76	
NONE	X	NO-HOV	Tfu_2842	Tfu_2842 hypothetical protein					17.4	
NONE	X	NO-HOV	Tfu_1457	Tfu_1457 hypothetical protein					18.57	
NONE	X	NO-HOV	Tfu_0404	Tfu_0404 hypothetical protein					18.8	0.884
NONE	X	NO-HOV	Tfu_2238	Tfu_2238 hypothetical protein		15.74	15.05		20.82	
NONE	X	NO-HOV	Tfu_0403	Tfu_0403 hypothetical protein	21.05	20.87	20.48	20.48	24.42	1.014
NONE	X	NO-HOV	Tfu_0484	Tfu_0484 hypothetical protein	14.8				18.53	0.88
NONE	X	NO-HOV	Tfu_1351	Tfu_1351 putative DNA-binding protein	16.72	15.71	14.32		19.62	
NONE	X	NO-HOV	Tfu_0959	Tfu_0959 hypothetical protein					16.84	
NONE	X	NO-HOV	Tfu_1596	Tfu_1596 CRISPR-associated CT1974 family protein					15.12	
NONE	X	NO-HOV	Tfu_1168	Tfu_1168 hypothetical protein					17.68	
NONE	X	NO-HOV	Tfu_1979	Tfu_1979 hypothetical protein					18	
NONE	X	NO-HOV	Tfu_1581	Tfu_1581 hypothetical protein	18.96	18.52	17.73	17.35	21.54	0.838
NONE	X	NO-HOV	Tfu_2073	Tfu_2073 putative secreted protein					17.88	
NONE	X	NO-HOV	Tfu_0499	Tfu_0499 hypothetical protein					14.87	
NONE	X	NO-HOV	Tfu_0515	Tfu_0515 hypothetical protein	17.67	17.54	17.73	17.17	21.91	1.055
NONE	X	NO-HOV	Tfu_0237	Tfu_0237 hypothetical protein	16.1	14.68	15.94	14.75	21.36	
NONE	X	NO-HOV	Tfu_2556	Tfu_2556 hypothetical protein					18.3	
NONE	X	NO-HOV	Tfu_2871	Tfu_2871 hypothetical protein					15.84	
NONE	X	NO-HOV	Tfu_1160	Tfu_1160 hypothetical protein		14.46			18.77	
NONE	X	NO-HOV	Tfu_2671	Tfu_2671 hypothetical protein					17.35	
NONE	X	NO-HOV	Tfu_3052	Tfu_3052 hypothetical protein					15.89	
NONE	X	NO-HOV	Tfu_0216	Tfu_0216 helix-turn-helix motif	13.68	14.27			19.46	0.703
NONE	X	NO-HOV	Tfu_0483	Tfu_0483 hypothetical protein		14.54	15.57	15.46	18.76	
NONE	X	NO-HOV	Tfu_0893	Tfu_0893 hypothetical protein	12.31		13.09	12.87	18.09	
NONE	X	NO-HOV	Tfu_0307	Tfu_0307 hypothetical protein					14.79	
NONE	X	NO-HOV	Tfu_0955	Tfu_0955 hypothetical protein	15.03	14.4			15.84	
NONE	X	NO-HOV	Tfu_0969	Tfu_0969 hypothetical protein					20.15	
NONE	X	NO-HOV	Tfu_1017	Tfu_1017 hypothetical protein		13.59	14.29	14.15	20.07	
NONE	X	NO-HOV	Tfu_2497	Tfu_2497 hypothetical protein					17.22	
NONE	X	NO-HOV	Tfu_2480	Tfu_2480 hypothetical protein					16.16	
NONE	X	NO-HOV	Tfu_0519	Tfu_0519 hypothetical protein	18.36	18.29	16.29	16.99	21.37	
NONE	X	NO-HOV	Tfu_1877	Tfu_1877 hypothetical protein	14.56	13.99	13.97	13.79	18.61	
NONE	X	NO-HOV	Tfu_2939	Tfu_2939 hypothetical protein		15.62				
NONE	X	NO-HOV	Tfu_2446	Tfu_2446 hypothetical protein				13.3	17.8	
NONE	X	NO-HOV	Tfu_1803	Tfu_1803 helix-turn-helix motif	16.43	15.24	15.25	14.96	20.03	

NONE	X	NO-HOV	Tfu_0998	Tfu_0998 hypothetical protein	18.25	18.06			18.17	
NONE	X	NO-HOV	Tfu_2760	Tfu_2760 hypothetical protein					18.58	
NONE	X	NO-HOV	Tfu_2266	Tfu_2266 hypothetical protein	13.99	15.23	14.09		18.43	
NONE	X	NO-HOV	Tfu_0410	Tfu_0410 hypothetical protein	19.65	19.27	18.1	18.48	21.48	0.492
NONE	X	NO-HOV	Tfu_0736	Tfu_0736 hypothetical protein	17.85	15.81	16.62	15.91	20.77	
NONE	X	NO-HOV	Tfu_1774	Tfu_1774 putative Lsr2-like protein	20.52	20.36	18.76	17.79	22.92	0.959
NONE	X	NO-HOV	Tfu_0602	Tfu_0602 hypothetical protein					16.48	
NONE	X	NO-HOV	Tfu_1070	Tfu_1070 hypothetical protein				15	19.27	0.702
NONE	X	NO-HOV	Tfu_1957	Tfu_1957 hypothetical protein	14.06	13.72			18.31	
NONE	X	NO-HOV	Tfu_0137	Tfu_0137 hypothetical protein		14.21		14.97	18.62	
NONE	X	NO-HOV	Tfu_1162	Tfu_1162 hypothetical protein	17.83	16.37	15.24	15.88	19.01	1.022
NONE	X	NO-HOV	Tfu_1121	Tfu_1121 hypothetical protein					16.14	
NONE	X	NO-HOV	Tfu_1321	Tfu_1321 hypothetical protein					16.33	
NONE	X	NO-HOV	Tfu_0971	Tfu_0971 putative DNA methylase	20.19	20.09	20.72	20.5	24.72	1.175
NONE	X	NO-HOV	Tfu_1049	Tfu_1049 hypothetical protein					15.68	
NONE	X	NO-HOV	Tfu_2543	Tfu_2543 hypothetical protein					17.16	
NONE	X	NO-HOV	Tfu_2328	Tfu_2328 hypothetical protein					19.56	
NONE	X	NO-HOV	Tfu_2513	Tfu_2513 hypothetical protein		14.01			17.93	
NONE	X	NO-HOV	Tfu_2834	Tfu_2834 hypothetical protein	16.13				21.03	0.914
NONE	X	NO-HOV	Tfu_1879	Tfu_1879 putative transcriptional regulator	17.17	15.51	16.38	15.52	19.79	0.819
NONE	X	NO-HOV	Tfu_2720	Tfu_2720 hypothetical protein	19.19	19.2	19.66	19.69	22.82	1.235
NONE	X	NO-HOV	Tfu_3074	Tfu_3074 hypothetical protein					16.42	
NONE	X	NO-HOV	Tfu_1237	Tfu_1237 hypothetical protein	16.08	15.96	19.23	19.33	22.62	
NONE	X	NO-HOV	Tfu_2084	Tfu_2084 hypothetical protein					18.33	
NONE	X	NO-HOV	Tfu_2918	Tfu_2918 hypothetical protein	16.19	15.78			17.2	
NONE	X	NO-HOV	Tfu_2287	Tfu_2287 hypothetical protein					17.44	
NONE	X	NO-HOV	Tfu_0094	Tfu_0094 hypothetical protein					16.28	
NONE	X	NO-HOV	Tfu_2077	Tfu_2077 hypothetical protein	15.96	15.81	14.4	15.94	20.23	
NONE	X	NO-HOV	Tfu_1035	Tfu_1035 hypothetical protein					18.5	
NONE	X	NO-HOV	Tfu_0239	Tfu_0239 hypothetical protein					17.6	
NONE	X	NO-HOV	Tfu_2499	Tfu_2499 hypothetical protein					17.19	
NONE	X	NO-HOV	Tfu_0355	Tfu_0355 putative integral membrane protein			13.63	13.05	18.23	
NONE	X	NO-HOV	Tfu_2046	Tfu_2046 hypothetical protein					19.96	
NONE	X	NO-HOV	Tfu_2912	Tfu_2912 hypothetical protein	12.34	14.21	14.8		20.65	
NONE	X	NO-HOV	Tfu_1886	Tfu_1886 hypothetical protein		14.9			17.6	
NONE	X	NO-HOV	Tfu_1823	Tfu_1823 hypothetical protein	17.02	16.65	15.24	15.58	17.8	
NONE	X	NO-HOV	Tfu_2506	Tfu_2506 hypothetical protein	15.92	15.39	17.15	17.02	21.56	1.301
NONE	X	NO-HOV	Tfu_1023	Tfu_1023 putative response regulator	16.28	16.13	19.03	18.67	22.61	
NONE	X	NO-HOV	Tfu_1965	Tfu_1965 hypothetical protein	18.11	18.06	17.84	18.11	22.83	

NONE	X	NO-HOV	Tfu_2321	Tfu_2321 hypothetical protein	18.92	18.95	18.26	18.5	21.91	
NONE	X	NO-HOV	Tfu_0974	Tfu_0974 helix-turn-helix motif					17.06	
NONE	X	NO-HOV	Tfu_0668	Tfu_0668 hypothetical protein					16.07	
NONE	X	NO-HOV	Tfu_1551	Tfu_1551 hypothetical protein					17.57	
NONE	X	NO-HOV	Tfu_0497	Tfu_0497 hypothetical protein					18.56	
NONE	X	NO-HOV	Tfu_0743	Tfu_0743 hypothetical protein	13.87				18.46	
NONE	X	NO-HOV	Tfu_0711	Tfu_0711 putative ATP/GTP binding protein	14.76				19.34	
NONE	X	NO-HOV	Tfu_2840	Tfu_2840 hypothetical protein					17.98	
NONE	X	NO-HOV	Tfu_2921	Tfu_2921 hypothetical protein			13.47		19.18	
NONE	X	NO-HOV	Tfu_2037	Tfu_2037 hypothetical protein	15.69				17.39	
NONE	X	NO-HOV	Tfu_1898	Tfu_1898 hypothetical protein	16.23	15.86			18.11	
NONE	X	NO-HOV	Tfu_3107	Tfu_3107 hypothetical protein			14.57		15.2	
NONE	X	NO-HOV	Tfu_0167	Tfu_0167 hypothetical protein					18.33	
NONE	X	NO-HOV	Tfu_0599	Tfu_0599 hypothetical protein	20.24	19.95	19.71	19.24	23.83	0.561
NONE	X	NO-HOV	Tfu_0380	Tfu_0380 hypothetical protein			14.91		19.53	
NONE	X	NO-HOV	Tfu_1067	Tfu_1067 hypothetical protein	19.22	19.5	20.11	19.74	23.82	1.201
NONE	X	NO-HOV	Tfu_0133	Tfu_0133 hypothetical protein					19.46	
NONE	X	NO-HOV	Tfu_0131	Tfu_0131 hypothetical protein	15.11	14.84		15.38	18.81	
NONE	X	NO-HOV	Tfu_2560	Tfu_2560 hypothetical protein					16.89	
NONE	X	NO-HOV	Tfu_2754	Tfu_2754 hypothetical protein					17.73	
NONE	X	NO-HOV	Tfu_2525	Tfu_2525 hypothetical protein					16.5	
NONE	X	NO-HOV	Tfu_1404	Tfu_1404 hypothetical protein			13.29		18.5	
NONE	X	NO-HOV	Tfu_3020	Tfu_3020 hypothetical protein					15.28	
NONE	X	NO-HOV	Tfu_2698	Tfu_2698 hypothetical protein					18.93	
NONE	X	NO-HOV	Tfu_2914	Tfu_2914 hypothetical protein				14.31	15.88	
NONE	X	NO-HOV	Tfu_1637	Tfu_1637 hypothetical protein						0.808
NONE	X	NO-HOV	Tfu_1536	Tfu_1536 hypothetical protein	16.6	16.22	15.49	15.6	21.56	
NONE	X	NO-HOV	Tfu_2991	Tfu_2991 hypothetical protein					16.66	
NONE	X	NO-HOV	Tfu_1533	Tfu_1533 hypothetical protein					18.73	
NONE	X	NO-HOV	Tfu_1654	Tfu_1654 hypothetical protein					16.32	1.027
NONE	X	NO-HOV	Tfu_2078	Tfu_2078 hypothetical protein	17.31	16.9			20.64	0.767
NONE	X	NO-HOV	Tfu_1315	Tfu_1315 hypothetical protein	17.89	17.57	16.52	16.74	21.91	
NONE	X	NO-HOV	Tfu_2448	Tfu_2448 hypothetical protein	17.23	18.56	18.27	17.74	22.48	
NONE	X	NO-HOV	Tfu_1338	Tfu_1338 ATPase			15.44	14.41	21.13	
NONE	X	NO-HOV	Tfu_1545	Tfu_1545 hypothetical protein	15.78	15.95	15.92	15.84	21.2	0.656
NONE	X	NO-HOV	Tfu_0871	Tfu_0871 hypothetical protein	18.06	16.83	16.09	16.13	19.82	
NONE	X	NO-HOV	Tfu_1364	Tfu_1364 hypothetical protein	14.36	14.13		14.79	18.29	
NONE	X	NO-HOV	Tfu_2877	Tfu_2877 putative Lsr2-like protein	20.07	19.86	19.55	19.54	23.62	1.53
NONE	X	NO-HOV	Tfu_1573	Tfu_1573 hypothetical protein					17.13	

NONE	X	NO-HOV	Tfu_0510	Tfu_0510 hypothetical protein					18.8	
NONE	X	NO-HOV	Tfu_2124	Tfu_2124 hypothetical protein	15.12	15.34			17.46	
NONE	X	NO-HOV	Tfu_2735	Tfu_2735 putative redoxin					16.54	
NONE	X	NO-HOV	Tfu_1947	Tfu_1947 hypothetical protein					18.56	
NONE	X	NO-HOV	Tfu_2388	Tfu_2388 hypothetical protein					15.84	
NONE	X	NO-HOV	Tfu_2927	Tfu_2927 hypothetical protein	14.54	14.58			20.13	1.258
NONE	X	NO-HOV	Tfu_2847	Tfu_2847 hypothetical protein					14.15	
NONE	X	NO-HOV	Tfu_0331	Tfu_0331 hypothetical protein					15.1	
NONE	X	NO-HOV	Tfu_1939	Tfu_1939 hypothetical protein			15.81	15.94	19.55	
NONE	X	NO-HOV	Tfu_0682	Tfu_0682 hypothetical protein					15.53	
NONE	X	NO-HOV	Tfu_0069	Tfu_0069 putative transcriptional regulator					18.32	
NONE	X	NO-HOV	Tfu_0026	Tfu_0026 hypothetical protein	16.91	17.02	15.4	15.16	20.3	
NONE	X	NO-HOV	Tfu_3000	Tfu_3000 hypothetical protein			14.91	14.87	19.62	
NONE	X	NO-HOV	Tfu_2080	Tfu_2080 hypothetical protein	15.86	16.28	14.8	16.29	20.35	
NONE	X	NO-HOV	Tfu_1962	Tfu_1962 hypothetical protein					15.25	
NONE	X	NO-HOV	Tfu_3070	Tfu_3070 hypothetical protein	17.71	17.65	19.14	18.43	23.45	1.888
NONE	X	NO-HOV	Tfu_0325	Tfu_0325 hypothetical protein	17.96	17.82	16.01	14.63	20.01	
NONE	X	NO-HOV	Tfu_2993	Tfu_2993 hypothetical protein				14.01	20.06	
NONE	X	NO-HOV	Tfu_1791	Tfu_1791 hypothetical protein	17.92	16.88	16.59	16.63	21.11	
NONE	X	NO-HOV	Tfu_0235	Tfu_0235 hypothetical protein					18.2	
NONE	X	NO-HOV	Tfu_2837	Tfu_2837 hypothetical protein					17.3	
NONE	X	NO-HOV	Tfu_1708	Tfu_1708 hypothetical protein		14.68			16.55	
NONE	X	NO-HOV	Tfu_2749	Tfu_2749 hypothetical protein						1.561
NONE	X	NO-HOV	Tfu_0488	Tfu_0488 putative peptidase	17.38	15.22	15.63	15.1	19.43	
NONE	X	NO-HOV	Tfu_2400	Tfu_2400 hypothetical protein	16.07	16.13	16.41	16.72	20.95	1.181
NONE	X	NO-HOV	Tfu_2981	Tfu_2981 hypothetical protein					16.83	
NONE	X	NO-HOV	Tfu_1599	Tfu_1599 hypothetical protein		13.47	14.26	14.44	19.18	
NONE	X	NO-HOV	Tfu_1516	Tfu_1516 hypothetical protein					16.95	
NONE	X	NO-HOV	Tfu_1180	Tfu_1180 hypothetical protein					16.98	
NONE	X	NO-HOV	Tfu_1735	Tfu_1735 putative regulator					13.35	
NONE	X	NO-HOV	Tfu_0738	Tfu_0738 hypothetical protein					18.01	
NONE	X	NO-HOV	Tfu_0070	Tfu_0070 hypothetical protein	15.01				17.68	
NONE	X	NO-HOV	Tfu_1072	Tfu_1072 hypothetical protein	15.45	14.67			18.09	
NONE	X	NO-HOV	Tfu_2969	Tfu_2969 hypothetical protein	20.36	20.16	18.33	16.87	22.01	1.245
NONE	X	NO-HOV	Tfu_1032	Tfu_1032 hypothetical protein	18	17.5	17.24	16.68	20.9	
NONE	X	NO-HOV	Tfu_2728	Tfu_2728 putative DNA methylase		13.71			19.49	
NONE	X	NO-HOV	Tfu_2677	Tfu_2677 hypothetical protein	18.38	17.99	18.34	18.18	21.75	
NONE	X	NO-HOV	Tfu_0362	Tfu_0362 hypothetical protein	15.99	15.73	14.29		19.96	1.163
NONE	X	NO-HOV	Tfu_1171	Tfu_1171 hypothetical protein		14.97	15.6	14.32	20.32	

NONE	X	NO-HOV	Tfu_0088	Tfu_0088 hypothetical protein			15.43	15.54	18.4	
NONE	X	NO-HOV	Tfu_2785	Tfu_2785 hypothetical protein					14.83	
NONE	X	NO-HOV	Tfu_0545	Tfu_0545 hypothetical protein	17.84	16.55			18.11	
NONE	X	NO-HOV	Tfu_0062	Tfu_0062 hypothetical protein					17.1	

Appendix - F - Unique Unreviewed Undetected(in past) Proteins in Cb2D

CELLULAR PROCESS				
Cell wall/membrane/envelope biogenesis				
Tfu_0471	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	M00096	C5 isoprenoid biosynthesis, non-mevalonate pathway	
Tfu_1715	Dihydrodipicolinate synthase	M00016; M00525; N	Lysine Biosynthesis	*Aspartate-->Lysisn*
Tfu_1709	UDP-glucose-4-epimerase			
ENVIRONMENTAL INFORMATION PROCESSING				
Inorganic ion transport and metabolism				
Tfu_0336	ABC-type cobalamin/Fe3+-siderophores transport systems AT	M00240	*Iron Transport*	
Tfu_0912; Tf	ABC-type dipeptide/oligopeptide/nickel transport systems, p	M00239	*Peptide Transport*	
Signal transduction mechanisms				
Tfu_0080	GAF domain protein			
Tfu_0691; Tf	Helix-turn-helix, Fis-type			
Tfu_2798	Putative DNA-binding protein			
GENETIC PROCESS				
Transcription				
Tfu_0273; Tf	Glucokinase ROK	M00001	Glycolysis	*Glucose-->Pyruvate*
Tfu_1605	Putative xylose repressor			
Tfu_0907	Regulatory protein, DeoR			
Translation, ribosomal structure and biogenesis				
Tfu_1854	Regulatory protein, DeoR		*Translation, ribosomal structure and biogenesis*	
METABOLIC PROCESS				
Amino acid transport and metabolism				
Tfu_1825	5-methyltetrahydrofolate--homocysteine methyltransferase	M00017	Methionine biosynthesis	*apartate-->homoserine-->methionine*
Tfu_0440	Cystathionine gamma-synthase	M00017	Methionine biosynthesis	*apartate-->homoserine-->methionine*
Tfu_2423	Threonine synthase	M00018	Threonine biosynthesis	*apartate-->homoserine-->threonine*
Tfu_1543	Arginase	M00029; M00134	Polyamine biosynthesis	arginine-->ornithine-->putrescine
Tfu_2425	Diaminopimelate decarboxylase	M00016; M00525; N	Lysine Biosynthesis	*aspartate-->Lysine*
Tfu_1715	Dihydrodipicolinate synthase	M00016; M00525; N	Lysine Biosynthesis	*aspartate-->Lysine*
Tfu_3053	Prephenate dehydratase	M00024	Phenylalanine biosynthesis	chorismate-->phenylalanine
Tfu_1165	Tryptophan synthase, beta chain	M00023	Tryptophan biosynthesis	chorismate-->tryptophan
Tfu_2708	Delta 1-pyrroline-5-carboxylate reductase	M00015	Proline Biosynthesis	*glutamate-->proline*
Tfu_0136	Phosphoserine phosphatase SerB:HAD-superfamily hydrolase	M00020	Serine Biosynthesis	*glycerate-3P-->serine*
Tfu_0821	Imidazolonepropionase	M00045	Histidine degradation	histidine-->N-formiminoglutamate-->glutamate
Tfu_0438	Cystathionine beta-synthase	M00035; M00338	Methionine degradation; Cysteine b	homocysteine+serine-->cysteine
Tfu_3025	Putative alcohol dehydrogenase	M00174	Methane oxidation methylotroph	methane-->CO2
Tfu_1635	Dehydroquinase, class II	M00022	Shikimate pathway	phosphoenolpyruvate+erythrose-4P-->chorismate
Tfu_2350	Phospho-2-dehydro-3-deoxyheptonate aldolase, subtype 1	M00022	Shikimate pathway	phosphoenolpyruvate+erythrose-4P-->chorismate
Tfu_2067	Shikimate 5-dehydrogenase	M00022	Shikimate pathway	phosphoenolpyruvate+erythrose-4P-->chorismate
Tfu_2223	Putative aminotransferase	M00026	Histidine biosynthesis	PRPP-->histidine
Tfu_0611	Acetolactate synthase I large subunit	M00019	Leucine biosynthesis	*pyruvate-->2-oxoisovalerate-->leucine*

Tfu_0617	2-isopropylmalate synthase	M00019; M00432	Leucine biosynthesis	*pyruvate-->2-oxoisovalerate-->leucine*
Tfu_2368	Cysteine synthase K/M	M00021	Cysteine biosynthesis	serine-->cysteine
Tfu_0921	Putative tryptophan 2,3-dioxygenase	M00038	Tryptophan metabolism	tryptophan-->kynurenine-->2-aminomuconate
Tfu_0075; Tf	ABC-type branched-chain amino acid transport systems ATPa	M00237	Branched-chain amino acid transport	
Tfu_1183	Branched-chain amino acid transport system permease prote	M00237	Branched-chain amino acid transport	
Tfu_2930	Glycine betaine/L-proline transport ATP-binding subunit	M00208	Glycine/Proline Transport	
Tfu_2929	Similar to ABC-type proline/glycine betaine transport system	M00208	Glycine/Proline Transport	
Tfu_0911; Tf	ABC-type dipeptide/oligopeptide/nickel transport systems, p	M00239	Peptide Transport	
Tfu_0306	ABC-type polar amino acid transport system ATPase compon	M00236	Polar Amino Acids Transport	
Tfu_0282	Polyamine ABC-transporter, inner membrane subunit	M00299	Spermidine/putrescine transport	
Tfu_1755	Alcohol dehydrogenase			
Tfu_2763	Arginine/ornithine transport system ATPase	2.7.-		
Tfu_1915	Ferredoxin/ferredoxin--NADP reductase, putative	1.18.1.2		
Tfu_1173	Glutamate synthase (ferredoxin)	1.4.1.13; 1.4.1.14		
Tfu_2012	N-carbamoyl-L-amino acid amidohydrolase	3.5.1.87		
Tfu_1856	Prolyl oligopeptidase	3.4.21.26		
Tfu_2332	Putative cholesterol oxidase	1.1.3.6		
Tfu_2263	Putative dehydrogenase			
Tfu_0284	Putative oxidoreductase			
Tfu_0595	Putative pyridoxal-phosphate-dependent aminotransferase	2.8.1.7		
Tfu_1741	Threonine dehydratase	4.3.1.19		
Carbohydrate transport and metabolism				
Tfu_2338; Tf	ABC-type glucosylglycerol transport system permease protein	M00201	alpha-Glucoside transport	
Tfu_1604	Xylulokinase	M00014	Glucuronate pathway (uronate pathway)	
Tfu_0188	2-dehydro-3-deoxyphosphogluconate aldolase / 4-hydroxy-2-	M00008; M00308	Glycolysis	glucose-6P-->glyceraldehyde-3P+pyruvate;gluconate-->g
Tfu_0273; Tf	Glucokinase ROK	M00001	Glycolysis	glucose-->pyruvate
Tfu_1837	Putative phosphatase	M00002	Glycolysis	
Tfu_0542	Histidinol-phosphate phosphatase, putative, inositol monoph	M00026	Histidine biosynthesis	PRPP-->histidine
Tfu_0831	Multiple sugar transport system permease protein	M00194	Maltose/maltodextrin transport	
Tfu_2202	Ribose-5-phosphate isomerase B	M00004; M00007; N	Pentose Phosphate Pathway	fructose6P-->ribose5P;glyceraldehyde-3P-->RuBP
Tfu_2005	Glucose-6-phosphate 1-dehydrogenase	M00004; M00006; N	Pentose Phosphate Pathway	fructose6P-->ribose5P;glyceraldehyde-3P-->RuBP
Tfu_2489	Putative phosphoenolpyruvate-dependent sugar phosphotra	M00265; M00266; N	PTS Sugar-specific II Transport	glucose,maltose,trehalose,arbutin,cellobioseandsalicin
Tfu_1716	Glycerone kinase	M00344		
Tfu_1010	Glycerate kinase	M00532		
Tfu_0586	Alpha-glucan phosphorylase	2.4.1.1		
Tfu_1615	Beta-galactosidase	3.2.1.23		
Tfu_0915	Beta-mannosidase	3.2.1.25		
Tfu_2114	Carbohydrate kinase, thermoresistant glucokinase	2.7.1.12		
Tfu_0580	Chitinase II	3.2.1.14		
Tfu_0341	Citryl-CoA lyase	4.1.3.34; 4.1.3.6		
Tfu_1891	Glycogen debranching enzyme GlgX	3.2.1.-		
Tfu_2205	Glycoside hydrolase, family 77	2.4.1.25		
Tfu_2038	HAD-superfamily hydrolase, subfamily IIA			
Tfu_1794	Major facilitator family transporter			

Tfu_2473	N-acetylglucosamine-6-phosphate deacetylase	3.5.1.25		
Tfu_2765	Phosphoenolpyruvate-protein phosphotransferase	2.7.3.9		
Tfu_1083	Putative aldose-1-epimerase			
Tfu_1012; Tf	Putative carbohydrate kinase			
Tfu_1885	Putative integral membrane protein			
Tfu_2725	Putative phosphoglycerate mutase			
Tfu_2129	Putative sugar kinase			
Tfu_2206	Putative transporter			
Tfu_1605	Putative xylose repressor			
Tfu_0907; Tf	Regulatory protein, DeoR			
Tfu_0259	Ribokinase, bacterial	2.7.1.15		
Tfu_1709	UDP-glucose-4-epimerase			
Coenzyme transport and metabolism				
Tfu_1051	Putative polyprenyl synthase / dimethylallyltranstransferase	M00364; M00365	C10-C20 isoprenoid biosynthesis	bacteria;C10-C20isoprenoidbiosynthesis
Tfu_0997	Adenosylcobinamide kinase / adenosylcobinamide-phosphat	M00122	Cobalamin biosynthesis	cobinamide-->cobalamin
Tfu_0312	Cob(I)yrinic acid a,c-diamide adenosyltransferase	M00122	Cobalamin biosynthesis	cobinamide-->cobalamin
Tfu_0309	Cobyric acid synthase	M00122	Cobalamin biosynthesis	cobinamide-->cobalamin
Tfu_2730	Porphobilinogen synthase	M00121	Heme biosynthesis	glutamate-->protoheme/siroheme
Tfu_0336	ABC-type cobalamin/Fe3+-siderophores transport systems AT	M00240	Iron complex transport system	
Tfu_0788	1,4-dihydroxy-2-naphthoate octaprenyltransferase,	M00116	Menaquinone biosynthesis	chorismate-->menaquinone
Tfu_1872	Isochorismate synthase	M00116	Menaquinone biosynthesis	chorismate-->menaquinone
Tfu_1409	Naphthoate synthase	M00116	Menaquinone biosynthesis	chorismate-->menaquinone
Tfu_2883	L-aspartate oxidase	M00115	NAD biosynthesis	aspartate-->NAD
Tfu_2171	Nicotinic acid mononucleotide adenyltransferase	M00115	NAD biosynthesis	aspartate-->NAD
Tfu_0876	5-amino-6-(5-phosphoribosylamino)uracil reductase	M00125	Riboflavin biosynthesis	GTP-->riboflavin/FMN/FAD
Tfu_0782	Cytidyltransferase-related	M00125	Riboflavin biosynthesis	GTP-->riboflavin/FMN/FAD
Tfu_1078	Lumazine-binding protein	M00125	Riboflavin biosynthesis	GTP-->riboflavin/FMN/FAD
Tfu_2890	7, 8-Dihydro-6-hydroxymethylpterin-pyrophosphokinase, HPI	M00126	Tetrahydrofolate biosynthesis	GTP-->THF
Tfu_2891	Dihydroneopterin aldolase family:Dihydroneopterin aldolase	M00126	Tetrahydrofolate biosynthesis	GTP-->THF
Tfu_2190	Folylpolyglutamate synthetase	M00126	Tetrahydrofolate biosynthesis	GTP-->THF
Tfu_0643	Thiamine monophosphate kinase	M00127	Thiamine biosynthesis	AIR-->thiamine-P/thiamine-2P
Tfu_0611	Acetolactate synthase I large subunit	M00019		
Tfu_0443	Magnesium chelatase subunit ChlI	6.6.1.1		
Tfu_0313	Mg-chelatase subunit ChlI	6.6.1.1		
Tfu_0538	Molybdenum cofactor biosynthesis protein E	2.-		
Tfu_0376	Molybdopterin binding domain			
Tfu_2373	Nicotinate phosphoribosyltransferase	2.4.2.11		
Tfu_0310	Precorrin-6x reductase CbiJ/CobK	1.3.1.54		
Tfu_2263	Putative dehydrogenase			
Tfu_1751	Putative methyltransferase			
Tfu_2115	Putative molybdopterin biosynthesis protein			
Tfu_2455	Putative monooxygenase (putative secreted protein)			
Tfu_2841	Putative rifampin monooxygenase			
Tfu_2727	Ribonuclease activity regulator protein RraA			

Tfu_2520	Similar to Methylase involved in ubiquinone/menaquinone biosynthesis			
Tfu_1038	Thiamine biosynthesis protein			
Energy production and conversion				
Tfu_0399	Putative fatty acid-CoA racemase	M00104	Bile acid biosynthesis	cholesterol-->cholate
Tfu_2675	Ferrodoxin oxidoreductase beta subunit	M00011; M00311	Citrate cycle, second carbon oxidati	2-oxoglutarate-->oxaloacetate
Tfu_0881	Cytochrome-c oxidase	M00155	Cytochrome c oxidase	
Tfu_0638	Putative cytochrome oxidase subunit I	M00153	Cytochrome d ubiquinol oxidase	
Tfu_2949	Succinate-semialdehyde dehydrogenase (NAD(P)+)	M00027	GABA (gamma-Aminobutyrate) shunt	
Tfu_1377	Isocitrate lyase	M00012	Glyoxylate cycle	
Tfu_1737	Oxidoreductase alpha (molybdopterin) subunit	M00174; M00347	Methane oxidation methylotroph; M	methane-->CO2;formate-->methane
Tfu_2971	Acetate kinase	M00357; M00377	Methanogenesis	acetate-->methane
Tfu_2691	ATP synthase subunit E	M00144	NADH:quinone oxidoreductase	
Tfu_2695	NADH dehydrogenase alpha subunit	M00144	NADH:quinone oxidoreductase	
Tfu_2686	NADH dehydrogenase subunit J	M00144	NADH:quinone oxidoreductase	
Tfu_2980	(S)-2-hydroxy-acid oxidase	M00532	Photorespiration	
Tfu_0247	Citrate synthase	M00009; M00010; M	TCA, first carbon oxidation	oxaloacetate-->2-oxoglutarate
Tfu_1287; Tf	Betaine-aldehyde dehydrogenase			
Tfu_2185	Elongator protein 3/MiaB/NifB			
Tfu_1624	Formate dehydrogenase accessory protein			
Tfu_2801	Glycerol dehydrogenase	1.1.1.6		
Tfu_0245	Glycerophosphoryl diester phosphodiesterase	3.1.4.46		
Tfu_2540	Glycerophosphoryl diester phosphodiesterase, putative	3.1.4.46		
Tfu_2902	Inorganic diphosphatase	3.6.1.1		
Tfu_0432; Tf	NADH dehydrogenase			
Tfu_0350	NADH dehydrogenase (quinone)			
Tfu_1303	NADH:flavin oxidoreductase, Old Yellow enzyme family			
Tfu_2293	Oxidoreductase			
Tfu_1302	Probable 6-carboxyhexanoate--COA ligase	6.2.1.14		
Tfu_1775	Putative alcohol dehydrogenase (zinc-binding)	1.1.1.1; 1.1.1.284		
Tfu_1706	Putative aldehyde dehydrogenase	1.2.1.4		
Tfu_2348	Putative ferredoxin reductase			
Tfu_2533	Putative glycerol 1-phosphate dehydrogenase	1.1.1.261		
Tfu_1930	Putative monooxygenase			
Tfu_0360; Tf	Putative monooxygenase (putative secreted protein)			
Tfu_0060	Putative oxidoreductase, oxygen dependent, FAD-dependent protein			
Tfu_1473	Putative pimeloyl-CoA synthetase			
Tfu_2841	Putative rifampin monooxygenase			
Tfu_1301	Similar to Coenzyme F420-dependent N5 N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductase			
Tfu_1982	SUF system FeS assembly protein			
Tfu_0340	Trimethylamine-N-oxide reductase (cytochrome c)	1.7.2.3		
Lipid Transport and Metabolism				
Tfu_0875	Thiolase	M00087; M00113	beta-Oxidation; Jasmonic acid biosynthesis	
Tfu_2485	Acyl-CoA dehydrogenase	M00013; M00036; M	beta-Oxidation; Malonate semialde	propanoyl-CoA-->Acetyl-CoA;leucine-->acetoacetate+ac
Tfu_1512	Putative acyl-CoA dehydrogenase	M00013; M00036; M	beta-Oxidation; Malonate semialde	propanoyl-CoA-->Acetyl-CoA;leucine-->acetoacetate+ac

Tfu_1512; Tf	Enoyl-CoA hydratase	M00013; M00032; M	beta-Oxidation; Malonate semialde	propanoyl-CoA-->Acetyl-CoA;leucine-->acetoacetate+ac
Tfu_1280; Tf	Putative enoyl-CoA hydratase/isomerase	M00013; M00032; M	beta-Oxidation; Malonate semialde	propanoyl-CoA-->Acetyl-CoA;leucine-->acetoacetate+ac
Tfu_0471	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	M00096	C5 isoprenoid biosynthesis, non-mevalonate pathway	
Tfu_2762	Methylmalonyl-CoA mutase	M00373; M00375; M	Ethylmalonyl pathway; Hydroxypro	pionate-hydroxybutylate cycle; 3-Hydroxypropionate bicy
Tfu_1682	3-ketoacyl-(acyl-carrier-protein) reductase	M00083	Fatty acid biosynthesis, elongation	
Tfu_1841	Putative 3-ketoacyl-CoA reductase	M00083	Fatty acid biosynthesis, elongation	
Tfu_0253	Acetyl-CoA acetyltransferase	M00088; M00095; M	Ketone body biosynthesis; C5 isopre	acetyl-CoA-->acetoacetate/3-hydroxybutyrate/acetone
Tfu_1520	Thiolase	M00088; M00095; M	Ketone body biosynthesis; C5 isopre	acetyl-CoA-->acetoacetate/3-hydroxybutyrate/acetone
Tfu_0948	Propionyl-CoA carboxylase	M00036	Leucine Degradation	leucine-->acetoacetate+acetyl-CoA
Tfu_0680	Phosphatidate cytidylyltransferase	M00093	Phosphatidylethanolamine (PE) bios	PA-->PS-->PE
Tfu_1417; Tf	Phospholipid/glycerol acyltransferase	M00089	Triacylglycerol biosynthesis	
Tfu_1298	2-deoxy-D-gluconate 3-dehydrogenase	1.1.1.125		
Tfu_1265	2-hydroxy-3-oxopropionate reductase	1.1.1.60		
Tfu_1873	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	1.3.1.28		
Tfu_1222	Actinorhodin polyketide synthase bifunctional cyclase/dehyd	4.2.1.-		
Tfu_0796	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltran	2.7.8.5		
Tfu_1300	DitJ-like CoA ligase (AMP forming), possibly related to diterpe	6.2.1.-		
Tfu_1496	FMNH2-dependent monooxygenase			
Tfu_2808	Putative acetyl-coenzyme A synthetase	6.2.1.1		
Tfu_2557	Putative acyl-CoA carboxylase, alpha subunit	6.3.4.14		
Tfu_2310; Tf	Putative acyl-CoA dehydrogenase			
Tfu_1546	Putative acyl-CoA synthetase	6.2.1.1		
Tfu_1393	Putative CDP-diacylglycerol--glycerol-3-phosphate 3-phospha	2.7.8.5		
Tfu_1544	Putative enoyl-CoA hydratase/isomerase family protein			
Tfu_1234	Putative hydrolase	1.14.14.-		
Tfu_2103	Putative membrane transferase	2.7.8.5		
Tfu_0275	Putative short chain dehydrogenase			
Tfu_1279; Tf	Short chain dehydrogenase			
Tfu_0154	Similar to Phospholipid N-methyltransferase			
Nucleotide transport and metabolism				
Tfu_2546	1-(5-Phosphoribosyl)-5-amino-4-imidazole- carboxylate (AIR)	M00048	Inosine monophosphate biosynthes	PRPP+glutamine-->IMP
Tfu_2547	Phosphoribosylaminoimidazole carboxylase, ATPase subunit	M00048	Inosine monophosphate biosynthes	PRPP+glutamine-->IMP
Tfu_0178	Phosphoribosylformylglycinamidine synthase	M00048	Inosine monophosphate biosynthes	PRPP+glutamine-->IMP
Tfu_2573	Phosphoribosylglycinamide formyltransferase	M00048	Inosine monophosphate biosynthes	PRPP+glutamine-->IMP
Tfu_3013	Phosphoribosylglycinamide synthetase	M00048	Inosine monophosphate biosynthes	PRPP+glutamine-->IMP
Tfu_1209	Cytidylate kinase	M00052	Pyrimidine ribonucleotide biosynth	UMP-->UDP/UTP;CDP/CTP
Tfu_1055	Dihydroorotase	M00051	Uridine monophosphate biosynthes	glutamine(+PRPP)-->UMP
Tfu_2563	Adenosine deaminase	3.5.4.4		
Tfu_0865	Deoxyguanosinetriphosphate triphosphohydrolase-like prote	3.1.5.1		
Tfu_2356	Formyltetrahydrofolate deformylase	3.5.1.10		
Tfu_2581	Inosine-uridine preferring nucleoside hydrolase	3.2.2.1		
Tfu_2242	Purine nucleoside phosphorylase	2.4.2.1		
Tfu_0431	Putative hydrolase	3.6.1.11; 3.6.1.40		
Tfu_2758	Putative mut-like protein			

Tfu_2973	Putative mutT-like protein			
Tfu_1518	Xanthine/uracil permease			
Secondary metabolites biosynthesis, transport and catabolism				
Tfu_1682	3-ketoacyl-(acyl-carrier-protein) reductase	M00083		infa
Tfu_1841	Putative 3-ketoacyl-CoA reductase	M00083		infa
Tfu_0821	Imidazolonepropionase	M00045		AddedinAminoacids
Tfu_1872	Isochorismate synthase	M00116		incoenzyme
Tfu_1298	2-deoxy-D-gluconate 3-dehydrogenase	1.1.1.125		
Tfu_1873	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	1.3.1.28		
Tfu_1866	Amino acid adenylation			
Tfu_1257	Cytochrome P450 monooxygenase			
Tfu_1300	DitJ-like CoA ligase (AMP forming), possibly related to diterpe	6.2.1.-		
Tfu_0080	GAF domain protein			
Tfu_0691; Tf	Helix-turn-helix, Fis-type			
Tfu_1478	Hypothetical protein			
Tfu_1868	Isochorismatase			
Tfu_1231	Modular polyketide synthase			
Tfu_2798	Putative DNA-binding protein			
Tfu_1869	Putative peptide monooxygenase			
Tfu_2374	Putative pyrazinamidase / nicotinamidase	3.5.1.-; 3.5.1.19		
Tfu_0275	Putative short chain dehydrogenase			
Tfu_1242; Tf	Short chain dehydrogenase			
OTHERS				
Tfu_1682; Tf	3-ketoacyl-(acyl-carrier-protein) reductase	M00083		
Tfu_3025	Putative alcohol dehydrogenase	M00174		
Tfu_1298	2-deoxy-D-gluconate 3-dehydrogenase	1.1.1.125		
Tfu_1873	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	1.3.1.28		
Tfu_1755	Alcohol dehydrogenase			
Tfu_1915	Ferredoxin/ferredoxin--NADP reductase, putative	1.18.1.2		
Tfu_0360	Putative oxidoreductase	1.6.5.5		
Tfu_0275; Tf	Short chain dehydrogenase			

Appendix - G - Secondary Metabolites Detected in Metabolomics Data

Count of KEGG IDs				
	Found in Both	Cellobiose	Avicel	Total
Alkaloids	**17**	**21**	**3**	**41**
Alkaloids derived by amination reactions	**1**	**6**	**1**	**8**
Acetate derived alkaloids	1			1
C10159 Methylconiine	1			1
Phenylalanine derived alkaloids		1		1
C02765 (+)-Pseudoephedrine		1		1
Steroid alkaloids		1		1
C10831 Zygadenine		1		1
Terpenoid alkaloids		4	1	5
C08681 Elatine		1		1
C08687 Hetisine		1		1
C08692 Jesaconitine		1		1
C08707 Songorine		1		1
C08712 Staphidine			1	1
Alkaloids derived from lysine	**4**	**2**		**6**
Indolizidine alkaloids		1		1
C06185 Slaframine		1		1
Piperidine alkaloids	3	1		4
C00408 L-Pipecolate	1			1
C10144 Fagomine	1			1
C10171 (-)-Sedamine	1			1
C10865 Pseudopelletierine		1		1
Quinolizidine alkaloids	1			1
C10758 Camoensine	1			1
Alkaloids derived from nicotinic acid	**2**	**2**		**4**
Pyridine alkaloids	2	2		4
C00253 Nicotinate		1		1
C00745 Nicotine		1		1
C06180 Anabasine	1			1
C10129 Arecoline	1			1
Alkaloids derived from ornithine	**1**	**7**	**1**	**9**
Pyrrolidine alkaloids			1	1
C10172 Stachydrine			1	1
Pyrrolizidine alkaloids	1			1
C06177 Retronecine	1			1
Tropane alkaloids		7		7
C10846 Bellendine		1		1
C10849 Brugine		1		1
C10858 Ecgonine		1		1
C10868 Tigloidine		1		1
C10869 Valeroidine		1		1
C12452 Acetyltropine		1		1
C12453 Acetylpseudotropine		1		1
Alkaloids derived from tryptophan and anthranilic ac	**3**	**1**	**1**	**5**
Indole alkaloids	1		1	2
C02673 Desacetoxyvindoline			1	1
C09160 Ergine	1			1

Quinoline alkaloids	2	1		3
C10701 Kokusaginine		1		1
C10713 Lunamarine	1			1
C10731 N-Methylflindersine	1			1
Alkaloids derived from tyrosine	**3**	**3**		**6**
Isoquinoline alkaloids	2	1		3
C09558 Laudanosine		1		1
C09573 Lophophorine	1			1
C09604 (-)-Pellotine	1			1
Thiazole alkaloids		1		1
C04327 4-Methyl-5-(2-phosphoethyl)-thiazole		1		1
Tyramine derivatives	1	1		2
C00483 Tyramine		1		1
C06199 Hordenine	1			1
Others	**3**			**3**
Purine alkaloids	3			3
C00262 Hypoxanthine	1			1
C00385 Xanthine	1			1
C00655 Xanthosine 5'-phosphate	1			1
Amino acid related compounds	**2**	**1**	**1**	**4**
Betalains	**2**	**1**	**1**	**4**
Cyanogenic glucosides derived from leucine	1			1
C08328 Cardiospermin	1			1
Cyanogenic glucosides derived from valine or isoleucin	1			1
C08340 Sarmentosin	1			1
Glucosinolates derived from alanine			1	1
C08404 Methyl glucosinolate			1	1
Glucosinolates derived from tryptophan		1		1
C05837 Glucobrassicin		1		1
Fatty acids related compounds	**2**			**2**
Fatty acids	**2**			**2**
Others	1			1
C16795 Hydnocarpic acid	1			1
Saturated fatty acids	1			1
C00249 Palmitic acid	1			1
Flavonoids	**1**		**1**	**2**
Flavonoids	**1**		**1**	**2**
Flavan 3,4-diols			1	1
C03648 cis-3,4-Leucopelargonidin			1	1
Flavonols	1			1
C00389 Quercetin	1			1
Others		**2**		**2**
Others		**1**		**1**
Others		1		1
C07090 Protoanemonin		1		1
Tannins and galloyl derivatives		**1**		**1**
Miscellaneous galloyl derivatives		1		1
C10242 Terminalin		1		1
Phenylpropanoids	**4**	**3**	**1**	**8**
Coumarins	**2**	**1**	**1**	**4**
Coumarins	1		1	2
C05851 Coumarin			1	1
C09315 Umbelliferone	1			1

Furanocoumarins	1	1		2
C01557 Bergapten		1		1
C02162 Isopimpinellin	1			1
Lignans	**2**	**1**		**3**
Lignans	2	1		3
C10636 Justicidin B	1			1
C10658 Magnoshinin		1		1
C10737 Phrymarolin I	1			1
Monolignols		**1**		**1**
Paracoumaryl alcohol derivatives		1		1
C00811 4-Coumarate		1		1
Polyketides		**4**		**4**
Others		**2**		**2**
Phloroglucinols		2		2
C10672 Aspidin		1		1
C10704 alpha-Kosin		1		1
Pyrones		**2**		**2**
Xanthenes		2		2
C10067 Irisxanthone		1		1
C10093 Swertianolin		1		1
Terpenoids	**12**	**6**	**7**	**25**
Carotenoids and apocarotenoids			**3**	**3**
Carotenoids			3	3
C08583 Canthaxanthin			1	1
C08585 Capsorubin			1	1
C08606 Neoxanthin			1	1
Diterpenoids (C20)	**4**		**1**	**5**
Clerodanes	1			1
C09070 Caryoptin	1			1
Gibberellins	1			1
C11863 Gibberellin A9	1			1
Grayanoids			1	1
C19992 Rhodojaponin I			1	1
Others	1			1
C09188 Spruceanol	1			1
Tiglianes	1			1
C09086 Diterpenoid EF-D	1			1
Hemiterpenoids (C5)		**1**		**1**
Isoprene		1		1
C16521 Isoprene		1		1
Monoterpenoids (C10)	**2**	**2**	**1**	**5**
Cyclic monoterpenes	1	2	1	4
C00843 (-)-Menthone		1		1
C01411 Borneol		1		1
C06577 p-Cumic aldehyde			1	1
C09837 (1S,2R,4S)-(-)-Bornyl acetate	1			1
Iridoids	1			1
C09801 Valtratum	1			1
Sesquiterpenoids (C15)	**3**	**3**	**1**	**7**
Germacrenes	2	1	1	4
C09290 Alatolide	1			1
C09297 Arctiopicrin	1			1
C09492 Laurenobiolide sesqui			1	1

C09568 epi-Tulipinolide diepoxide		1		1
Others	1	1		2
C09633 Chamazulene		1		1
C09645 Cuauhtemone	1			1
Pseudoguaianolide		1		1
C09559 Tetraneurin A		1		1
Steroids	**3**			**3**
Bufanolide	3			3
C08853 Bryotoxin A	1			1
C08872 Lanceotoxin A	1			1
C08880 Scilliroside	1			1
Triterpenoids (C30)			**1**	**1**
Oleananes			1	1
C08972 Quillaic acid			1	1
Total	**38**	**37**	**13**	**88**

VITA

Niti Vanee was born on December 20, 1984 in Kanpur, India and she is currently a citizen of Republic of India. Niti received her school education in India and graduated with Bachelors in Technology from College of Engineering and Technology IILM, India in 2006, majoring in Biotechnology. She graduated as an outstanding student in her Masters in Bioinformatics, with a GPA of 3.86. She was nominated as the member of Honor Society of Phi Kappa Phi in 2008.